

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2004, 22:29:22 ; Search time 5963.83 Seconds
(without alignments)
17340.609 Million cell updates/sec

Title: US-10-067-449-10

Perfect score: 2386

Sequence: 1 tcgactctagaggtccctc.....ctggactttctccagttg 2386

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb.ba.*
2: gb.htg.*
3: gb.in.*
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5: gb.ov.*
6: gb.pat.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2386	100.0	2386	6	AX573332 Sequence
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3	1528.2	64.0	2482	10	J04524 Rat insulin
4	1528.2	64.0	2506	10	D28561 Rat insulin
5	1526.6	64.0	2447	10	M25482 Rat insulin
6	1490.4	62.5	2338	6	AX573334 Sequence
7	1488.8	62.4	2338	6	AX573335 Sequence
8	1485.6	62.3	2338	6	AX573336 Sequence
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16	1206.2	50.6	1544	4	AY458600 Bos tauru
17	1191.8	49.9	2642	4	D63150 Bos tauru
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19	1066.4	44.7	2592	6	AX057563 Sequence
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31	679	28.5	2856	6	AR281087 Sequence
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ALIGNMENTS

RESULT 1	AX573332	AX573332	2386 bp	DNA	linear	PAT 29-NOV-2002
LOCUS	Sequence 10 from Patent WO02064784.					
DEFINITION	Sequence 10 from Patent WO02064784.					
ACCESSION	AX573332					
VERSION	AX573332.1	GI:26005218				
KEYWORDS	Rattus norvegicus (Norway rat)					
SOURCE	Rattus norvegicus					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;					
	Rattus.					
REFERENCE	1					
AUTHORS	Mueller,G., Koller,K.P., Boles,B., Wiczorke,R. and Dlugai,S.					
TITLE	Yeast strain of saccharomyces cerevisiae with functional expression					

of a glut transporter
JOURNAL Patent: WO 02064784-A 10 23-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION Rat mRNA for insulin-regulatable glucose transport (IRGT).
ACCESSION X14771
VERSION X14771.1 GI:56501
KEYWORDS glucose transport.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2086)
AUTHORS James,D.E., Strube,M. and Mueckler,M.
TITLE Molecular cloning and characterization of an insulin-regulatable
glucose transporter
JOURNAL Nature 338 (6210), 83-87 (1989)
MEDLINE 89143771
PUBMED 2645527
COMMENT Data kindly reviewed (23-MAY-1990) by Mueckler M.
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Db 201 TCAGCAGCGAGTGACTGGGACACTGGTCTTGTGTTATTTCTCAGCTGTGCTTGGCTCCCT 260
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1581 TGACCAAGATCTCGGCACCTTCCGACGACACCTTCTCTTGTAGAGGAGGTTGAAC 1640
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1701 GAGCCACCTCTCC 1713

RESULT 3
RATIRGT
LOCUS
DEFINITION
Rat insulin-responsive glucose transporter (Gr) mRNA, complete cds.
ACCESSION
J04524
VERSION
J04524.1 GI:204979
KEYWORDS
glucose transporter.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 2482)
AUTHORS
Charon,M.J., Brosius,F.C. III, Alper,S.L. and Lodish,H.F.
TITLE
A glucose transport protein expressed predominately in
insulin-responsive tissues
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 86 (8), 2535-2539 (1989)
MEDLINE
89202363
FURNED
2649883
COMMENT
Original source text: Rattus norvegicus (strain Sprague-Dawley)
male soleus cDNA to mRNA.
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Best Local Similarity 98.2; Pred. No. 0;
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DB 110 CTTTAAAAAANAGATGCGTGGGTTTCCAGCAGATCGGCTCTGAAGATGGGAAACCCCC 169
QY 515 TCAGCAGGAGTGAATGGGACACTGGTCTTGTGTATTCAGCTGTGCTGGTCTCCCT 574
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QY 575 TCAGTTTGGCTATAAATTTGGAGTCATCAAGCCGCCACAGAAAGTATTGAACAGAGCTA 634
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QY 635 CAATGCAACTTGGCTGGTAGGAGGCTCTGGGGGACCGGACTCCATCCCAACAGGAC 694
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DB 470 TGTCTTGGCTGTGTGGGGGCGCCCTCATGGGCTTAGCCCAATGCCGGGCTCCTATGCA 529
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QY 1055 GGGCAGAGTACCTGTGGCCATTGCTTCTGGCTATCAGAGTATCTCCCTGTCTCTCTGCA 1114
DB 710 GGGCAGAGTACCTGTGGCCATTGCTTCTGGCTATCAGAGTATCTCCCTGTCTCTCTGCA 769
QY 1115 GCTGCTTCTGTGGCTTCTGTCTCTGAGAGCCCGGACCTCTATCATCATCCGGAACCT 1174
DB 770 GCTGCTTCTGTGGCTTCTGTCTCTGAGAGCCCGGACCTCTATCATCATCCGGAACCT 829

Qy	1175	GGAGGGCGCTCCCGAAGAGTCTAAAGCGCCTGACAGGCTGGGCTGATGTGTCTGATGC	1234
Db	830	GGAGGGCGCTCCCGAAGAGTCTAAAGCGCCTGACAGGCTGGGCTGATGTGTCTGATGC	889
Qy	1235	ACTGGCTGAGCTGAAGAGTGAAGAACGGAAGTTCGGAAGAGAGCGTCCACTGTCCTTGCT	1294
Db	890	ACTGGCTGAGCTGAAGAGTGAAGAACGGAAGTTCGGAAGAGAGCGTCCACTGTCCTTGCT	949
Qy	1295	GCAGCTCTCTGGGCACGCGCACCCACCGCAGCCTCTGATTAATTGCACTGGTGTCTGCAGCT	1354
Db	950	GCAGCTCTCTGGGCACGCGCACCCACCGCAGCCTCTGATTAATTGCACTGGTGTCTGCAGCT	1009
Qy	1355	GAGCCAGCAGCTCTCAGGCATCAATGCTGTTTCTACTATTAACACGACATCTTTGAGTT	1414
Db	1010	GAGCCAGCAGCTCTCAGGCATCAATGCTGTTTCTACTATTAACACGACATCTTTGAGTT	1069
Qy	1415	AGCTGGGGTGGAAACAGCCAGCCTACGCCACCATAGGAGCTGGTGTGCTCAATACCGTCTT	1474
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Qy	1475	CACGTTGCTCTCGGTGCTCTTAGTAGAGCAGCTTGGCGACGGACATCTCCATCTCTCGGG	1534
Db	1130	CACGTTGCTCTCGGTGCTCTTAGTAGAGCAGCTTGGCGACGGACATCTCCATCTCTCGGG	1189
Qy	1535	CCTGGCAGGCATGTGTGGCTGTGCCATCTTGATGACGGTGGCTCTGCTGCTGTGAGACG	1594
Db	1190	CCTGGCAGGCATGTGTGGCTGTGCCATCTTGATGACGGTGGCTCTGCTGCTGTGAGACG	1249
Qy	1595	GTTTCCATCCAGATTAAGTGTCCATGCTGGGCCATATTTGGCTTTGTGGCTTCTTTTGA	1654
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Qy	1655	GATTTGCTCTGGCCCCCATCCCTGGTTCATTTGTGGCGAGCTCTTCAGCCAGGGCCCCCG	1714
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Qy	1715	CCACGACGCATGGCTGTAGCTGGTCTTCCAACTGGACCTGTAACTTCATCGTTGGCAT	1774
Db	1370	CCACGACGCATGGCTGTAGCTGGTCTTCCAACTGGACCTGTAACTTCATCGTTGGCAT	1429
Qy	1775	GGGTTTCCAGTATGTTGGGATGCTATGGGTCCCTACGGTCTTCCTTATTTGCGGTCCT	1834
Db	1430	GGGTTTCCAGTATGTTGGGATGCTATGGGTCCCTACGGTCTTCCTTATTTGCGGTCCT	1489
Qy	1835	CCTGCTTGGCTCTTTCATCTTCACCTTCCTAAGAGTGCCTTGAACACAGAGCGCGACATT	1894
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Qy	1895	TGACACAGATCTCGGCCACCTTCCGACGACACCTTCTCTCTTAGAGCAGGAGGTGAACCC	1954
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Qy	1955	CAGTACAGAACTTGAATACTATTAGGGCCAGATGAGAATGACTAATTCGATTTGAAGTGAGAC	2014
Db	1610	CAGTACAGAACTTGAATACTATTAGGGCCAGATGAGAATGACTAATTCGATTTGAAGTGAGAC	1669
Qy	2015	GCTCCATCATCTC 2027	
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RESULT	4
LOCUS	RATGLUT4
DEFINITION	Rattus norvegicus mRNA for glucose transporter, GLUT4.
ACCESSION	D28561
VERSION	D28561.1 GI:464195
KEYWORDS	GLUT4; glucose transporter.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE	AUTHORS	TITLE	JOURNAL	MDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL
1	(sites)	Kasahara, T. and Kasahara, M.	Characterization of rat Glut4 glucose transporter expressed in the yeast <i>Saccharomyces cerevisiae</i> : comparison with Glut1 glucose transporter	Biochim. Biophys. Acta	1324	(1), 111-119	(1997)	97212686	
2	(bases 1 to 2506)	Kasahara, M.	Direct Submission	Submitted (18-FEB-1994)	Michihiro Kasahara, Teikyo University, School of Medicine, Laboratory of Biophysics, 359 Ohtsuka, Hachioji, Tokyo 192-03, Japan	(E-mail: mkasa@tansei.cc.u-tokyo.ac.jp, Tel: 0426-75-8211 (ex. 262), Fax: 0426-75-0025)	Location/Qualifiers	1. .2506	
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								/db_xref="taxon:10116"	
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								/product="glucose transporter"	
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								/db_xref="GI:538355"	
								/translation="MPSGQQIGSEBPEPQQRVTGLVLAVSFASVLSIQFGVNIQVINAPOKIEQSYNATWLGRCGGPDSIPQGTITLTWALSVAFSVGGMISFLIGII	
								SOWLGRKRLANNVLAVGLANLAASVEILIGRLICAYSGLTSGLVPMVV	
								GETAPLHRCALCTNOLAIVIGILVAQVLGSEMLGTATLPLLLAITVLPALLQLL	
								LLPFCSPESRYLIIRINLEGPARKSLKRLTGWADVSDALAEKDEKRLERPLSLLL	
								QLGSRTHROPLIAIVLQSLQGINAVFYTSTIFELAGVEQPAIATIGAGVNV	
								VFTLSVLVFRAGRRTLLHLAGCMGCALMTVALLLERVPSSMSYIVAVGTV	
								AFPEIGPGPTPWFIVAEILFSQGRPAAMAVAGSNMTCNFIVGMGQYVADAMGPYVF	
								DLFVALLLGFFIFTFLRVPTGRGTFDQISATPRRTPSLLEQVKPSTELXYLGPDSN	
								D"	
								2506	
								polyA_site	
								ORIGIN	
								Query Match	64.0%; Score 1528.2; DB 10; Length 2506;
								Best Local Similarity	98.3%; Pred. No. 0;
								Matches 1545; Conservative	0; Mismatches 28; Indels 0; Gaps 0;
Qy	455	CTTATAAGCAACATAATGTCGTAATCCAGCAGATCGGCTCTGAAATGGGAAACCCCC	514						
Db	128	CTTTTAAACAAGATGCGTCGGGTTTCCAGCAGATCGGCTCTGAAGATGGGAAACCCCC	187						
Qy	515	TCAGCAGGAGTCACTGGGACATGGTCCTTGCTGTATTCTTCAGCTGTGCTTGGCTCCCT	574						
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Qy	575	TCAGTTGGCTATAACATTGGAGTCATCAACGCCCCACACAGAAAGTGAATGAACAGAGCTA	634						
Db	248	TCAGTTGGCTATAACATTGGAGTCATCAACGCCCCACACAGAAAGTGAATGAACAGAGCTA	307						
Qy	635	CAATGCAACTTGGCTGGGTAGGCAGGGTCTCTGGGGGACCGGACTCCATCCACAAAGGCAC	694						
Db	308	CAATGCAACTTGGCTGGGTAGGCAGGGTCTCTGGGGGACCGGACTCCATCCACAAAGGCAC	367						
Qy	695	CCTCACTACCCCTTGGGCTCTCTCCGTGGGCATCTTCTCTGTGGGTGGCATGATTTCTTC	754						
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Qy	755	CTTTCTCATTTGGCATCATTTTCTCAATGGTTGGGAAGGAAAAGGCTATGCTGGCCACAA	814						
Db	428	CTTTCTCATTTGGCATCATTTTCTCAATGGTTGGGAAGGAAAAGGCTATGCTGGCCACAA	487						
Qy	815	TGCTTGGCTGTGCTGGGGGGCGCCCTCATGGGCTTAGCCAAATGCCCGGCTCCTTATGA	874						

Db 488 TGTCTTGGCTGTGCTGGGGGGCCCTCATGGCCCTAGCCAAATGCGCGGCTCCTATGA 547
QY 875 GATACATCTTCGGACGGTTCCTCATTTGGGCCCTACTCAGGGCTAAACATCAGGTTGGT 934
Db 548 GATACATCTTCGGACGGTTCCTCATTTGGGCCCTACTCAGGGCTAAACATCAGGTTGGT 607
QY 935 GCTATGTATGTGGGAGAAATCCGCCCACTCATCTTCGGGGTGCTTTGGGAACACTCAA 994
Db 608 GCTATGTATGTGGGAGAAATCCGCCCACTCATCTTCGGGGTGCTTTGGGAACACTCAA 667
QY 995 CCAATGGCCATCGTCAATTTGGCAATCTGTTGGCCAGGTGTTGGTTGGAGTCTATGCT 1054
Db 668 CCAATGGCCATCGTCAATTTGGCAATCTGTTGGCCAGGTGTTGGTTGGAGTCTATGCT 727
QY 1055 GGGCAGACTACCTGTGGCCATTCCTTGCCCTATACAGTACTCCCTGCTCTCTGCA 1114
Db 728 GGGCAGACTACCTGTGGCCATTCCTTGCCCTATACAGTACTCCCTGCTCTCTGCA 787
QY 1115 GCTGCTTCTGTTGCCCTTCTGCTCGAGAGCCCGGATACCTTACATCATCCGGAACCT 1174
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QY 1355 GAGCCAGAGCTCTCAGGCATCAATGCTGTTTCTATCTATTAACACAGCATCTTTGAGTT 1414
Db 1028 GAGCCAGAGCTCTCAGGCATCAATGCTGTTTCTATCTATTAACACAGCATCTTTGAGTT 1087
QY 1415 AGCTGGGTGGAAACAGCAGCTACGCCACCATAGGAGCTGGTGGTCAATACCGTCT 1474
Db 1088 AGCTGGGTGGAAACAGCAGCTACGCCACCATAGGAGCTGGTGGTCAATACCGTCT 1147
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QY 1895 TGACCATGCTCTGGGACCTTCCGAGGACACTTCTCTCTTAGAGGAGGAGGTAAC 1954
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Db 1628 CAGTACAGAACTTCAATCTTAGGGCCAGATGAGAATGACTAATCGATTTGAAGTGAC 1687
QY 2015 GCTCCATCATCTC 2027
Db 1688 GAGCCACCTCCC 1700

RESULT 5

RAT1GTSPM

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

CDS

polyA_signal

polyA_site

ORIGIN

Query Match

Best Local Similarity

Matches 1544; Conservative

QY 455

Db 93

QY 515

Db 153

Score 1526.6; DB 10; Length 2447;

Pred. No. 0;

Mismatches 29; Indels 0; Gaps 0;

QY 455

Db 93

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Db 153

Score 1526.6; DB 10; Length 2447;

Pred. No. 0;

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Score 1526.6; DB 10; Length 2447;

Pred. No. 0;

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QY 455

Db 93

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Db 153

Score 1526.6; DB 10; Length 2447;

Pred. No. 0;

Mismatches 29; Indels 0; Gaps 0;

575 TCAGTTGGCTATAACATTGGAGTCTATCAACGCCCAAGAAAGTGAATTGAACAGAGCTA 634
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Db CAATGCAACTTGGCTGGGTAGGAGAGGCTCTCGGGGACCGCACTCCATCCCAAGGCAC 332
695 CTTCTCACTTGGCTCTCTCGGGGACCGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 754
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2015 GCTCCATCATCTC 2027
Db GCTCCATCATCTC 1653
1653 GAGCCACCTCC 1665

RESULT 6
AX573334 LOCUS 2338 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 12 from Patent WO2064784.
ACCESSION AX573334
VERSION AX573334.1 GI:26005220
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1
AUTHORS Mueller,G., Koller,K.P., Boles,E., Wisczorzke,R. and Dlugai,S.
TITLE Yeast strain of saccharomyces cerevisiae with functional expression
of a glut transporter
JOURNAL Patent: WO 02064784-A 12 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DB)
FEATURES Location/Qualifiers
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Query Match 62.5%; Score 1490.4; DB 6; Length 2338;
Best Local Similarity 77.8%; Pred. No. 0;
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AX573335 AX573335 2338 bp DNA linear PAT 29-NOV-2002
LOCUS Sequence 13 from Patent WO02064784.
DEFINITION AX573335
ACCESSION AX573335
VERSION AX573335.1 GI:26005221
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Mueller, G., Koller, K.P., Boles, E., Wiczorke, R. and Dlugai, S.
TITLE Yeast strain of saccharomyces cerevisiae with functional expression
of a glut transporter
JOURNAL Patent: WO 02064784-A 13 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:10116"
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Query Match 62.4%; Score 1488.8; DB 6; Length 2338;
Best Local Similarity 77.8%; Pred. No. 0;
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DB 61 TAACCTAATAAATTTCCGAATCTTTTCTACGCGTTTCTTCGGGAACTAGATAG 120
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ACCESSION AX573336
VERSION AX573336.1 GI:26005222
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SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Mueller,G., Koller,K.P., Boles,E., Wiczorke,R. and Dlugai,S.
TITLE Yeast strain of saccharomyces cerevisiae with functional expression
of a glut transporter
JOURNAL Patent: WO 02064784-A 14 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

FEATURES

Location/Qualifiers

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 Age-dependent changes in phenotypes and candidate gene analysis in a polygenic animal model of Type II diabetes mellitus; NSY mouse Diabetologia 43 (7), 932-938 (2000)
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 PUBLISHED 10952468
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 Ueda, H., Ikegami, H. and Kawaguchi, Y.
 Direct Submission
 Submitted (23-OCT-1997) Hiroshi Ikegami, Osaka University Medical School, Department of Geriatric Medicine; 2-2 Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail: ikegami@geriat.med.osaka-u.ac.jp, Tel: 06-879-3852, Fax: 06-879-3859)
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FEATURES
 source

gene
 CDS

ORIGIN

Query Match 59.3%; Score 1415.4; DB 10; Length 1572;
 Best Local Similarity 95.1%; Pred. No. 0;
 Matches 1461; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
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 Db 1 AAACAGATGCCGTGGGTTCAGAGCAGATCGGCTCTGACGATGGGAAACCCCTCGGCA 60
 Qy 521 GCGAGTCACTGGGACACTGGTCTTGTGTTATCTCAGCTGTGCTTGGCTCCCTTCAGTT 580
 Db 61 GCGAGTCACTGGAAACACTGGTCTTGTGTTATCTCAGCTGTGCTTGGCTCCCTTCAGTT 120
 Qy 581 TGGCTATAACATTCGAGTCAATCAACGCCCCACAGAAAGTGAACAGAGCTTCAATGC 640
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QY 1589 GGAGCGGTTCCATCCATGAGTATATGTCCATCGTGGCCATATTTGGCTTTTGGCCTT 1648
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 QY 1649 CTTTGAGATTGGTCTCGGCCCATCCCTGCTTCATTTGTGGCGAGCTCTTCAGCCAGGG 1708
 DB 1341 CTTTGAGATTGGCTGGCCCATCCCTGCTTCATTTGTGGCGAGCTCTTCAGCCAGGG 1397
 QY 1709 CCCCAGCCAGCCATGCTGAGTGTGTTCTCAACTGGACCTGTAACTTTCATCGT 1768
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 DB 1518 CGTCTCTCTGCTGCTTCATCTTCACTTCCCTAAAGAGTGCCTGAAACAGAGCCG 1577
 QY 1889 GACATTTGACAGATCTCGGCCACCTTCCAGCGACACCTTCTCTTTAGAGCAGGAGT 1948
 DB 1578 GAGCTTTGACAGATCTCGGCCACCTTCCAGCGACACCTTCTCTTTAGAGCAGGAGT 1637
 QY 1949 GAAACCCAGTACAGAACTTGAATCTTAGGGCCAGATGAGAACTAA 1997
 DB 1638 GAAACCCAGTACAGAACTTGAATCTTAGGGCCAGATGAGAACTAA 1686

RESULT 12

AF531753
 LOCUS 1539 bp mRNA linear MAM 21-AUG-2002
 DEFINITION Equus caballus glucose transporter type 4 (GLUT4) mRNA, complete cds.

ACCESSION AF531753.1 GI:22347677

VERSION

KEYWORDS Equus caballus (horse)

SOURCE

ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE

AUTHORS 1 (bases 1 to 1539) Jose-Cunilleras, E., Hayes, K.A., Toribio, R.E., Mathes, L.E. and Hinchcliff, K.W.

TITLE Equus caballus insulin-responsive glucose transporter, glucose transporter type 4 (GLUT4) mRNA

JOURNAL Unpublished

REFERENCE

AUTHORS 2 (bases 1 to 1539) Jose-Cunilleras, E., Hayes, K.A., Toribio, R.E., Mathes, L.E. and Hinchcliff, K.W.

TITLE Direct Submission

JOURNAL Submitted (21-JUL-2002) Veterinary Clinical Sciences, The Ohio State University, 601 Vernon L. Tharp St, Columbus, OH 43210, USA

FEATURES

source Location/Qualifiers

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gene

CDS

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VERSION	AX573331.1 GI:26005217		
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Mueller,G., Koller,K.P., Boles,E., Wiczorke,R. and Dlugai,S.		
TITLE	Yeast strain of saccharomyces cerevisiae with functional expression of a glut transporter		
JOURNAL	Patent: WO 02064784-A 2 29-AUG-2002;		
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TITLE		Direct Submission	
JOURNAL		Submitted (11-JUL-2003) Anatomy and Cell Biology, Martin Luther University Halle-Wittenberg, Gr. Steinstrasse 52, Halle (Saale), Sachsen-Anhalt 06097, Germany	
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Matches 1334; Conservative 0; Mismatches 200; Indels 0; Gaps 0;			
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Job time : 5972.83 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-067-449-10

Perfect score: 2386

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1485.6	62.3	2338	6	AAL49315 Rat Glut1
5	1229	51.5	7828	6	AAL49310 Human Glu
6	1066.4	44.7	2592	5	Aaf81396 Coding se
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8	682.2	28.6	2587	2	Aaql1148 GTP-gene
9	679	28.5	1815	2	Aat56495 Human glu
10	679	28.5	2544	6	Abi99628 Mouse isc
11	679	28.5	2571	9	Adbs3698 Primary r
12	679	28.5	2854	7	Abx74453 Human cdn
13	679	28.5	2856	3	Aac65871 Human cdn
14	679	28.5	2856	6	Abk83784 Human cdn
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16	679	28.5	2856	6	Abf49090 Human lun
17	679	28.5	2856	6	Abn95630 Gene #212
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19	679	28.5	2856	7	Abx76166 Lung canc
20	679	28.5	2856	8	Ada28225 Human cdn
21	679	28.5	2856	9	Ades3430 Human lun
22	679	28.5	2893	6	Aaf98714 Human lat
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25	678.2	28.4	2778	7	ABT31931	Abt31931 Human bre
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27	667.4	28.0	2683	6	ABSS1820	Abss1820 Novel hum
28	663	27.8	2349	6	ABK35243	Abk35243 Human cdn
29	639.2	26.8	2919	6	ABSS1822	Abss1822 Novel hum
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31	631.8	26.5	2850	2	AAZ24632	Aaz24632 Human lun
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40	464.6	19.5	2126	6	ABQ76439	Abq76439 S. cerevi
41	456.2	19.1	3168	6	ABN95601	Abn95601 Gene #209
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ALIGNMENTS

RESULT 1

AAL49311

ID AAL49311 standard; DNA; 2386 BP.

XX AC AAL49311;

XX DT 07-NOV-2002 (first entry)

XX DE Rat Glut4 containing vector H2rg4g2.

XX KW Rat; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;

XX KW vector; ds.

XX OS Rattus norvegicus.

XX PN WO200264784-A2.

XX PD 22-AUG-2002.

XX PF 09-FEB-2002; 2002WO-EP001373.

XX PR 14-FEB-2001; 2001DE-01006718.

XX PA (AVET) AVENTIS PHARMA DEUT GMBH.

XX PI Mueller G, Koller K, Boles E, Wleczorke R, Dlugai S;

XX DR WPI; 2002-636632/68.

XX PT New strains of yeast, useful in screening for modulators of hexose

XX PT transport, potential antidiabetic and antiobesity agents, lack native

XX PT hexose-transport function.

XX PS Claim 10; Page 36-37; 58pp; German.

XX CC The present invention relates to a strain of Saccharomyces cerevisiae

XX CC carbon but the ability to grow on such substrates is restored when the

XX CC GLUT4 gene is expressed. A strain transformed to express the GLUT1 or

XX CC GLUT4 genes can be used to identify compounds that increase/reduce hexose

XX CC transport by these proteins. These compounds, optionally after

XX CC development, are potential drugs for treating diabetes and obesity. The

XX CC present sequence is a vector containing the rat Glut4 coding sequence as

XX CC used in the invention

XX SQ Sequence 2386 BP; 560 A; 610 C; 542 G; 674 T; 0 U; 0 Other;

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Matches 2386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy	1	TCGACTCTAGAGATCCCTTAAAGCTAATCCCTTATGAATCGGAGAAAAGCGGGTCTTT	60				
Db	1	TCGACTCTAGAGATCCCTTAAAGCTAATCCCTTATGAATCGGAGAAAAGCGGGTCTTT	60				
Qy	61	TAACTCAATAAATTTTCGGAATCCTTTTCTACGGCTTTTCTTCGGGAACCTAGATAG	120				
Db	61	TAACTCAATAAATTTTCGGAATCCTTTTCTACGGCTTTTCTTCGGGAACCTAGATAG	120				
Qy	121	GTGGCTCTTCCACCTGTTTTTCATCATTTAGTTTTTCGAAAGCATGCGTGCTTTTC	180				
Db	121	GTGGCTCTTCCACCTGTTTTTCATCATTTAGTTTTTCGAAAGCATGCGTGCTTTTC	180				
Qy	181	GTTTTTGCGATGCGAAAGAGGCTGGAAAAATTAACGGTACGCGCCTAACGATAGTAA	240				
Db	181	GTTTTTGCGATGCGAAAGAGGCTGGAAAAATTAACGGTACGCGCCTAACGATAGTAA	240				
Qy	241	TAGGCACGCAACTGGGTGGAGCAACAATAAGTCGCCCATTTTATGTTTTCAAAA	300				
Db	241	TAGGCACGCAACTGGGTGGAGCAACAATAAGTCGCCCATTTTATGTTTTCAAAA	300				
Qy	301	CCTAGCAACCCCAACAACTTGTCTATCGTTCCCGGATTCAAAATGATATAAAAAGCGA	360				
Db	301	CCTAGCAACCCCAACAACTTGTCTATCGTTCCCGGATTCAAAATGATATAAAAAGCGA	360				
Qy	361	TTACAATTCTCATTTCTAACCAAGATTGAGATTTCTCTTCTCAATTCCTTTATATTA	420				
Db	361	TTACAATTCTCATTTCTAACCAAGATTGAGATTTCTCTTCTCAATTCCTTTATATTA	420				
Qy	421	GATTATAGAAACAATAATTAATAAAGACTTATAAGCAACAATAATGTCGAAT	480				
Db	421	GATTATAGAAACAATAATTAATAAAGACTTATAAAGCAACAATAATGTCGAAT	480				
Qy	481	TCACGAGATCGGCTCTGAAGATGGGAACCCCTCAGCAGGAGTGACTGGGACACTGG	540				
Db	481	TCACGAGATCGGCTCTGAAGATGGGAACCCCTCAGCAGGAGTGACTGGGACACTGG	540				
Qy	541	TCCTTGCTGTATCTCAGCTGTGCTTGCTCCCTTTCAGTTTGGCTATAAACAATGGAGTCA	600				
Db	541	TCCTTGCTGTATCTCAGCTGTGCTTGCTCCCTTTCAGTTTGGCTATAAACAATGGAGTCA	600				
Qy	601	TCAGGCCCAACAGAAAGTGAACAGAGCTACAATGCAACTTGGCTGGGTAGGACAGG	660				
Db	601	TCAGGCCCAACAGAAAGTGAACAGAGCTACAATGCAACTTGGCTGGGTAGGACAGG	660				
Qy	661	GTCTGGGGGACCGGACTCCATCCCAAGGCAACCTCAGTACCTTTGGGCTCTCTCCG	720				
Db	661	GTCTGGGGGACCGGACTCCATCCCAAGGCAACCTCAGTACCTTTGGGCTCTCTCCG	720				
Qy	721	TGGCCATCTTCTGTGGGTGGCATGATTTCTCTTCTCATTTGGCATCAATTTCTCAAT	780				
Db	721	TGGCCATCTTCTGTGGGTGGCATGATTTCTCTTCTCATTTGGCATCAATTTCTCAAT	780				
Qy	781	GGTTGGGAAGAAAAGGGCTATGCTGGCAACAATGCTTGCTGGTGGGGGGCGCC	840				
Db	781	GGTTGGGAAGAAAAGGGCTATGCTGGCAACAATGCTTGCTGGTGGGGGGCGCC	840				
Qy	841	TCATGGGCTAGCCAATGCGGGCTCTCTATGAGATACTCAATTCGGACGGTTCCTCA	900				
Db	841	TCATGGGCTAGCCAATGCGGGCTCTCTATGAGATACTCAATTCGGACGGTTCCTCA	900				
Qy	901	TTGGGCGCTTACTCAGGGCTAAACATCAGGGTTGGTGCTTATGATGAGAAATTCGCC	960				
Db	901	TTGGGCGCTTACTCAGGGCTAAACATCAGGGTTGGTGCTTATGATGAGAAATTCGCC	960				
Qy	961	CACTCATCTTCGGGGTGGGAAACACTCAACCAATTTGGCCATCGTCAITGGCATTC	1020				
Db	961	CACTCATCTTCGGGGTGGGAAACACTCAACCAATTTGGCCATCGTCAITGGCATTC	1020				
Qy	1021	TGTTGCCAGGCTTGGGTTGGAGTCTATGCTGGGCACAGCTACCTGTGGCCATTGC	1080				
Db	1021	TGTTGCCAGGCTTGGGTTGGAGTCTATGCTGGGCACAGCTACCTGTGGCCATTGC	1080				
Qy	1081	TTCTGGCTATCACAGTACTCCCTGCTCTCTGCTGAGCTGCTTCTGTGCCCCCTCTCTCTG	1140				
Db	1081	TTCTGGCTATCACAGTACTCCCTGCTCTCTGCTGAGCTGCTTCTGTGCCCCCTCTCTCTG	1140				
Qy	1141	AGAGCCCCGATACCTCTACATCATCGGACCTGGAGGGGCTGCCCGAAGAGCTCTAA	1200				
Db	1141	AGAGCCCCGATACCTCTACATCATCGGACCTGGAGGGGCTGCCCGAAGAGCTCTAA	1200				
Qy	1201	AGGCGCTGACAGGCTGGGCTGATGCTGATGCACTGGCTGAGCTGAAGATGAGAAAC	1260				
Db	1201	AGGCGCTGACAGGCTGGGCTGATGCTGATGCACTGGCTGAGCTGAAGATGAGAAAC	1260				
Qy	1261	GGAAATGGAAAAGAGAGCGTCCAATGCTTGTGCTGAGCTCTTGGGACCGCCACCCACC	1320				
Db	1261	GGAAATGGAAAAGAGAGCGTCCAATGCTTGTGCTGAGCTCTTGGGACCGCCACCCACC	1320				
Qy	1321	GGCAGCCTCTGATTTTCAACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCCAGCTACG	1380				
Db	1321	GGCAGCCTCTGATTTTCAACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCCAGCTACG	1380				
Qy	1381	CTGTTTCTACTATTCAACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCCAGCTACG	1440				
Db	1381	CTGTTTCTACTATTCAACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCCAGCTACG	1440				
Qy	1441	CCACATAGAGCTGGTGTCAATACCGTCTTCAACCGTCTTCAACCGTCTTCAACCGTCTT	1500				
Db	1441	CCACATAGAGCTGGTGTCAATACCGTCTTCAACCGTCTTCAACCGTCTTCAACCGTCTT	1500				
Qy	1501	AGCAGCTGGGCGACGACACTCCATCTCTGGGCTGGCAGGAGTGTGGCTGGCCA	1560				
Db	1501	AGCAGCTGGGCGACGACACTCCATCTCTGGGCTGGCAGGAGTGTGGCTGGCCA	1560				
Qy	1561	TCCTTGAAGAGGCTGGCTCTGCTGCTGGAGCGGGTTCATCCATGAGTTATGTTGCTCA	1620				
Db	1561	TCCTTGAAGAGGCTGGCTCTGCTGCTGGAGCGGGTTCATCCATGAGTTATGTTGCTCA	1620				
Qy	1621	TCGTTGGCCATATTTGGCTTTTGGCTCTTGTGAGTTGGTCTGGGCCCATCCCTGGT	1680				
Db	1621	TCGTTGGCCATATTTGGCTTTTGGCTCTTGTGAGTTGGTCTGGGCCCATCCCTGGT	1680				
Qy	1681	TCATTGGCGGAGCTCTTCAAGCAGGCCCCCGCCAGCAGCCATGCTGTGCTGGT	1740				
Db	1681	TCATTGGCGGAGCTCTTCAAGCAGGCCCCCGCCAGCAGCCATGCTGTGCTGGT	1740				
Qy	1741	TCTCCAACTGGACCTGTAACCTTCAATCGTTGGCATGGGTTTCCAGTATGTCGGATGCTA	1800				
Db	1741	TCTCCAACTGGACCTGTAACCTTCAATCGTTGGCATGGGTTTCCAGTATGTCGGATGCTA	1800				
Qy	1801	TGGTCCCTAGCTCTTCTTATTTGGCGTCTCTGCTTGGCTTCTTCACTTTCACT	1860				
Db	1801	TGGTCCCTAGCTCTTCTTATTTGGCGTCTCTGCTTGGCTTCTTCACTTTCACT	1860				
Qy	1861	TCCTAAGAGTGCCTGAAACAGAGCGCGACATTTGACAGATCTCGGCCACTTCCGAC	1920				
Db	1861	TCCTAAGAGTGCCTGAAACAGAGCGCGACATTTGACAGATCTCGGCCACTTCCGAC	1920				
Qy	1921	GGACACCTTCTCTCTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATCTTAGGGC	1980				
Db	1921	GGACACCTTCTCTCTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATCTTAGGGC	1980				
Qy	1981	CAGATGAGATGACTAATCGATTTGAGTGAAGCTCCATCATCTCTTAAATTTTCA	2040				
Db	1981	CAGATGAGATGACTAATCGATTTGAGTGAAGCTCCATCATCTCTTAAATTTTCA	2040				
Qy	2041	TGACTGAGCTTTTCTTCAATTTTAAATTTATCATAGTATTTGTTGAAAAAATAAAAAA	2100				
Db	2041	TGACTGAGCTTTTCTTCAATTTTAAATTTATCATAGTATTTGTTGAAAAAATAAAAAA	2100				
Qy	2101	AATTTCCCTTATCAATGATATCTTACGATTATATAAATTCCTTACCTAAACCTATTAT	2160				


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QY 1141 AGAGCCCCGATACCTCTACATCATCCGAAACCTGGAGGGCCCTGCCGAAAGAGTCTAA 1200
DB 1096 AGAGCCCCGCTCTCTGCTCATCATCTGTAACGAGGAGAAACGGGGCAAGAGTGTGTA 1155
QY 1201 AGCGCTGACAGGCTGGCTGATGTCTGATGCACTGGCTGAGCTGAAGATGAGAAAC 1260
DB 1156 AAAAGCTTCGAGGGACAGCCGATGTGACCCGAGAGCTTCGAGGAGATGAAAGAGGGTC 1215
QY 1261 GGAAGTTGGAAGAGAGGCTCCACTGTCTCTGCTGAGCTCCTGGGAGCGCCACCCACC 1320
DB 1216 GGCAGATGATGCGGAGAGAGAGGTCACCATCTTGGAGCTGTTCCGCTCACCCGCCCTACC 1275
QY 1321 GGCAGCTCTGATTAATGTCAGTGGTGTGTCAGCTGAGCAGCAGCTCTCAGGCATCAATG 1380
DB 1276 GGCAGCCCATCTCATCGCGTGGTGTGTCGAGCTGTCCAGCAGCTGTGCGGATCAATG 1335
QY 1381 CTGTTTCTTACTATTCAACAGCATCTTTTGATGATGCTGGGTGGAACAGCAGCCTACG 1440
DB 1336 CTGTGTTCTACTACTCAAGCAGCATCTTCGAGAGGCGAGGTGTGCAGCAGCCTGTGTATG 1395
QY 1441 CCACCATAGGAGCTGGTGTGTCATACGCTCTTCACTGTTGCTCGTGCTCTTAGTAG 1500
DB 1396 CCACCATCGGCTCGGATATCGTCAACACGCGCTTCACTGTGGTGTGCTGTGCTGTG 1455
QY 1501 AGCAGCTGGGCGAGCGACACTCCATCTCTGGGCTGCGCAGGCGATGTGGCTGTGCCA 1560
DB 1456 AGCAGCTGGGCGTGGACCTCGCATCTCATTTGCTGTGGCTGBCATGCGCGGCTGTGCTG 1515
QY 1561 TCTTGATGACGGTGGCTCTGCTGCTGCTGGAGCGGGTTCATCCATGATGATGATGTCGA 1620
DB 1516 TGCTCATGACCATGCCCTGGCCCTGCTGGAGCAGCTGCCCTGGATGCTCTATCTGAGTA 1575
QY 1621 TGTGGCCATATTTGGCTTTTGGCTTTCTTTGAGATTTGGTCTCGGCCCATCTCCCTGGT 1680
DB 1576 TGTGGCCATCTTTGGCTTTTGGCTTTCTTTGAGTAGGGCCCTGGTCTCTATTCCTATG 1635
QY 1681 TCATTGTGGCCAGCTCTTTCAGCCAGGCGCCCGCCGAGCAGCATGCTGTAGCTGTT 1740
DB 1636 TCATTGTGGCCAGCTTTTCAGCCAGGCGCCCGCCGAGCAGCTGTGCTGTGCTGTGCTG 1695
QY 1741 TCTCAACTGGACCTGTAACTTCATCTGTTGGCATGGGTTTCCAGTATGTTCCGATGCTA 1800
DB 1696 TCTCAACTGGACCTCAAACTTCATCTGTTGGCATGGTCTTCCATATATGAGCAACTGT 1755
QY 1801 TGGTCCCTACGCTCTCTCTTAATTTGGCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
DB 1756 GTGGCCCTTACGCTCTCTCACTATCTTTCAGCGTGTGCTGCTGCTGCTGCTGCTGCT 1815
QY 1861 TCTAAGAGTGTCTGAAACCCAGAGCGCGCATTTTGACAGATCTCGGCCACCTTCCGAC 1920
DB 1816 ACTTCMAAGTTCCTGAGACCAAGCCGAGCCTTCGATGATGCTTCCGGCTTCCGGC 1875
QY 1921 GGACACCTTCTCTCTAGACGAGGAGGTGAACCCAGTACAGAACTTGAATPACTTAGGGC 1980
DB 1876 AGGGGGTGC---CAGCCAGAGCGACAAGACACCTTGAGAGCTCTTCCACCTCTGGGG 1932
QY 1981 CAGATGAGATGACTAATCGATTGAAGTGAAGAGCGCTCCATCATCTCTTAATTTTCA 2040
DB 1933 CTGACTCCCAAGTGAATCGATTGAAGTGAAGAGCGCTCCATCATCTCTCTTAATTTTCA 1992
QY 2041 TGACTGACGTTTTTCTTCATTTAATTAATATCATAGTATTTGTTGAAAAAAGAAAAA 2100
DB 1993 TGACTGACGTTTTTCTTCATTTAATTAATATCATAGTATTTGTTGAAAAAAGAAAAA 2052
QY 2101 AATTTCCCTTATCAATGATATCTTACGATTATATAAATCTTACCTTAACCTATTATT 2160
DB 2053 AATTTCCCTTATCAATGATATCTTACGATTATATAAATCTTACCTTAACCTATTATT 2112
QY 2161 TGTGTACATATATCAGAGTATTTATACATATATACCTTTTCTTAAACAGAAAAA 2220
DB 2113 TGTGTACATATATCAGAGTATTTATACATATATACCTTTTCTTCTTAAACAGAAAAA 2172
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QY 2221 AAAAGAAAAAGATAACATGCTCTGCCATCTTTTGTTCACCGAGCAAAATTAATAACGCAA 2280
DB 2173 AAAAGAAAAAGATAACATGCTCTGCCATCTTTTGTTCACCGAGCAAAATTAATAACGCAA 2232
QY 2281 AATGAATTTGCTCCCTATGAAATTTAAGGACCAATCACCAGACTTATCTCTGGGGGT 2340
DB 2233 AATGAATTTGCTCCCTATGAAATTTAAGGACCAATCACCAGACTTATCTCTGGGGGT 2292
QY 2341 CCTCTAGAAAATGAGTCAGGTACTTGTCTGACCTTCTTCCAGTTG 2386
DB 2293 CCTCTAGAAAATGAGTCAGGTACTTGTCTGACCTTCTTCCAGTTG 2338

RESULT 3
ID AAL49314 standard; DNA; 2338 BP.
XX AAL49314;
XX AC
XX 07-NOV-2002 (first entry)
XX Rat Glut1 mutant 69M coding sequence.
XX Rat; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
XX vector; mutant; ds.
XX Rattus norvegicus.
XX Synthetic.
XX WO200264784-A2.
XX 22-AUG-2002.
XX 09-FEB-2002; 2002WO-EP001373.
XX 14-FEB-2001; 2001DE-01006718.
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
XX Mueller G, Koller K, Boles E, Wieszorke R, Dlugai S;
XX WPI; 2002-636632/68.
XX New strains of yeast, useful in screening for modulators of hexose
XX transport, potential antidiabetic and antiobesity agents, lack native
XX hexose-transport function.
XX Claim 19; Page 41-42; 58pp; German.
XX The present invention relates to a strain of Saccharomyces cerevisiae
XX that cannot grow on a substrate containing hexose as the only source of
XX carbon but the ability to grow on such substrates is restored when the
XX GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
XX GLUT4 genes can be used to identify compounds that increase/reduce hexose
XX transport by these proteins. These compounds, optionally after
XX development, are potential drugs for treating diabetes and obesity. The
XX present sequence is a mutant version of the rat Glut1 coding sequence as
XX used in the invention
XX Sequence 2338 BP; 539 A; 611 C; 538 G; 650 T; 0 U; 0 Other;

Query Match 62.4%; Score 1488.8; DB 6; Length 2338;
Best Local Similarity 77.8%; Pred. No. 0;
Matches 1856; Conservative 0; Mismatches 482; Indels 48; Gaps 3;

QY 1 TCGACTCTAGAGGATCCCTTAACTAATCTTATGATATCCGAGAAAGCGGGTCTTT 60
DB 1 TCGACTCTAGAGGATCCCTTAACTAATCTTATGATATCCGAGAAAGCGGGTCTTT 60
QY 61 TAACCTCAATAAATTTTCCGAAATCCTTTTCTACCGGTTTCTTCCGGAACCTAGATAG 120
DB 61 TAACCTCAATAAATTTTCCGAAATCCTTTTCTACCGGTTTCTTCCGGAACCTAGATAG 120
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QY 121 GTGGCTCTCCACTGTTTTCATCATTTTGTGTTTTCGAAAGCAATGCGTCCCTTTTC 180
DB 121 GTGGCTCTCCACTGTTTTCATCATTTTGTGTTTTCGAAAGCAATGCGTCCCTTTTC 180
QY 181 GTTTTTCGATGCGAACAGGCTCGAAATTTAAAGGTACCGCTTAACCATAGTAA 240
DB 181 GTTTTTCGATGCGAACAGGCTCGAAATTTAAAGGTACCGCTTAACCATAGTAA 240
QY 241 TAGGCCACGCAACTGGCGTGGAGCAACAAATAGTCCGCCATTTTATGTTTCAAAA 300
DB 241 TAGGCCACGCAACTGGCGTGGAGCAACAAATAGTCCGCCATTTTATGTTTCAAAA 300
QY 301 CTTAGCAACCCCAACCAACTGTGTATGTTCCCGGATTCACAAATGATATAAAGCGA 360
DB 301 CTTAGCAACCCCAACCAACTGTGTATGTTCCCGGATTCACAAATGATATAAAGCGA 360
QY 361 TTACAATTTACATCTTAACAGATTTGAGATTTCTCTTCTCAATTTCTCTTATATTA 420
DB 361 TTACAATTTACATCTTAACAGATTTGAGATTTCTCTTCTCAATTTCTCTTATATTA 420
QY 421 GATTATAAGAAACAAATTAATTAACAAAGACTTTATAAGCAACATATGTTCTGAAT 480
DB 421 GATTATAAGAAACAAATTAATTAACAAAGACTTTATAAGCAACATATGTTCTGAAT 480
QY 481 TCCAGCAGATCGGCTCTGAAGATGGGAAACCCCTCTAGCAGCAGTGAATGGGACACTGG 540
DB 481 TCAGCAAGA-----AGGTGACGGGCGGCTTA 507
QY 541 TCCCTGCTGTATTTCTCAGCTGTCTGGCTCCCTCAGTTTGGCTATTAACATTTGGAGTCA 600
DB 508 TGTGGCGGTGGAGGGGAGTGTCTGGATCCCTTGCAAGTTTGGCTATAACACCGGTGTCA 567
QY 601 TCAACGCCCAACAGAAAGTGAATGAACAGAGCTACAAATGCAATCTTGGCTGGTAGGCAGG 660
DB 568 TCAACGCCCAACAGAAAGTGAATGAAGAGTGTCTACAAATCAACATGAACACCGCTATG 627
QY 661 GTCCCTGGGGACCGGACTCATCCCAACAGGCAACCTCTACATCCCTTGGGCTCTCTCCG 720
DB 628 G-----AGAGTCCATCCCACTCCACCACTCACCACACTCTGGTCTCTCTCCA 675
QY 721 TGGCCATCTCTGTGGGTGGCATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCAAT 780
DB 676 TGGCCATCTCTGTGGGTGGCATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 735
QY 781 GGTGGGAAGAAAGGGCTATGCTGGCCCAACAAATCTTGGCTGTCTGGGGGGGGCCCC 840
DB 736 GCTTTGGCAGCGGAACCTCATGCTGATGATGAACCTGTTGGCTTTGTCTGCGGTGC 795
QY 841 TCATGGGCTTAGCCAAATGCGCGGCTCTCTATGAGATCTCATCTCGGACGTTCTCTCA 900
DB 796 TTATGGGTTTCTCCAAACTGGGCAAGTCTTTGAGATGCTGATCTCTGGGCGGCTTCATCA 855
QY 901 TTGGCGCTTACTCAGGCTTAACATCAGGTTGCTGCTATGATGTTGGGGAATCGCCC 960
DB 856 TTGGAGTGTACTGTGGCTTACCACCGGCTTTGTGCCATGATGTTGGGGAGGTGTAC 915
QY 961 CCACTCATCTTGGGGTGGCTTGGGAACACTCAACAAATTTGGCCATCGTCAATTTGGCATTC 1020
DB 916 CCACAGCTCTTGTGGAGCCCTGGGACCCCTGACCCAGCTGGGCACTGTTGGGATCC 975
QY 1021 TGGTGGCCAGGTGTTGGGTTTGGAGTCTATGCTGGGCAACAGTACCTCTGTGGCCATGTC 1080
DB 976 TTATTTGCCAGGTGTTGGGCTTAGACTTCACTCATATGAGGCAATGAGACTTTGGGCTCTAC 1035
QY 1081 TTCTGGCTATCACAGTACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
DB 1036 TGCTCAGTGTCTCTCATCCAGCCCTGTCTACAGTGTATCTCTGTGCTCTCTCTCTCTCTCT 1095
QY 1141 AGAGCCCCGATACCTCTACATCATCCGAACTGGAGGGGCTGCGCCGAAAGAGTCTAA 1200
DB 1096 AGAGCCCCGCTTCT 1155
QY 1201 AGCGCTGACAGGCTGGGCTGTGTGTCTGATGCACTGGCTGAGCTGAAGGATGAGAAAC 1260

DB 1156 AAAAGCTTCGAGGGAAGCGGATGTGACCCGAGACCTGCGAGGATGAAGAAAGAGGGTC 1215
QY 1261 GGAAGTTTGAAGAGAGAGGCTCCACTGCTCTGCTGAGCTCTCTGGGCGAGCCGACCCACC 1320
DB 1216 GGCAGATGATCGGGAAGAAGGTCAACATCTTGGAGCTGTTCCGCTCAACCGCTTACC 1275
QY 1321 GGCAGCTCTGATTTATTTGAGTGGTCTGCTGAGCTGAGCCAGCAGCTCTCAGGCAATCAATG 1380
DB 1276 GCCAGCCCATCTCTCATCGCGTGGTCTGAGCTGTCCCAGCAGCTGTGCGGCATCAATG 1335
QY 1381 CTGTTTTCTACTATTCAACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCCAGCTTACG 1440
DB 1336 CTGTGTTTACTACTCAACAGCATCTTCGAGAAGCAGGTGTGACAGCAGCTGTGTATG 1395
QY 1441 CCACCATAGGAGCTGTGTGTTCAATACCGTCTTCACTGTTGGTCTGGTCTCTTAGTAG 1500
DB 1396 CCACCATGGCTCGGTGATGCTCAACAGGCTTCACTGTTGGTCTGGTCTCTTAGTAG 1455
QY 1501 AGCAGCTGGGGAAGGACACTCTCTCTGGGCTGGCAGGCAATGTGTGGTGTGCCA 1560
DB 1456 AGCAGCTGGGCTGGGACCTCTCATCTCACTGCTGTGGCTGGCATGGGCGCTGTGCTG 1515
QY 1561 TCTTGATGAGGCTGCTCTGCTGCTGAGGCGGTTCCATCCATGAGTTATGTGCCA 1620
DB 1516 TGCTCATGACCATCGCCCTGGCCCTGCTGAGCAGCTGCCCCTGATGCTCTATCTAGTA 1575
QY 1621 TGTGGCCATATTTGGCTTTTGGCTCTCTTTCAGATTTGCTCTGCGCCCATCCCTGCT 1680
DB 1576 TGTGGCCATCTTTGGCTTTTGGCTCTCTTTCAGATTTGCTCTGCGCCCATCCCTGCT 1635
QY 1681 TCATTTGGCCGAGCTCTTTCAGCAGGCGCCCGCCAGCAGCAGCTAGCTGTAGCTGTT 1740
DB 1636 TCATTTGGCCGAGCTTTCAGCAGGCGCCCGCCAGCAGCTGCTGTGCTGTGGCTGCT 1695
QY 1741 TCTCAGCTGAGCTGTAACTTTCATCTGTTGGCATGAGTTTCCAGTATGTTGGGATGCTA 1800
DB 1696 TCTCTAACTGGACCTCAAACTTCATCTGTTGGCATGTTCTTCAATATGTTGGAGCACTGT 1755
QY 1801 TGGGCTCCCTAGCTTCTCTTCTTATTTGCGCTCTCTGCTGCTGCTGCTCTTCTTCACTT 1860
DB 1756 GTGGCCCTTACGCTTCTTCTATCTTCACTTCCAGGCTGCTGCTGCTCTTCTTCTTCACT 1815
QY 1861 TCTAAGAGTGGCTGAAACAGAGGCGGCACTTTGACAGAGCTCTCGGCCACCTTCCGAC 1920
DB 1816 ACTTCAAAGTCTCTGAGACCAAGGCGGACCTTTCGATGAGATCGCTTCCGGCTTCCGGC 1875
QY 1921 GGCACCTTCTCTTTAGAGCAGGAGGTGAACCCAGTACAGAACTTTGAATATCTTAGGGC 1980
DB 1876 AGGGGGTGC---CAGCCAGAGCGCAAGACACTGAGGAGCTCTTCCACCTCTGGGGG 1932
QY 1981 CAGATGAGAACTGAATTAATCGATTTGAAGTGAGAGCTCCATCATCTCTCTTAAATTTTCA 2040
DB 1933 CTGACTCCCAAGTGAATCGATTTGAAGTGAGAGCTCCATCATCTCTCTTAAATTTTCA 1992
QY 2041 TGACTGACGTTTTTCTTCTTCAATTTAATATCATAGTATTTGTTGAAAAAATAAAAAA 2100
DB 1993 TGACTGACGTTTTTCTTCTTCAATTTAATATCATAGTATTTGTTGAAAAAATAAAAAA 2052
QY 2101 AATTTCCCTTATCAATGATATCTTACGATTTATATAAATCTTACCTAAACCTTATTT 2160
DB 2053 AATTTCCCTTATCAATGATATCTTACGATTTATATAAATCTTACCTAAACCTTATTT 2112
QY 2161 TGTGTACATATATCAGAGTATTTATACATATATAAATCTTCTTAAACAGGAAAAA 2220
DB 2113 TGTGTACATATATCAGAGTATTTATACATATATAAATCTTCTTAAACAGGAAAAA 2172
QY 2221 AAAAGAAAAAGTAAACATGCTCTGCCATCTTTGTTTCCGAGCAAAATTTAAAAACGCA 2280
DB 2173 AAAAGAAAAAGTAAACATGCTCTGCCATCTTTGTTTCCGAGCAAAATTTAAAAACGCA 2232
QY 2281 AATGAATTTGCTTATGAATTTATTAAGGACCATATCACCAGACTTATCTCTGGGGGT 2340

Db 2233 AATGAATTGTCCTATGAAATTAATAAGGACCACATCACAGACTTATCTCTGGGGGT 2292

Qy 2341 CCTCTAGAAATAAGTCAAGTACTTGCCTGGACTTCTTCCAGTTG 2386

Db 2293 CCTCTAGAAATAAGTCAAGTACTTGCCTGGACTTCTTCCAGTTG 2338

RESULT 4

AAI49315

ID AAL49315 standard; DNA; 2338 BP.

XX

AC AAL49315;

XX

DT 07-NOV-2002 (first entry)

XX

DE Rat Glut1 mutant 70M coding sequence.

XX

KW Rat; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;

XX

KW vector; mutant; ds.

XX

OS Rattus norvegicus.

OS Synthetic.

XX

PN WO200264784-A2.

XX

PD 22-AUG-2002.

XX

PF 09-FEB-2002; 2002WO-EP001373.

XX

PR 14-FEB-2001; 2001DE-01006718.

XX

PA (AVET) AVENTIS PHARMA DEUT GMBH.

XX

PI Mueller G, Koller K, Boles E, Wiczorke R, Dlugai S;

XX

DR WPI; 2002-636632/68.

XX

PT New strains of yeast, useful in screening for modulators of hexose

PT transport, potential antidiabetic and antiobesity agents, lack native

PT hexose-transport function.

XX

PS Claim 24; Page 42-43; 58pp; German.

XX

CC The present invention relates to a strain of *Saccharomyces cerevisiae*

CC that cannot grow on a substrate containing hexose as the only source of

CC carbon but the ability to grow on such substrates is restored when the

CC GLUT4 gene is expressed. A strain transformed to express the GLUT1 or

CC GLUT4 genes can be used to identify compounds that increase/reduce hexose

CC transport by these proteins. These compounds, optionally after

CC development, are potential drugs for treating diabetes and obesity. The

CC present sequence is a mutant version of the rat Glut1 coding sequence as

CC used in the invention

XX

SQ Sequence 2338 BP; 539 A; 609 C; 539 G; 651 T; 0 U; 0 Other;

Query Match 62.3%; Score 1485.6; DB 6; Length 2338;

Best Local Similarity 77.7%; Pred No. 0;

Matches 1854; Conservative 0; Mismatches 484; Indels 48; Gaps 3;

Qy 1 TCGACTCTAGAGATCCCTTAAAGCTAATCCTTATGAATCCGAGAAAGCGGGTCTTT 60

Db 1 TCGACTCTAGAGATCCCTTAAAGCTAATCCTTATGAATCCGAGAAAGCGGGTCTTT 60

Qy 61 TAACTCAATAAATTTTCGAAATCCTTTTCTACGGGTTTCTTCGGGAAGTATAG 120

Db 61 TAACTCAATAAATTTTCGAAATCCTTTTCTACGGGTTTCTTCGGGAAGTATAG 120

Qy 121 GTGGCTCTTCCACCTGTTTTTCATCATTTTAGTTTTCGCAAGCATGCGTCTTTC 180

Db 121 GTGGCTCTTCCACCTGTTTTTCATCATTTTAGTTTTCGCAAGCATGCGTCTTTC 180

Qy 181 GTTTTTCGATCGGCAACGAGGCTGGAAAAATTAACGGTACGCGCTTAACGATAGTAA 240

Db 181 GTTTTTCGATCGGCAACGAGGCTGGAAAAATTAACGGTACGCGCTTAACGATAGTAA 240

Qy 241 TAGGCCACGCAACTGGCGTGGACGACAAATATAGTGCCTTATTTTATGTTTCAAAA 300

Db 241 TAGGCCACGCAACTGGCGTGGACGACAAATATAGTGCCTTATTTTATGTTTCAAAA 300

Qy 301 CCTAGCAACCCCAACCAAACTTGTCTGTTCCCGGATTACAAATGATATAAAAAGCGA 360

Db 301 CCTAGCAACCCCAACCAAACTTGTCTGTTCCCGGATTACAAATGATATAAAAAGCGA 360

Qy 361 TTACAATTTACATTTTAAACAGATTTTCAATTTCTCTCAATTTCTCTTATATA 420

Db 361 TTACAATTTACATTTTAAACAGATTTTCAATTTCTCTCTTCTCAATTTCTCTTATATA 420

Qy 421 GATTATAGCAACAAATTAATAAATTAACAAGACTTATAAGCAACATATGTTCTGAT 480

Db 421 GATTATAGCAACAAATTAATAAATTAACAAGACTTATAAGCAACATATGTTCTGAT 480

Qy 481 TCCAGCAGATCGGCTCTGAAGATGGGAAACCCCTCAGCAGCGAGTGAACCACTGG 540

Db 481 TCAGCAAGA-----AGGTGACGGGCGCCTTA 507

Qy 541 TCCTTGCTGATTTCTCAGCTGTGCTTGGCTCCCTTCACTTTGGGCTATTAACATGGAGTCA 600

Db 508 TGTGGCGGTGGAGGGGCGAGTCTCGGATCCCTGCACTTCCGCTATTAACACCGGTGTCA 567

Qy 601 TCACGCGCCACAGAAAGTGAATGAACAGAGTCAATGCAACTTGGCTGGGTAGGCAGG 660

Db 568 TCAACGCGCCCAAGAGGTAATTGAGGAGTTCTCAATCAAAACATGGAAACCAACCGCTATG 627

Qy 661 GTCCTGGGGACCGGACTCCATCCCAAGGCAACCTCCTTACCTTGGGCTCTCTCCG 720

Db 628 G-----AGAGTCCATCCATCCACCACTCACCACACTCTGGTCTCTCTCCG 675

Qy 721 TGGCCATCTTCTGTTGGGTGGCAATGTTCTCTTCTCATTTGGCAATCATTTCTCAAT 780

Db 676 TGATGATCTTCTGTCGGGGCATGATTTGGTTCCTTCTCTGTGGGCTCTTTGTTAATC 735

Qy 781 GGTGGGAAGGAAGGGCTATGCTGGCAACATGTTCTGGCTCTGCTGGGGGGCGCC 840

Db 736 GCTTTGGCAGGCGGAATCCATGCTGATGATGAACCTGTTGGCCTTTGTGTCTGGCTGC 795

Qy 841 TCATGGCCCTAGCAATCGCGCGCTCTCTATGAGACTCATTTCTCGGACGGTTCTCTCA 900

Db 796 TTATGGGTTCTTCAAACTGGCAAGTCTTTGAGATGCTGATCTTGGGCGCTTCACTCA 855

Qy 901 TTGGCGCTTACTCAGGCTAACATCAGGTTGGTGGCTTATGATGTGGGAGAAATCGCC 960

Db 856 TTGAGTGTACTGTGGCTGACCAACCGGCTTTGTGCCCATGTATGTGGGGAGGTGTAC 915

Qy 961 CCATCATCTTGGGGTGGCTTGGGAACACTCAACCAATTCGCCCATCTGTTGGCATTC 1020

Db 916 CCACAGCTCTTGTGGAGCGCTGGGCAACCTGCAACCTGCGGCACTGTTGGATCC 975

Qy 1021 TGGTTGCCAGGTTTGGGTTTGGAGTCTATGCTGGGCAACAGTACCTTGTGGCCATTCG 1080

Db 976 TTATGGCCAGGTTTGGCTTAGACTCCATCATGGGCAATGACAGACTTGTGGCTCTAC 1035

Qy 1081 TTTGGGCTATCAGTACTCTCTCTCTGAGTGTCTTGTGGCTCTCTGCTCTCTGCTG 1140

Db 1036 TGCTCAGTGTATCTTCAACCGCTGCTACAGTGTATCTGTTGGCTCTCTGCTCTG 1095

Qy 1141 AGAGCCCCGATACCTCTACATCATCGGAACCTGGAGGGCGCTGCGGAAAGAGTCTAA 1200

Db 1096 AGAGCCCCGCTTCTCTCTCATCAATGTAACAGAGGAACCGGGCCAGAGTGTGCTGA 1155

Qy 1201 AGCGCTTACAGGCTGGGCTGATGTGTGTGATGCACTGGCTGAGCTGAAGGATGAGAAAC 1260

Db 1156 AAAAGCTTCGAGGGACAGCGGATGTGACCCGAGACCTGACAGAGATGAAGAAGAGGTC 1215

Qy 1261 GGAAGTTGGAAGAGAGGCTCCACTGCTTGTGCTGAGCTCTCTGGGAGCGGCAACCCACC 1320

Db 1216 GGCAGATGATGCGGGAGGAAGAGGTCCACTTCTTGGAGCTGTTCGCTCAACCCGCTACC 1275

RESULT 5	
AAAL49310	
ID	AAAL49310 standard; DNA; 7828 BP.
XX	
XX	AAAL49310;
XX	
DT	07-NOV-2002 (first entry)
XX	
DB	Human Glut4 containing vector YEP4H7-HsGLUT4.
XX	
XX	Human; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
KW	vector; ds.
KW	
XX	
OS	Homo sapiens.
XX	
XX	WO200264784-A2.
PN	
XX	
PD	22-AUG-2002.
XX	
PF	09-FEB-2002; 2002WO-EP001373.
XX	
XX	
PR	14-FEB-2001; 2001DE-01006718.
XX	
XX	(AVET) AVENTIS PHARMA DEUT GMBH.
PA	
XX	
PI	Mueller G, Koller K, Boles E, Wieszorke R, Dlugai S;
XX	
XX	WPI; 2002-636632/68.
DR	
XX	
PT	New strains of yeast, useful in screening for modulators of hexose
PT	transport, potential antidiabetic and antiobesity agents, lack native
PT	hexose-transport function.
XX	
PS	Claim 10; Page 34-36; 58pp; German.
XX	
CC	The present invention relates to a strain of Saccharomyces cerevisiae
CC	that cannot grow on a substrate containing hexose as the only source of
CC	carbon but the ability to grow on such substrates is restored when the
CC	GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
CC	GLUT4 genes can be used to identify compounds that increase/reduce hexose
CC	transport by these proteins. These compounds, optionally after
CC	development, are potential drugs for treating diabetes and obesity. The
CC	present sequence is a vector containing the human Glut4 coding sequence
CC	as used in the invention
XX	
SQ	Sequence 7828 BP; 2009 A; 1928 C; 1771 G; 2120 T; 0 U; 0 Other;
Query Match	51.5%; Score 1229; DB 6; Length 7828;
Best Local Similarity	85.8%; Pred. No. 2e-290;
Matches 1364; Conservative	0; Mismatches 225; Indels 0; Gaps 0
Qy	468 ATATGTCGTGAATTCACGACATCGGCTCTGAAGATGGGAAACCCCTCAGCAGCGAGTG 527
DB	1 ATGCGTCGGGCTTCCAAACAGATAGGCTCCGAAGATGGGAAACCCCTCAGCAGCGAGTG 60
Qy	528 ACTGGGACATGGTCCTTGCTGTATTCTCAGCTGTGCTTGGCTCCCTTCAGTTTGGCTAT 587
DB	61 ACTGGGACCTCGTGCCTTGCTGTGTTCTCTCGGTGCTTGGCTCCCTGCACTTGGGTAC 120
Qy	588 AACATTGGAGTCATCAACGCCGCCACAGAAAGTGATTGAACAGAGCTACAAATGCAACTGG 647
DB	121 AACATTGGGTGTCATCAATGCCCCCTCAGAGGTGATTGAACAGAGCTACAAATGAGACGTG 180
Qy	648 CTGGGTAGGCGAGGTCTCTGGGGGACCGGACTCCATCCCAAGGCAACCTCACTACCTTT 707
DB	181 CTGGGAGGCGAGGGGCTCTGAGGGAACCCAGCTCCATCCCTCTCAGGCAACCTCAACCCCTC 240
Qy	708 TGGGCTCTCTCCGTGGGCATCTTCTCTGTGGGTGCGATGATTTCTCTCTTCTCTCATTTGG 767
DB	241 TGGGCCCTCTCCGTGGGCATCTTTTTCGTGGGCGCATGATTTCTCTCTTCTCTCATTTGT 300
Qy	768 ATCATTTTCTCAATGGTTGGGAAGAAAGGGCTATGCTGGCCAAACAATGCTTTGGCTGTG 827

Db 301 ATCATCTCTCAGTGGCTTGGAAAGGAAAGGGCCATCTGCTGCTCAACAATGCTCGCGGTG 360
QY 828 CTGGGGGGCGCCCTCATATGGCCCTAGCCATATCGCGGGCTCTATGATGATCTATCTTC 887
Db 361 CTGGGGGGGAGCTCTCATATGGGGCTGGCCAAAGCTGCTGCTCTCTATGAAATCTCATCC 420
QY 888 GGACGGTCTCTCATATGGGGCCCTACTCAGGGCTTAACATCAGGGTGGTGGCTATGATGTG 947
Db 421 GGACGATCTCTCATATGGGGCCCTACTCAGGGCTGACATCAGGGCTGGTGGCCATGTACGTG 480
QY 948 GGAGAAATCGCCCGCCCATCATCTTCTGGGGTGGCTTGGGAAACATCAACAAATGGCCCATC 1007
Db 481 GGAGAAATGTCTCCCACTCACCTCGCGGGCGCCCTGGGGAGCGCTCAACCAATGGCCCAT 540
QY 1008 GTCAATGGCAATCTGGTGGCCAGGTGTGGGTTGGAGTCTATGCTGGGACAGCTACC 1067
Db 541 GTTATCGGCAATCTGATCGCCAGGTGTGGGCTTGGAGTCCCTCGGGCACTGCCAGC 600
QY 1068 CTGTGGCCATCTGCTTCTGGCTATCAGTACTCCTGCTCTGCTGAGCTGCTTCTGTG 1127
Db 601 CTGTGGCCATCTGCTTCTGGGCTCAGTGTACTCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 1128 CCTTCTGTCTGAGAGCCCGCATACCTCTATCATATCCGGAACCTGGAGGGCCCTGCC 1187
Db 661 CCTTCTGTCTGAGAGCCCGCATACCTCTATCATATCCGGAATCTCGAGGGCCCTGCC 720
QY 1188 CGAAGAGTCTAAGGCGCTGACAGGCTGGGCTGATGTCTGATGCTGCTGCTGCTGCTG 1247
Db 721 AGAAGAGTCTAAGGCGCTGACAGGCTGGGCGGATGTTCTGGAGTCTGGGCTGAGCTG 780
QY 1248 AAGGATGAGAAACGGAAGTTGGAAGAGAGCTCCACTGCTGCTGCTGCTGCTGCTGCTG 1307
Db 781 AAGGATGAGAAACGGAAGTTGGAAGAGAGCTGAGGCGTGAAGGCGCACTGCTGCTGCTG 840
QY 1308 AGCGGACCCACCGGAGCTCTGATTAATGAGTGGTGTGCTGCTGCTGCTGCTGCTGCTG 1367
Db 841 AGCGGTACCCACCGGAGCTCTGATTAATGAGTGGTGTGCTGCTGCTGCTGCTGCTGCTG 900
QY 1368 TCAGGCTCATGCTGCTTCTTCTATTTCAACAGAGCTTCTGAGTGGTGGGCTGGAA 1427
Db 901 TCTGGCATCAATGCTGCTTCTTCTATTTCAACAGAGCTTCTGAGAGAGAGGCTGAGG 960
QY 1428 CAGCAGCTCAGCCACCATAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1487
Db 961 CAGCCTGCTATGCCACCATAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1488 GTGCTCTTATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1547
Db 1021 GTGCTTGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1548 TGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1607
Db 1081 TGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1608 AGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1667
Db 1141 AGCTAGCTCTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1668 CCCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1727
Db 1201 CCCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1728 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1787
Db 1261 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1788 GTTGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1847
Db 1321 GTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1848 TTCATCTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1907

Db 1381 TTCATCTTCCATCTTCTTAAAGAGTACCTGAAACTCGAGCCGAGCGTTTGGACAGATCTCA 1440
QY 1508 GCCACCTTCCGAGCAGACACCTTCTCTCTAGAGCAGAGGTGAACCCAGTACAGACTT 1967
Db 1441 GCTGCCCTTCCACCGGACACCTCTCTCTTCTAGCAGAGGTTGAACCCAGCAGACTT 1500
QY 1568 GAATACTTAGGGCCAGATGAGAAATGACTTAATTCGATTTTGAAGTGAGAGCTCCATCATCTC 2027
Db 1501 GAGTATTTAGGGCCAGATGAGAAACGACTGATAAGCTTATCATCCGCTCGAGCTCGAGTC 1560
QY 2028 TCTTAATTTTCAGTACGAGTGTTC 2056
Db 1561 ATGTAATTAGTTATGTCAAGCTTACATTC 1589

RESULT 6

AAF81396

ID AAF81396 standard; cDNA; 2592 BP.

XX AAF81396;

XX AC AAF81396;

XX DT 05-JUN-2001 (first entry)

XX XX Coding sequence for modified GLUT4.

XX XX GLUT4 glucose transporter; insulin; protein translocation;

XX KW insulin resistance; adult-onset diabetes; obesity;

XX KW polycystic ovary syndrome; ss.

XX OS Unidentified.

XX XX WO200075188-A1.

XX XX 14-DEC-2000.

XX XX 09-JUN-2000; 2000WO-US015904.

XX XX 09-JUN-1999; 99US-0138237P.

XX XX 15-SEP-1999; 99US-0154078P.

XX XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX XX (GEHO) GEN HOSPITAL CORP.

XX XX Bogan JS, Lodish H;

XX XX WPI; 2001-050022/06.

XX XX P-PSDB; AAB80940.

XX XX Assessing translocation of proteins such as glucose transporter GLUT4,

XX XX cystic fibrosis transmembrane conductance regulator by using modified

XX XX protein of interest comprising the protein and detectable tags.

XX XX Disclosure; Fig 8; 75pp; English.

XX XX The present sequence is the coding sequence for a modified GLUT4 glucose

XX XX transporter. Insulin stimulates glucose uptake in muscle and adipose

XX XX tissue by causing translocation of the GLUT4 glucose transporter from an

XX XX intracellular compartment to the plasma membrane. This results in an

XX XX increase in the number of cell-surface GLUT4 transporters and therefore

XX XX an increased rate of glucose entry into cells. The modified GLUT4

XX XX protein of interest (e.g. GLUT4) from an intracellular location to the

XX XX plasma membrane in mammalian cells, when the cells are exposed to a

XX XX condition or a stimulus. The method is useful for assessing the effect

XX XX of a drug on translocation of a protein such as GLUT4. Such drugs are

XX XX useful in treating insulin resistance such as in adult-onset diabetes,

XX XX obesity and polycystic ovary syndrome. The modified GLUT4 transporter

XX XX CC encoded by the present sequence has myc epitope tags (see AAB80939) and a

XX XX GFP fluorescent tag

XX XX

SQ Sequence 2592 BP; 545 A; 767 C; 733 G; 547 T; 0 U; 0 Other;

Query Match

44.7%; Score 1066.4; DB 5; Length 2592;


```
Best Local Similarity 87.5%; Pred. No. 8.7e-251;
Matches 1166; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 663 CTGGGGGACCGGACTCCATCCACAGGACACCTCACTACCTCTTGGGCTCTCTCCGTG 722
Db 511 CTTAAGGACCCAGCTCCATCCCTCAGGACACCTCAACACCTCTGGGCTCTCCGTG 570
QY 723 GCATCTTCTCTGGGTGCGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db 571 GCATCTTCTCTGGGTGCGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 630
QY 783 TTGGGAAGGAAGAGGCTATGCTGGGCAACAATGCTCTGGCTCTGGGGGGGCGCCCTC 842
Db 631 CTTGGGAAGGAAGAGGCTATGCTGGGCAACAATGCTCTGGCTCTGGGGGGGCGCCCTC 690
QY 843 ATGGGCTCTAGCAATGCGCGGCTCTCTATGAGATCTCATTTCTCGGACGGTTCTCAIT 902
Db 691 ATGGGCTCTAGCAATGCGCGGCTCTCTATGAGATCTCATTTCTCGGACGGTTCTCAIT 750
QY 903 GGGGCTCTACAGGGCTAATCATCAGGGTTGGTGGCTATGATGTGGAGAAATCGCCCCC 962
Db 751 GGGGCTCTACAGGGCTAATCATCAGGGCTGGTGGCTATGATGTGGAGAAATCGCCCCC 810
QY 963 ACTCATCTTGGGGTCTTGGGAACACTCAACCAATGGCCATCGTCAATGGCATTCG 1022
Db 811 ACTCATCTTGGGGTCTTGGGAACACTCAACCAATGGCCATCGTCAATGGCATTCG 870
QY 1023 GTTGGCCAGGTGTGGGTTTGGAGTCTATCTGGGACAGCTACCTCTGGGCCATTTGCTT 1082
Db 871 ATGGCCAGGTGTGGGTTTGGAGTCTATCTGGGACAGCTACCTCTGGGCCATTTGCTT 930
QY 1083 CTGGCTATCAGATCTCCCTGCTCTCTGACGTCTCTGTGGCTCTCTGTCTCTCTGAG 1142
Db 931 CTGGCTATCAGATCTCCCTGCTCTCTGACGTCTCTGTGGCTCTCTGTCTCTCTGAG 990
QY 1143 AGCCCGGATACCTCTACATCATCCGNACTCGGAGGGCTCGCCGAAAGAGCTCTAAG 1202
Db 991 AGCCCGGATACCTCTACATCATCCGNACTCGGAGGGCTCGCCGAAAGAGCTCTAAG 1050
QY 1203 CGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTGAAGATGAGAAACGG 1262
Db 1051 CGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTGAAGATGAGAAACGG 1110
QY 1263 AAGTTGGAAGAGAGCTGCTCACTGTCTCTGCTGAGCTCTGGGAGCGCCACCCACGG 1322
Db 1111 AAGTTGGAAGAGAGCTGCTCACTGTCTCTGCTGAGCTCTGGGAGCGCCACCCACGG 1170
QY 1323 CAGCTCTGATTTATTCAGTGTGTCTGACGTGAGCCAGCAGCTCTCAGGCATCAATGCT 1382
Db 1171 CAGCTCTGATTTATTCAGTGTGTCTGACGTGAGCCAGCAGCTCTCTGGCATCAATGCT 1230
QY 1383 GTTTTCTACTATTCAACCAAGCATCTTTAGTTAGCTGGGTTGGAACAGCAGCCTACGCC 1442
Db 1231 GTTTTCTACTATTCAACCAAGCATCTTTAGTTAGCTGGGTTGGAACAGCAGCCTACGCC 1290
QY 1443 ACCATAGGAGCTGGTGTGTCANAACGCTTTCAGCTGTCTGGGAGCGCCACCCACGG 1502
Db 1291 ACCATAGGAGCTGGTGTGTCANAACGCTTTCAGCTGTCTGGGAGCGCCACCCACGG 1350
QY 1503 CGAGCTGGGAGCGGACATCTCCATCTCTGGGCTGGCAGCATGTGGCTGTGCCATC 1562
Db 1351 CGAGCTGGGAGCGGACATCTCCATCTCTGGGCTGGCAGCATGTGGCTGTGCCATC 1410
QY 1563 TTGATGACGGTGGCTCTGTCTGTCTGGAGCGGTTCCATCCATGATGTTATGTGCCATC 1622
Db 1411 TTGATGACGGTGGCTCTGTCTGTCTGGAGCGGTTCCATCCATGATGTTATGTGCCATC 1470
QY 1623 GTGGCCATATTTGGCTTTGGGCTCTTTGAGATTTGGTCTGGCCCCCATCCCTGGTTC 1682
Db 1471 GTGGCCATATTTGGCTTTGGGCTCTTTGAGATTTGGTCTGGCCCCCATCCCTGGTTC 1530
QY 1683 ATTGTGGCCAGCTCTTTGAGCAAGGCCCCCGCCAGCAGCATGCTGTAGCTGGTTTC 1742
Db 1742 ATTGTGGCCAGCTCTTTGAGCAAGGCCCCCGCCAGCAGCATGCTGTAGCTGGTTTC 1700

Db 1531 ATGCTGGCGAGCTCTTACGACGAGGACCCCGCCGACGCAATGGCTGTGGCTGTTTC 1590
QY 1743 TCCAACTGGACCTGTAACTTTCATCGTTGGCATGGGTTTCCAGTATGTTGGGATGCTATG 1802
Db 1591 TCCAACTGGACGAGCAACTTTCATCGTTGGCATGGGTTTCCAGTATGTTGGGAGGCTATG 1650
QY 1803 GGTCCCTAGCTCTCTCTCTATTTTGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1862
Db 1651 GGGCCCTAGCTCTCTCTCTATTTTGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1710
QY 1863 CTAAGAGTCTCTGAAACACGAGCGCGGACATTTGACAGATCTCGGCCACCTTCCGACGG 1922
Db 1711 TTAAGAGTCTCTGAAACTCGAGCCCGAGCTTTGACAGATCTCGGCTGCTTCCACCG 1770
QY 1923 ACACCTTCTCTTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATACTTAGGSCCA 1982
Db 1771 ACACCTTCTCTTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATACTTAGGSCCA 1830
QY 1983 GATGAGAAATGAC 1994
Db 1831 GATGAGAAATGAC 1842

RESULT 7
ABL41106
ID ABL41106 standard; DNA; 2592 BP.
XX
AC ABL41106;
XX
DT 12-AUG-2002 (first entry)
XX
DE Modified GLUT4 encoding nucleotide sequence.
XX
KW Protein translocation; plasma membrane; GLUT-4; diabetes mellitus;
insulin; gene; GFP; green fluorescent protein; ds.
XX
OS Synthetic.
XX
Key Location/Qualifiers
CDS 1..2592
FT /*tag= a
FT /product= "modified GLUT4"
FT /note= "contains myc epitope tags and GFP"
FT misc_feature 1873..2592
FT /*tag= b
FT /note= "GFP"
XX
US2002052012-A1.
XX
PD 02-MAY-2002.
XX
XX 28-JUN-2001; 2001US-00894927.
XX
XX 22-MAY-1997; 97US-0047433P.
PR 09-JUN-1999; 99US-0138237P.
PR 15-SEP-1999; 99US-0154078P.
PR 09-JUN-2000; 2000US-00591025.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Bogan JS, Lodish HF;
XX
XX WPI; 2002-443696/47.
DR P-PSDB; ABB07975.
XX
XX Determining protein translocation to the plasma membrane of a mammalian
cell using a modified protein with an intracellular fluorescent tag and
an extracellular group tag, useful in finding new drugs, particularly to
treat diabetes.
XX
XX Example 1; Fig 8a-b; 34pp; English.
XX
XX The invention relates to determining if a protein translocates from an
```

CC intracellular location to the plasma membrane of a mammalian cell in the
CC presence of a condition or stimulus. The method involves modifying the
CC protein with a group tag in the extracellular domain and a fluorescent
CC tag in the intracellular domain and determining the proportion of total
CC protein which is at the membrane. The method is used to identify a drug
CC which enhances translocation of a protein from an intracellular location
CC to the plasma membrane of a mammalian cell. The method is particularly
CC used to measure GLUT-4 protein translocation to identify drugs to treat
CC insulin resistance in adult-onset diabetes mellitus. The invention
CC provides a less labour intensive quantitative method for measuring GLUT4
CC translocation than prior art methods. The present sequence represents a
CC modified GLUT4 nucleotide sequence, containing myc epitope tags and green
CC fluorescent protein (GFP) sequences
XX
SQ

Sequence 2592 BP; 545 A; 767 C; 733 G; 547 T; 0 U; 0 Other;

Query Match 44.7%; Score 1066.4; DB 6; Length 2592;
Best Local Similarity 87.5%; Pred. No. 8.7e-251;
Matches 1166; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 663 CTGGGGACCGGACTCCATCCCAAGGACCCCTCACTACGCTTGGGCTCTCCGTG 722
DB 511 CTTAAGGGACCCAGCTCCATCCCTCCAGGCAACCTCAACCCCTCTGGGCTCTCCGTG 570
QY 723 GCCATCTTCTGTGGGTGGCATGATTTCCCTTCTCATTTGGCATCATTTCTCAATGG 782
DB 571 GCCATCTTCTGTGGGTGGCATGATTTCCCTTCTCATTTGGCATCATTTCTCAATGG 630
QY 783 TTGGGAAGAAAGGGCTATGTGCGCAACAATGTTTGGGTGTGTGGGGGGCGCCCTC 842
DB 631 CTTGGAAGAAAGGGCTATGTGCGCAACAATGTTTGGGTGTGTGGGGGGCGAGCCTC 690
QY 843 ATGGGCTAGCAATGCGCGCCCTCTATGATGATCTATCTCGGACGGTTCCTCATTT 902
DB 691 ATGGGCTAGCAATGCGCGCCCTCTATGATGATCTATCTCGGACGGTTCCTCATTT 750
QY 903 GCGGCTACTCAGGGCTTAACATCAGGGTGTGTGCTATGATGATGAGAAATCGCCCC 962
DB 751 GCGGCTACTCAGGGCTGACATCAGGGTGTGTGCTATGATGATGAGAAATCGCCCC 810
QY 963 ACTCATTTTGGGGTGGCTTGGGAACATCAACCAATTTGGCATCGTCAATGGCATCTG 1022
DB 811 ACTCATTTTGGGGTGGCTTGGGAACATCAACCAATTTGGCATCGTCAATGGCATCTG 870
QY 1023 GTTGGCCAGGTCTGGGTGGAGTCTATGCTGGGACAGCTACCTGTGGCCATGCTT 1082
DB 871 ATCGCCCGAGGTCTGGGTGGAGTCTATGCTGGGACAGCTACCTGTGGCCATGCTT 930
QY 1083 CTGGCTATCACAGTACTCCCTGCTCTCTGCGAGTGTCTTCTGTGGCCCTCTGCTCTGAG 1142
DB 931 CTGGGCTCACAGTGTACTGCTGCTCTCTGCGAGTGTCTTCTGTGGCCCTCTGCTCTGAG 990
QY 1143 AGCCCGGATACCTTACATCATCCGAACTTGGAGGGGCTGCGGAAAGAGTCTAAAG 1202
DB 991 AGCCCGGATACCTTACATCATCCGAACTTGGAGGGGCTGCGGAAAGAGTCTGAG 1050
QY 1203 CGCCTGACAGGCTGGGTGATGTCTGATGCACTGGCTGAGCTGAGGATGAGAAAG 1262
DB 1051 CGCCTGACAGGCTGGGTGATGTCTGATGCACTGGCTGAGCTGAGGATGAGAAAG 1110
QY 1263 AAGTTGGAAAGAGCGCTCCACTGTCTTGTGCGAGTCTCTGGGCGAGCCGCCACCCCG 1322
DB 1111 AAGTTGGAGCGTGGAGCGGCTGCTGCTCTGCTGCGAGTCTCTGGGCGAGCCGTA 1170
QY 1323 CAGCTCTGATTTATGCGAGTGTGTGCGAGTGGAGCGAGCTCTCAAGCATCAATGCT 1382
DB 1171 CAGCCCTGATCATTTGCGGTGTGTGCGAGTGGAGCGAGCTCTCTGGCATCAATGCT 1230
QY 1383 GTTTTCTACTATTCAACAGCATCTTTTCAAGTGTGTGGGTGGAAACAGCCGCTAGCC 1442
DB 1231 GTTTTCTATTATTCAGCAGCATCTTCGAGCAGAGGGGTAGGCCAGCTGCTATGCC 1290
QY 1443 ACCATAGGAGCTGGTGTGGTCAATACCGTCTTTCAGTTGGTCTCGGTCTCTAGTAGAG 1502

DB 1291 ACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACTTGGTCTCGGTCTTGTGGTGGAG 1350
QY 1503 CGAGCTGGGCGAGCGACACTCCATCTCTTGGCCCTGGCAGCAGTGTGGCTGTGCCATC 1562
DB 1351 CGGCGCGGCGCGCGAGCTCCATCTCTTGGCCCTGGCAGCAGTGTGGCTGTGCCATC 1410
QY 1563 TTGATGACGGTGGTCTCTGCTGCTGCTGAGCGGGTCCATCCATGAGTTATGTGTCATC 1622
DB 1411 CTGATGACTGTGGTCTGCTCTCTGAGGCGAGTTCAGGCATGAGCTACGTCTCCATT 1470
QY 1623 GTGGCCATATTTGGCTTTTGTGGCTTCTTTCAGATTTGCTTGGCCCATCCCTGGTTTC 1682
DB 1471 GTGGCCATCTTGGCTTCTGCTGCTGAGTTCATTTTGGATTTGGCCCTGGCCCATTCCTTGGTTTC 1530
QY 1683 ATTGTGGCGAGCTCTTTCAGCAGGCGCCCGCCAGCAGCATGCTGTAGCTGTGGTTTC 1742
DB 1531 ATCTGGCGCGAGCTCTTTCAGCAGGCGCCCGCCAGCAGCATGCTGTAGCTGTGGTTTC 1590
QY 1743 TCCAACTGGACCTGTAACCTTTCATCTTGGCATGGTTCAGATGTTTCCAGTATGTTGGGAGCTATG 1802
DB 1591 TCCAACTGGAGGAGCAACTTCATCTTGGCATGGTTCAGATGTTTCCAGTATGTTGGGAGCTATG 1650
QY 1803 GGTCCCTACGTCTTCTTCTTATTTGGCGTCTCTCTGCTTGGCTTCTTCACTTTCACCTTC 1862
DB 1651 GGGCCCTACGTCTTCTTCTTATTTGGCGTCTCTCTGCTGGCTTCTTCACTTTCACCTTC 1710
QY 1863 CTAAGAGTCCCTGAAACCCAGAGCGCGGACATTTGACACAGATCTCGGCCACCTTCCGACGG 1922
DB 1711 TTAAGAGTACCTGAAACTCGAGGCGCGACGTTTGACACAGATCTCGGCTGCGCTTCCACCG 1770
QY 1923 ACACCTTCTCTTATGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATACCTTAGGGCCA 1982
DB 1771 ACACCTTCTCTTATGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATACCTTAGGGCCA 1830
QY 1983 GATGAGAATGAC 1994
DB 1831 GATGAGAATGAC 1842

RESULT 8

AAQ11148
ID AAQ11148 standard; cDNA; 2587 BP.

XX AAQ11148;

AC AAQ11148;

XX 04-JUN-1991 (first entry)

XX GTP-gene from Chinese Hamster Ovary cells.

XX Glucose transporter protein; serum-independence; CHO;

XX insulin-independence; ds.

XX Crictetus sp.

XX Key Location/Qualifiers

FT CDS 191..1669

FT /*tag= a

FT /product= "Glucose Transporter Protein"

XX WO9103554-A.

XX 21-MAR-1991.

XX 01-SEP-1989; 89US-00402204.

XX 01-SEP-1989; 89US-00402204.

XX 20-JUN-1990; 90US-00541426.

XX (GETH) GENENTECH INC.

XX Thomas JN, Williams SR;

XX

XX		23-OCT-1995;	95US-00546934.	
XX	PR	(TEXA) UNIV TEXAS SYSTEM.		
XX	PA	(BETA-) BETAGENE INC..		
XX	XX	Newgard CB, Clark SA, Thigpen AE, Normington KD; WPI; 1997-297737/27. P-PSDB; AAW17835.		
XX	PT	- used in negative and double selection protocols and screening methods, for cancer treatment and treatment of diabetes.		
XX	XX	Claim 138; Page 104-106; 169pp; English.		
XX	CC	This cDNA sequence codes for human glucose transporter GLUT-1 (AAW17835). A claimed polynucleotide comprises a contiguous nucleic acid sequence from human GLUT-1 cDNA and rat GLUT-2 cDNA (see AAW17835) . It encodes a GLUT-1/GLUT-2 chimeric transporter that confers glucose sensing capacity to a cell but which does not render the cell subject to diabetic immune destruction, and which does not transport streptozotocin. The claimed polynucleotide can be administered to a patient to treat diabetes, or expressed in a cell to prepare a recombinant cell that secretes insulin in response to glucose and which can be administered to a patient to treat diabetes		
XX	SS	Sequence 1815 BP; 324 A; 572 C; 520 G; 399 T; 0 U; 0 Other;		
QY		Query Match 28.5%; Score 679; DB 2; Length 1815; Best Local Similarity 68.1%; Pred. No. 7.2e-156; Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;		
QY	S0	506 GGAAACCCCCTCAGGCGAGTGACTGGGCACGTGGTTCCTTGCTGTATTTCTCAGCTGTGCT 565		
Dd		167 GGAGCCCCAGCAGCAAGAAGCTGACGGGTCCCTCATCTGGCTGTGGGAGGACGAGTGTCT 226		
QY		566 TGCGTCCCTTCAGTTTGCTATTACAATTGGAGTCATCAACGCCCCACAGAAAGTAGTTGA 625		
Dd		227 TGCTGCCCTGCAGTTTGCTATAAACACTGGAGTCATCAATGCCCCCCAGAGAGGTGATCGA 286		
QY		626 ACAGAGCTACAATGCAACTTGCTTGCTGGGTAGGCAGGGTCTCTGGGGGACCGCGACTCCATCCC 685		
Dd		287 GGAGTTCTACAACAGACATGGGTCCAACCGCTATGG-----GGAGAGCATCTCT 334		
QY		686 ACAAGCACCTCTACTACCTTTGGGGTCTCTCGGTGGCCATCTCTCTGTGGGTGGCAT 745		
Dd		335 GCCACCACGCTCCACGCTGTGTCTCTCAAGTGGCCATCTTTCTGTGTGGGGGCAT 394		
QY		746 GAATTTCTCTTTCTCATTTGSCATFATTTCTCAATGGTTGGGAGAAAGGCTATGCT 805		
Dd		395 GAATGGCTCTCTCTGTGGGCCCTTTTGTTAACCCCTTTGGCGCGCGGAATTCATGCT 454		
QY		806 GGCCAAACAATGTCTTGGCTGTGCTGGGGGCGCCCTCATGGGCCCTAGCAAATGCCGCGC 865		
Dd		455 GATGATGAACCTGCTGGCCCTTCGTGTCGCGCGTCTCATGGCTCTCGAAACTGGGCAA 514		
QY		866 CTCCTATGAGATACATCATFTCGGACGGTTCTCATTTGGCGCCCTACTCAGGGCTTAACATC 925		
Dd		515 GTCCCTTTGAGATGCTGATCCTTGGGCCCTTCATCATCGGTGTGTACTGCGGCTGACCAAC 574		
QY		926 AGGGTGTGCTGCTATGATGTGGGAGAAATCGCCCCCATCATCTTCGGGGTGCTTGGG 985		
Dd		575 AGGCTTCGTGGCCCATGTATGTGGGTGAAGTGTCAACCAACAGCCTTTCTGTGGGGCCCTGGG 634		
QY		986 AACACTCAACAANTTGGCCATCGTCATTTGGCATTTCTGGTTGCCAGGTGTGTGGGTTTTGGA 1045		
Dd		635 CACCCTGCACAGCTGGGCATCGTCTGCGCATCTCTATCGCCAGGTGTTCCGGCTGGA 694		
QY		1046 GTCTATGCTGGGCAAGCTACCTCTGTGGCCATTGCTTCTGGCTATCACAGTACTCCCTGTC 1105		
Dd		695 CTCCATCATGGGCAACAGGACCTGTGGCCCTGTCTGCTGAGCATCATCTTCATCCCGGC 754		

PN W0200188188-A2.
 XX 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-JP004192.
 XX 18-MAY-2000; 2000JP-00145977.
 XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX WPI; 2002-034733/04.
 DR P-PSDB; ABB57244.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 1637-1641; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischemic condition (e.g. compressive
 CC ischemia, occlusive ischemia or vasospastic ischemia) by measuring
 CC expression levels of particular genes (ABI999202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischemic condition-improving drugs or
 CC therapeutics for ischemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 2544 BP; 514 A; 719 C; 679 G; 632 T; 0 U; 0 Other;
 Query Match 28.5%; Score 679; DB 6; Length 2544;
 Best Local Similarity 68.1%; Pred. No. 8.5e-156;
 Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;
 506 GGAACCCCTCAGCAGCGAGTGAATGGGACACTGGTCTCTGTATTTCTCAGCTGTGCT 565
 192 GGATCCCGAGCAGCAAGAGTGAACGGCCGCTCATGTGGCTGTGGGAGGAGCAGTGCT 251
 566 TGCTCCCTTCAGTTTGGCTATACATTTGAGTCAATCAACGCCGCCACAGAAAGTATGA 625
 252 CGGATCACTGAGTTCGGCTATACACTGGTGTATCAACGCCGCCCGGAGAGGTTATGA 311
 626 ACAGAGCTACAAATGCAACTTGGCTGGGTAGGAGGCTCTGGGGAGCCGACTCCATCCC 685
 312 GGAGTTCTACATCAATCAATGAAACACCGCATCGG-----AGAGCCCATCCC 359
 686 ACAAGGACCCCTCACTACCTTTGGGCTCTCTCGTGGCCATCTTCTCTGTGGGTGGCAT 745
 360 ATCCACACACTACACAGCTTTGGTCTCTCTCGTGGCCATCTTCTCTGTGGGGGCGAT 419
 746 GATTTCTCTCTTCTCATTTGGCATCATTTCTCAATGTTGGGAAGAAAGGGGTATGCT 805
 420 GATTTGGTCTCTCTCTGCGGCTCTTTGTTAATCGCTTTGGCAGGCGGAACCTCCATGCT 479
 806 GGCCAAACAAATGCTTTGGCTGTGGGGGCGCCCTCATGGGCTACCCAAATGCGGGGC 865
 480 GATGATGAACCTGTTGGCTTTTGGCTGTGGTGTGCTATGAGGCTTCTCCAACTGGGCAA 539
 866 CTCCTATGAGATCACTCACTTCGAGCGGTTCTCTCAATTTGGGCGCTTACTCAGGGCTAAATC 925
 540 GTCTTTTGGATGCTGATCTCTGGGCGCTTCTCATCTCGGTGTGTACTTGGGCGCTGACTAC 599
 926 AGGTTGGTGGCTATGATGTGGAGAAATCGCCCCCAGCTCATCTTCTGGGGGTGCTGGG 985

600 TGCTTTTGGCCCATGTATGTGGAGAGGTGTCACTACAGTCTACGTGAGAGCCCTAGG 659
 986 AACACTCAACCAATTTGGCCCATGTGTGATTTGGCATTTCTGGTTCGCCAGGTGTGGGTTTGA 1045
 660 CACACTGCACAGCTGGGATCGTGTGGCATCTTATTTGCCAGGTGTGGCTTTAGA 719
 1046 GTCTATGTGGGACAGCTACCTGTGGCCATTTGCTTCTGGCTATCAAGTACTTCTCTGC 1105
 720 CTCATCATGGCAATGCAGACTTGTGGCTCTGTCTCAGTGTCTCTTCTGTCTCCAGC 779
 1106 TCTCTCTGAGCTGCTTCTGTGCTCTGTCTGAGAGCCCGGATACCTCTATCATCAT 1165
 780 CTTGCTACAGTGTATCTGTGCTCTTCTGCCCCGAGAGCCCGCTTCTCTGCTCATCAA 839
 1166 CCGGAACCTGAGGGGCTGCCCCGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGT 1225
 840 TCGTAACGAGAGAACCGGSCCAAGAGTGTGCTGAGAGAGCTTCGAGGGACAGCCGATGT 899
 1226 GTCTGATGCACTGGCTGAGCTGAAGGATGAGAAACGGAAGTTGGAAAGAGAGCGCTCCACT 1285
 900 GACCCGAGACTTCAGGAGATGAAGAGAGGGTTCGGCAGATGATGCGGGAGAGAAAGGT 959
 1286 GTCTTGTGCTGAGCTCTGCGGAGCGCACCCACCGGAGCGCTCTGATATTGTCAGTGT 1345
 960 CACCATCTTGGAGCTGTTCGCTCACCCGCTTACCGGAGCCCATCTCATCGCTGTGT 1019
 1346 GCTGAGCTGAGCAGCAGCTCTCAGGCATCAATGCTGTGTTTCTTACTATTCAACAGCAT 1405
 1020 GCTGAGCTGTCCAGCAGCTGTGCGGTATCAATGCTGTGTTCTTACTTACTCAACAGCAT 1079
 1406 CTTTGTAGTTAGTGGGTGGAACAGCCAGCTTAGCCACCATAGGAGCTGGTGTGTCAT 1465
 1080 CTTTCGAGAGGAGGAGTGTGAGCAGCTGTGTGTCGCCACCATCGGCTTCGGTATTCGTC 1139
 1466 TACGCTCTTACCTGCTCTGCGTGTCTTGTAGAGCGAGCTGGGGAGCGAGCAGCTCCA 1525
 1140 CACGGCTTCTACTGTGTGCTGTGTTGTTGTAGAGCGAGCTGGAGCAGCGAGCCCTGCA 1199
 1526 TCTCTGGGCTGGCAGGATGTGTGGCTGTGCTGCTGATGACGGTGGCTCTGTGCT 1585
 1200 CTTATTTGGCTGGCTGGCATGGCAGGCTGTGCTGTGCTCATGACCATCGCCCTGGCTT 1259
 1586 GCTGGAGCGGTTCCATCCATGAGTATGTGTCCATGTGGCCATATTTGGCTTTGTGGC 1645
 1260 GCTGGAACCGCTGCTTGGATGCTTATCTGAGCATCGTGGCCATCTTTGGCTTTGTGGC 1319
 1646 CTTCTTTGAGATTGCTGCGCCCATCCCTGCTTCAATGTCGCGAGCTCTTTCAGCCA 1705
 1320 CTTCTTTGAAAGTAGGCGCTGCTTCTATTCATGTTGTTGGCCGAGCTGTTCAGCCA 1379
 1706 GGGCCCCCGCCAGCAGCATGGCTGTAGCTGGTTCCTCAACTGGACCTGTAACTTCAT 1765
 1380 GGGGCCCCGCTGCTGCTGATTTGCTGTGGCTGGCTTCTCCACTGGACCTCAAACTTCAT 1439
 1766 CGTTGGCATGGGTTTCAGTATGTTGGGATGCTATGGGTCCCTTACGCTTCTTCTTATT 1825
 1440 TGTGGGCGATGTGCTTCAGTATGTGGAGCAACTGTGGGCGCCCTTACGCTTCTTCTTCT 1499
 1826 TGGGCTCTCTGCTTGGCTTCTTCACTTCTTCACTTCTTCAAGAGTGTCTGAAACAGAGG 1885
 1500 CAGGTGTCTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1559
 1886 CCGGACATTTGACAGATCTCGGCCAGCTTTCGAGCG 1922
 1560 CCGAACCTTCGATGAGATCGCTTCCGGCTTCCGGCAG 1596

RESULT 11
 ADB53698
 ID ADB53698 standard; DNA; 2571 BP.
 XX AC ADB53698;
 XX

DT 04-DEC-2003 (first entry)
 XX Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4240.
 XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
 KW toxicity marker; toxicity progression; drug screening;
 KW primary rat hepatocyte toxicity modelling; gene; ds.
 XX
 OS Rattus norvegicus.
 XX
 XX WO2003065993-A2.
 PN
 XX 14-AUG-2003.
 PD
 XX
 XX 04-FEB-2003; 2003WO-US003482.
 XX
 PR 04-FEB-2002; 2002US-0353171P.
 PR 13-MAR-2002; 2002US-0363534P.
 PR 08-APR-2002; 2002US-0370249P.
 PR 10-APR-2002; 2002US-0371134P.
 PR 10-APR-2002; 2002US-0371135P.
 PR 10-APR-2002; 2002US-0371150P.
 PR 11-APR-2002; 2002US-0371413P.
 PR 19-APR-2002; 2002US-0373601P.
 PR 19-APR-2002; 2002US-0373602P.
 PR 22-APR-2002; 2002US-0374139P.
 PR 08-MAY-2002; 2002US-0378370P.
 PR 09-MAY-2002; 2002US-0378652P.
 PR 09-MAY-2002; 2002US-0378653P.
 PR 09-MAY-2002; 2002US-0378665P.
 PR 09-JUL-2002; 2002US-0394230P.
 PR 04-SEP-2002; 2002US-0394253P.
 PR 04-SEP-2002; 2002US-0407688P.
 PR 28-JAN-2003; 2003US-0442900P.
 XX
 XX (GENE-) GENE LOGIC INC.
 XX Mendrick D, Porter M, Johnson K, Higge B, Castle A, Orr M;
 PI Elashoff M;
 XX WPI; 2003-731472/69.
 DR
 XX Determining if a compound induces a toxic effect on a tissue or cell, for
 PT identifying hepatotoxic compounds, comprises comparing a gene expression
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
 PT mean values.
 XX
 XX Claim 44; SEQ ID NO 4240; 874pp; English.
 PS
 XX The present invention describes a method for determining whether a
 CC compound induces a toxic effect on a tissue or cell. The method comprises
 CC preparing a gene expression profile of a tissue or cell sample exposed to
 CC the compound, and comparing the gene expression profile to a database
 CC comprising data or information on the Tox mean and non-Tox mean value.
 CC The method is useful for predicting or identifying at least one toxic
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The
 CC genes listed in the specification are useful as diagnostic or toxicity
 CC markers for the prediction or identification of the physiological state
 CC of tissue or cell sample that has been exposed to a compound, or to
 CC identify or predict the toxic effects of a compound or an agent. These
 CC may also be used as markers for monitoring toxicity progression or for
 CC drug screening. The present sequence represents a primary rat hepatocyte
 CC toxicity modelling related gene sequence from the present invention.
 XX
 XX Sequence 2571 BP; 528 A; 714 C; 686 G; 643 T; 0 U; 0 Other;
 SQ
 Query Match 28.5%; Score 679; DB 9; Length 2571;
 Best Local Similarity 68.1%; Pred. No. 8.5e-156;
 Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;
 506 GGAAACCCCTCAGCAGCGAGTACCTGGGACACTGGCTCTCTGCTGTAATTCCTCAGCTGGCT 565
 211 GGAGGCCAGCAGCAAGAAGGTGACGGCGCCCTTATGTTGGCCGTGGGAGGGGCGAGTGGCT 270

QY 566 TGGCTCCCTTCAGTTTGGCTATACATTGGAGTCATCAACGCCCCACACAGAAAGTCATTCA 625
 DB 271 CGGATCCTCGAGTTTGGCTATACACCGGTGTATCAACGCCCCCCACAGAAAGTAAATGA 330
 QY 626 ACAGAGCTACAAATCAATTTGGCTGGGTAGCAGGGTCTTGGGGACCGGACTCCATCCC 685
 DB 331 GGAGTTCTACAATCAAAACATGGAACACCGCTATGG-----AGAGTCCATCCC 378
 QY 686 ACAAGGCAACCTCACTACCCCTTTGGGCTCTCTCCGTGGGCCATCTTCTCTGTGGGTGGCAT 745
 DB 379 ATCCACCAACATCACCACACTCTCTGTCTCTCCGTGGGCCATCTTCTCTGTCTGGGGCAT 438
 QY 746 GATTTCT 805
 DB 439 GATTTGGTTCCTTCT 498
 QY 806 GGCCAAACAATGTCTTTGGCTGTCTGGGGGGGGCCCTCATGGGCCCTPAGCAATGCCGCGGC 865
 DB 499 GATGATGAACCTGTGGGCTTTGTCTGCGCTGTCTTATGGTTTCTCCAACTGGCAA 558
 QY 866 CTCCTATGAGATCACTCTCGGACCGGTCTCTCATTTGGCGCCTACTCAGGGCTAACATC 925
 DB 559 GTCTTTTGAATGCTGATCTCTGGGCCGCTTCTCATTTGAGTGTACTGTGGGCTGACCA 618
 QY 926 AGGGTGTGTCTATGTATGTGGGAGAAATCGCCCACTCATCTTTCGGGGTGCCTTGGG 985
 DB 619 CGGCTTTGTGCCCATGTATGTGGGGAGGTGTCAACCAAGCTCTTCTGTGGAGCCTTGG 678
 QY 986 AACACTCAACCAATTTGGCCATCGTCAATTGGCAATCTGGTTGCCCAAGTGTGGGTTTGA 1045
 DB 679 CACCTGCACCAAGCTGGGCATCGTCTGGGATCCTTATTGCCCAAGTGTTCGGCTTAGA 738
 QY 1046 GTCTATGCTGGGACAGCTACCTGTGGCCATGTCTTCTGGCTATCAGAGTACTCCCTGC 1105
 DB 739 CTCATCATGGGCAATGCAGACTTTGGGCTCTACTGCTCAGTGTCTCTTCTCATCCCAGC 798
 QY 1106 TCTCTCAGCTGTCTTCTTGTCCCTTCTGTCTCAGAGAGCCCGATACCTCTACATCAT 1165
 DB 799 CTGCTACAGTGTATCTCTTGTCCCTTCTGTCCCTCAGAGAGCCCGCTTCTCTCTCATCA 858
 QY 1166 CCGGAACCTTGAGGGGCTGCTCCGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGT 1225
 DB 859 TCGTAACGAGAGAAACCGGCAAGAGTGTCTGCTGAAAGCTTCGAGGACAGCCGATGT 918
 QY 1226 GTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1285
 DB 919 GACCCGAGACCTGCAGGAGATGAAGAAGAGGGTTCGGCAGATGATGCGGGAGAGAAGGT 978
 QY 1286 GTCTCTGCTGAGCTCTGAGGACCGCCACCCAGCGAGCTCTGATTTATTTGAGTGTGT 1345
 DB 979 CACATCTTGGAGTGTTCGCTCACCGCTTACCGCAGGCCATCTCTCATCGCGTGT 1038
 QY 1346 GTGTCAGCTGAGCCAGCAGCTCTCAGGCACTCAATGCTGTTTTTCTACTATTTCAACAGCAT 1405
 DB 1039 GCTGCACTGTCCAGCAGCTGTGCGGCATCAATGCTGTCTTCTACTACTCAACAGCAT 1098
 QY 1406 CTTTGTAGTGTGGGTGGAAAGCAGCAGCTACGCCACCATAGAGCTGTGTGTGTGTCAA 1465
 DB 1099 CTTTCGAGAAGGAGGTGTGACAGAGCTGTGTGTATGCCACCATCGGCTCGGGTATCGTCAA 1158
 QY 1466 TACCGTCTTCACTGTGTGTCTCGGTGCTTCTTGTAGAGAGCTGGGCGACGACACTCCA 1525
 DB 1159 CAGGCTTCTACTGTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1218
 QY 1526 TCTCTCGGCTTGGCAGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1585
 DB 1219 TCTCATTTGGTCTGGCTGGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1278
 QY 1586 GCTGGAGGGGTTCCATCCATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1645
 DB 1279 GCTGGAGGAGCTGCTCCCTGGATGCTCTATCTGAGTATCGTGCCATCTTTTGTGTGTGT 1338

Db 530 GTCTTTGAGATGCTGATCTCTGGCGCGCTTCATCATCGGTGTGTACTCGCGCTGACCAC 589
QY 926 AGGGTTGGTGGCTATGTATGGAGAAATCCGCCCACTCATCTTCGGGGTGCTTGGG 985
Db 590 AGGCTTGTGCCCATGTATGTGGGTGAAGTGTACCCACAGCTTTCGTGGGGCCTGGG 649
QY 986 AACACTCAACAAATGGCCATCGTCAITTTGGCATTTCTGGTTCGCCAGGTGTGGGTTTGGG 1045
Db 650 CACCTGTGACCAAGCTGGGATCGTCTGGCATCTCATGCCCAAGGTGTTCGGGCTGGA 709
QY 1046 GTCTATGTGGGACAGACTACCTGTGGCAATGCTTCTGGTATFACAGTACTCCCTGC 1105
Db 710 CTCATATATGGGCAACAGGACCTGTGGCCCTGCTGTGAGCATFATCTTCATCCCGGC 769
QY 1106 TCTCTGTGAGTGTCTTCTGTGGCTTCTGTCTGAGAGCCCGATACCTCTCATCAT 1165
Db 770 CTGTGTGATGTCATGTGTGCTCCCTTCTGTCCCGAGAGTCCCGCTTCCTGTCTCATCA 829
QY 1166 CCGGAACCTGGAGGGGCTGCGGAAGAGTCTAAAGCGCTGACAGGCTGGCTGTATGT 1225
Db 830 CCGCAACGAGGAGAACCGGGCCCAAGAGTGTCTAAAGAGCTGCGCGGACAGCTGACGT 889
QY 1226 GTCTGATGACCTGGCTGAGCTGAAGGATGAGAAACGGAAGTTGAAAGAGAGCGTCCACT 1285
Db 890 GACCATGACCTGCGAGGAGATGAGGAAGAGAGTGTGCGAGATGATGCGGGAGAAAGGT 949
QY 1286 GTCTTGTGTGAGCTTCTGTGGGCGAGCGCACCCAGCGAGCTCTGATTATTGAGTGGT 1345
Db 950 CACCATCTGTGAGCTGTCTCGCTCCCGCTTACCGCGAGCCCATCTCATCGCTGTGGT 1009
QY 1346 GCTGAGCTGTGACCGAGCAGCTCTCAGGCAATCAATGCTGTTTCTACTATTCAACAGCAT 1405
~ Db 1010 GCTGAGCTGTCCAGCAGCTGTCTGSCATCAAGCTGTCTTCTATTACTCCAGAGCAT 1069
QY 1406 CTTTGTAGTGTGGGTGGGAAACAGCAGCCTTACCCACATAGAGTGTGTGTGTCAA 1465
Db 1070 CTTGAGAGGGGGGGTGTGACAGCCTGTGTATGCCACCATTTGGCTCCGGTATCGTCAA 1129
QY 1466 TACCGTCTTACGTTGTCTGTGGTCTCTTGTAGTACGAGCTGGCGACGAGCACTCCA 1525
Db 1130 CAGGCTTCTATGCTGTGCTGTCTGTGTGGTGGAGCAGAGCGCGGACCTGTGCA 1189
QY 1526 TCTCTGGGCGCTGGCAGGATGTGGCTGTGCCATCTTGTATGAGCGGTCTGTCTGCT 1585
Db 1190 CTTATAGGCTCGCTGGCATGGCGGGTGTGCCATCTCATGACCATCGCGCTAGCACT 1249
QY 1586 GCTGAGCGGGTTCATCATGAGTATGTGTCCATCTGTGCCATATTTGGCTTTGTGGC 1645
Db 1250 GCTGAGCAGCTACCTGTGATGTCTATCTGAGCATGTGGCCATCTTTGGCTTTGTGGC 1309
QY 1646 CTTCTTTGAGATTGTCTGGCGCCATCCCTGTGTTTCAITTTGGCGAGCTCTTCAGCA 1705
Db 1310 CTTCTTTGAGTGGTCTGGCGCCATCCATGTTTCAITTTGGCTGAACTCTTCAGCCA 1369
QY 1706 GGGCCCCCGCCAGCAGCATGGCTGTAGTGTGTTTCTTCAACTGGACCTGTAACTTCAT 1765
Db 1370 GGGTCCAGCTCCAGCTGCCATTGGCGTGTGAGGCTTCTTCAACTGGACCTCAAAATTCAT 1429
QY 1766 CGTTGCGATGGGTTTCCAGTATGTGGGAGTGTATGGGTCCCTACGTCCTCTCTATT 1825
Db 1430 TGTGGGCATGTGCTTCCAGATGTGGAGCACTGTGTGGTCCCTACGTCCTTCATCATCT 1489
QY 1826 TCGGCTCTCTCTGCTTGGCTTCTTCACTTCACTTCTTCAAGAGTGTCTGAAACAGAGG 1885
Db 1490 CACTGTGCTCTCTGCTTCTTCTTCACTTCTTCAAGTTCCTGAGACTTAAAGG 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTCCGACGG 1922
Db 1550 CCGGACCTTCGATGAGATCGCTTCCGGCTTCCGGCAG 1586

RESULT 15
ABV77983

ID XX ABV77983 standard; DNA; 2856 BP.
XX AC ABV77983;
XX DT 12-NOV-2002 (first entry)
XX DE Hypoxia-regulated protein coding sequence #3.
XX KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW antiinflammatory; vulnary; gynecological; ophthalmological; vaccine;
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW preclapmsia; atherosclerosis; inflammatory condition; wound healing;
KW inflammation; erythropoiesis; hair loss; human; gene; ds.
XX OS Homo sapiens.
XX FN WO200246465-A2.
XX PD 13-JUN-2002.
XX XX 10-DEC-2001; 2001WO-GB005458.
XX PF 08-DEC-2000; 2000GB-00030076.
XX PR 08-FEB-2001; 2001GB-00003156.
XX PR 25-OCT-2001; 2001GB-00025666.
XX XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX PA White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
XX PI Rayner WN;
XX PI WPI; 2002-627238/67.
XX DR
XX FT Identifying a gene involved in disease for treating hypoxia-regulated
XX PT conditions, comprises comparing the transcriptome/proteome of two cell
XX PT types under different conditions and identifying a differentially
XX PT regulated gene.
XX PS Claim 37; Page 333; 538pp; English.
XX CC The present invention relates to methods for identifying genes and
XX CC proteins that are implicated in a specific disease or physiological
XX CC condition. The method comprises comparing the transcriptome/proteome of a
XX CC specialised cell type implicated in a disease or condition with that of a
XX CC second specialised cell type, under two experimental conditions, and
XX CC identifying a gene that is differentially regulated in the two
XX CC specialised cell types under experimental conditions. ABV77873-ABV78116
XX CC and ABP65061-ABP65257 were identified using the methods of the invention.
XX CC The coding sequences and proteins are useful for treating a disease in a
XX CC patient, for manufacture of a medicament for treating hypoxia-regulated
XX CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
XX CC biological response to hypoxia conditions, or hypoxic-associated
XX CC pathology in a patient. The coding sequences and proteins are also useful
XX CC for monitoring the therapeutic treatment of a disease or physiological
XX CC condition, such as cancer, ischaemic conditions, reperfusion injury,
XX CC retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory
XX CC conditions, wound healing, inflammation, erythropoiesis or hair loss
XX CC

SQ Sequence 2856 BP; 602 A; 804 C; 753 G; 697 T; 0 U; 0 Other;

Query Match 28.5%; Score 679; DB 6; Length 2856;
Best Local Similarity 68.1%; Pred. No. 9e-156;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

Qy 506 GGAAACCCCTCAGCAGCAGTGTGACCTGGGACACTGGTCTCTGCTGTATTCTCAGCTGTGCT 565
Db 182 GGAGCCCGCAGCAAGAAAGCTGACGGGTGCGCTCATGCTGGCTGTGGGAGGACGAGTGTCT 241
Qy 566 TGGCTCCCTTCAGTTTGGCTATACATTGGAGTCAATCAACGCCCCACACAGAAAGTCAATCA 625
Db 242 TGGCTCCCTTCAGTTTGGCTATACATTGGAGTCAATCAATGCCCCCAGAGGATCAATCA 301

Qy	626	ACAGAGTACAAATGGCAACTTGGCTGGGTGAGCAGGGTCTCTGGGGGACCGGAGCTCCATCC	685
Db	302	GGAGTTTACAAACAGACATGGGTCCACCGCTATGG-----GGAGAGCATCTCT	349
Qy	686	ACAAGGCACCCCTCACTACCTTTTGGGCTCTCTCGTGGGCCATCTTCTCTGTGTGGTGGCAT	745
Db	350	GCCACACACGGCTAACACAGCTCTCTGGTCCCTCTCAGTGGCCATCTTTTCTGTGTGGGGGCAT	409
Qy	746	GATTTCTCTTTTCTCATTTGGSCATATTTCTCAATGGTTGGGAAGGAAAAGGCTATGCT	805
Db	410	GATTTGGCTCTCTCTCTGTGGSCCTTTTCGTTTAAACCGCTTTTGGCCGGGAAATTCAAATGCT	469
Qy	806	GGCCAAACAAATGCTTTGGGTGTGTGGGGGGGGCCCTCATGGGCTAGACCAATGCCGGGC	865
Db	470	GATGATGAACCTGCTGGCCCTTCGTGTGCCGCGTCTCATGSGGCTTCGAAAACGTGGGC	529
Qy	866	CTCCTATGAGATATCATTTCTCGACAGSTTCTCATTTGGGCGCTACTCAGGGCTAAATC	925
Db	530	GTCCTTTTGGATGCTGATCTTGGGCCGCTTCATCATCGGTGTGTACGCGCCTGACCAC	589
Qy	926	AGGGTTGGTGCCTATGTATGTGGGAGAAATCGCCCCCACTCATCTTCGGGGTGCCTTGGG	985
Db	590	AGGCTTCGTGCCCATGTATGTGGGTGAAGTGTCAACCCACAGCCCTTCGTGGGGCCCTGGG	649
Qy	986	AACACTCAACAAATTTGGCCATCTGTATGTGGATTTCTGGTTGCCAGAGTGTGGTTTGG	1045
Db	650	CACCTTGACACAGCTGGGCATCTGTCTGTGGCATCTCATCGCCGAGGTTCGCGCCCTGGA	709
Qy	1046	GTCTATGCTGGGCACAGTACCTCTGGGCCATTTGCTTCTGGCTATCACAGTACTCCCTGC	1105
Db	710	CTCCATCATTTGGGCACAAAGAACCTTGTGGCCCTGCTGCTGAGCATCATCTTCATCCCGGC	769
Qy	1106	TCTCCTGCAGCTGCTTCTGTTTGGCCCTTCTGTCTCTGAGAGCCCCGATACCTCTACATCAT	1165
Db	770	CCTGCTGCAGTGCACTGTTGTGCCCTTCTGCCCGAGAGTCCCCGCTTCTCTGCTCATCAA	829
Qy	1166	CCGAAACCTGGAGGGGCTGCCGAAAGAGTCTAAAGGCGCTGACAGGCTGGGCTGATGT	1225
Db	830	CCGCAACGAGGAGAACCCGGGCCAAGAGTGTGCTAAAGAGCTGCGCGGACAGCTGACGT	889
Qy	1226	GTCGTATGCACTGCTGAGCTGAGGATGAGAACGGAAGTTGGMAAGAGAGCGTCCACT	1285
Db	890	GACCCATGACCTGCAGGAGATGAAAGGAAGAGATCGGCAGATGATGCGGAGAGAAGGT	949
Qy	1286	GTCCTTGTCTGAGCTCTCTGGGCACCGCACCCACCGGCAGCTCTGATATTGCAGTGT	1345
Db	950	CACCATCTTGGAGCTGTCTCGCTCCCGCGCTACCGCCAGCCCATCTCATCTGCTGTGT	1009
Qy	1346	GCTGCAGCTGAGCAGCAGCTCTCAGGCATCAATGCTGTGTTTTCTPACTATTCAACCAAGCAT	1405
Db	1010	GCTGCAGCTGTCCACGACGTGTCTGGCATCAACGCTGTCTTCTATTACTCCACGAGCAT	1069
Qy	1406	CTTTGAGTTAGCTGGGTGGNAAGCCAGCCCTACGCCACCATAGGAGCTGGTGTGTCAA	1465
Db	1070	CTTCGAGAAGCGGGGTGCAGCAGCTGTGTATGCCCACCATTTGGCTCCGGTATCGTCAA	1129
Qy	1466	TACCGTCTTTCACGTTTGTCTCGGTGCTCTTAGTAGCGGAGCTGGGCGACGCACTCCA	1525
Db	1130	CACGGCTTCACTGTGTGTGCTGTGTTGTGGTGGAGCAGCAGCCGGCGGACCTTGCA	1189
Qy	1526	TCTCCTGGGCTGCGACGCAATGTGTGCTGTGGCCATCTTGATGACGGTGGCTCTGTGCT	1585
Db	1190	CCTCATAGGCCCTGCTGGCATGGCGGGTTGTGCCATACTCATGACCATCGCGCTAGCACT	1249
Qy	1586	GCTGGAGGGGTTCCATCCATGAGTTATGTGTCCATCGTGGCCATATTTGGCTTTTGGC	1645
Db	1250	GCTGGAGCAGCTACCTCGGATGCTCTATCTGAGCATCGTGGCCATCTTTTGGCTTTTGGC	1309
Qy	1646	CTTCTTTGAGATTGGTCTGSCCCCATCCCTCGTTTCAATGTGCGCGAGCTCTTCAGCCA	1705
Db	1310	CTTCTTTGAAGTGGGTCTGSGCCCATCCCATCATGTTTCTGTTGCTGAACTCTTCAGCCA	1369
Qy	1706	GGGCCCCCGCCGACGAGCCATGGCTGTAGCTGGTTTCTCCAACTGGACCTGTAACTTCAT	1765

Search completed: May 16, 2004, 01:32:07
Job time : 566.671 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 00:27:52 ; Search time 3702.57 Seconds
(without alignments)
19243.679 Million cell updates/sec

Title: US-10-067-449-10
Perfect score: 2386
Sequence: 1 tcgactctagagatccctc.....ctggactttcttcagttg 2386

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esti:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1203.4	50.4	1497	29	AY421217 Mus muscu
2	1157.8	48.5	3049	11	BC034387
3	1035.4	43.4	1497	29	AY421215 Homo sapi
4	1018.8	42.7	1814	14	CD014068 90134560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1	AY421217	AY421217	1497 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY421217	Mus musculus SLC2A4 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	AY421217	Genomic survey sequence.				
ACCESSION	AY421217	GI:39777174				
VERSION	AY421217.1	GI:39777174				
KEYWORDS	GSS.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1 (bases 1 to 1497)					
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J., Adams, M.D. and Cargill, M.					
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	14671302					
REFERENCE	2 (bases 1 to 1497)					
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J., Adams, M.D. and Cargill, M.					
TITLE	Direct Submission					

Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 50 Row: h Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4507010
 This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5187454"
 /tissue types="Colon, Kidney, Stomach, adult, whole pooled"
 /clone_lib="NIH MGC_116"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 48.5%; Score 1157.8; DB 11; Length 3049;
 Best Local Similarity 83.0%; Pred. No. 9.9e-213;
 Matches 1359; Conservative 0; Mismatches 217; Indels 61; Gaps 1;
 455 CTTTAAAGCAACATAATGCTCTGAATCCAGAGATCGGCTCTGAAGATGGGAACCC 514
 Db |||||
 188 CTTTAAAGCAACATAATGCTCTGAATCCAGAGATCGGCTCTGAAGATGGGAACCC 247
 |||||
 515 TCAGCAGCAGTCACTGGGACACTGGTCTCTGTGTTATCTCAGCTGTGCTGGCTCCCT 574
 Db |||||
 248 TCAGCAGCAGTCACTGGGACACTGGTCTCTGTGTTATCTCAGCTGTGCTGGCTCCCT 307
 |||||
 575 TCAGTTTGGCTATAACATTGGAGTCAATCAAGCCCAAGAAAGTGAATGAACAGAGCTA 634
 Db |||||
 308 GCAGTTTGGGTACAAATTGGGGTCAATGCTCCATGCTCCAGAGGATGATTGAACAGAGCTA 367
 |||||
 635 CAATGCACTTGGCTGGTAGGAGGAGGCTCTGGGGGACCGGACTCCATCCCAAGGCAC 694
 Db |||||
 368 CAATGAGACGTGGCTGGGAGGAGGAGGCTGGAGGACCGAGCTCCATCCCTCCAGGCAC 427
 |||||
 695 CCTCACTACCTTTGGGCTCTCTCCGTGGCCATCTCTCTGTGGGTGGCATGATTTCCCTC 754
 Db |||||
 428 CCTCACACCTCTGGGCCCTCTCCGTGGCCATCTCTCTGTGGGTGGCATGATTTCCCTC 487
 |||||
 755 CTTTCTCATTTGGCATCATTTCTCAATGGTTGGAAAGAAAGGGCTATGCTGCCCAACAA 814
 Db |||||
 488 CTTTCTCATTTGGTATCATCTCTCAGTGGCTTGGAAAGAAAGGGCTATGCTGGTCAACAA 547
 |||||
 815 TGTCTTGGCTGTCTGGGGGGCCCTCATGGGCTAGCAATGCCGGCCCTCTATGA 874
 Db |||||
 548 TGTCTTGGGCTGTCTGGGGGGAGCCCTCATGGGCTGGCCCAAGCTGCTGCTCTATGA 607
 |||||
 875 GATACTCATTTCTCGGAGCGTTCTCTCATTTGGCGCTACTCAGGGCTAAACATCAGGGTTGGT 934
 Db |||||
 608 AATGCTCATCTTGGAGCATCTCTCATTTGGCGCTACTCAGGGCTGACATCAGGGCTGGT 667
 |||||
 935 GCCTATGATATGTGGGAAATCGCCCACTCATTTCTGGGGTGGCTTGGGAACACTCAA 994
 Db |||||
 668 GCCCATGTAGTGGGGAGATTGCTCCCACTCACTTGGGGGGCCCTGGGGGAGCTCAA 727
 |||||
 995 CCAATGGCCCATGTCATTTGGCATTTGGTTGGCCAGGTGTTGGGTGGAGTCTATGCT 1054
 Db |||||
 728 CCAACTGGCCATTTGTTATGGGCATTTGATCGCCAGGGTCTGGGCTTGGAGTCCCTCT 787
 |||||
 1055 GGGCAGCAGCTTACCTCTGGGCAATGCTTCTGGGCTATCAGAGTACTCCCTGCTCTCTGCA 1114
 Db |||||
 788 GGGCAGCTGCGAGCTGTGGCCACTGCTCTTGGGCTTACAGTGTCTACCTGCTCTCTGCA 847
 |||||

RESULT 3

AY421215

LOCUS

DEFINITION

AY421215 1497 bp DNA linear GSS 17-DEC-2003
 Homo sapiens SLC2A4 gene, VIRTUAL TRANSCRIPT, partial sequence,

QY 1115 GCTGCTTCTGTTGGCCCTTCTGCTCTGAGAGCCCCCGATACCTCTACATCATCCGGAACCT 1174
 Db |||||
 848 GCTGTGCTCTGCTGCTCTTCTGCTCCGAGAGCCCCCGCTACTCTATCATATCCAGAATCT 907
 |||||
 QY 1175 GGAGGGGCTGCCCCGAAAGAGTCTAAAGCGCCTGACAGGCTGGGCTGATGTTCTGATGC 1234
 Db |||||
 908 CGAGGGGCTTCCGAAAGAGTCTGAAGCGCTTGAAGCGCTTGAAGCGCTTGAAGCGCTTGAAGCGT 967
 |||||
 QY 1235 ACTGGCTGAGCTGAAGGATGAGAAACGGAAGTTTGGAAAGAGAGCGTCCACTGCTCTTGGCT 1294
 Db |||||
 968 GCTGGCTGAGCTGAAGGATGAGAAACGGAAGCTGGAGCGTGGAGCGGCACTGTCCTGCT 1027
 |||||
 QY 1295 GAGCTCTCTGGGAGCGGACCCACCGGAGCCTCTGATATTATTTGAGTGGTGTGCTGAGCT 1354
 Db |||||
 1028 CCAGCTCTCTGGGAGCGCTTACCCACCGGAGCGCTTATGCTGCTGCTGCTGCTGCTGCTGCT 1087
 |||||
 QY 1355 GAGCCAGAGCTCTCAGGAGCATCAATGCTGTTTTTCTACTATTCAACAGAGCATCTTTGAGTT 1414
 Db |||||
 1088 GAGCCAGAGCTCTCTGGCATCAATGCTGTTTTTCTATTATTCGACAGAGCATCTTCGAGAC 1147
 |||||
 QY 1415 AGCTGGGTTGGAAACAGCCAGCCTTACGCCACCATAGGAGCTGGTGTGCTCAATACCGTCTT 1474
 Db |||||
 1148 AGCAGGGGTAGGCCAGCTGCTATGCCACCATAGGAGCTGGTGTGCTCAACAGAGCTT 1207
 |||||
 QY 1475 CAGTTGGTCTC----- 1486
 |||||
 Db 1208 CACTTGGTCTCGGTAACTGCTCACCTCTGGAATGGCCCGAGCACTGGGCTTCACTCC 1267
 |||||
 QY 1487 -----GGTCTCTTAGTAGAGCAGCTGGGGAGCGACACTCCATCTCTCTGG 1533
 |||||
 Db 1268 TGGGTCTCCGGAGGTGTTGGTGGAGCGGGCGGGCGCGAGCGCTCCATCTCTCTGG 1327
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 QY 1534 GCCTGGCAGGCAATGTGGCTGTGCCATCTTGTATGACGGTGGCTGTGCTGCTGCTGAGC 1593
 Db |||||
 1328 GCCTGGCAGGCAATGTGGCTGTGCCATCTCTGATGACTGTGGCTGTGCTGCTGCTGAGC 1387
 |||||
 QY 1594 GGGTTCATCCATGATTTATGTCATCGTGGCCATATTGGCTTGTGGCCCTCTCTTG 1653
 Db |||||
 1388 GAGTTCCAGCCATAGCTAGCTTCCATTTGTGGCCATCTTTGGCTTCTGTTGGCATTTTGG 1447
 |||||
 QY 1654 AGATTGCTCTGGCCCCCATCCCTGGTTCATTGTGGCCGAGCTCTTCAGCCAGGGCCCC 1713
 |||||
 Db 1448 AGATTGGCCCTGGCCCCCATCTTGGTTTCATCGTGGCCGAGCTCTTCAGCCAGGGCCCC 1507
 |||||
 QY 1714 GCCCAGCAGCCATGGCTGTAGCTGGTTTCTCCTCAACTGGAGCTGTAACCTTCATGTTGGCA 1773
 |||||
 Db 1508 GCCCAGCAGCCATGGCTGTGGCTGGTTTCTCCTCAACTGGAGCACTTCATCATTTGGCA 1567
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 QY 1774 TGGGTTCCAGTATGTTGGGATGCTATGGGTCCCTACGTTCTCTCTTATTTGGCGTCC 1833
 Db |||||
 1568 TGGGTTTCCAGTATGTTGGGAGGCTATGGGGCCCTACGTTCTCTTCTTATTTGGCGTCC 1627
 |||||
 QY 1834 TCTGCTTGGCTTCTTCTCATCTTCCACCTTCTTAAGAGTGGCTGAAACAGAGGGCGGACAT 1893
 |||||
 Db 1628 TCTGCTGGGCTTCTTCTCATCTTCCACCTTCTTAAGAGTGGCTGAAACAGAGGGCGGACAT 1687
 |||||
 QY 1894 TTGACAGATCTCGGCACTTCCGAGCGACCTTCTCTCTTTAGAGCAGGAGGTGAAC 1953
 Db |||||
 1688 TTGACAGATCTCAGCTGCTTCCACCGGACACCTCTCTTTTAGAGCAGGAGGTGAAC 1747
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 QY 1954 CAGTACAGACTTGAATATTAGGCGCAGATGAGATGACTAATGATTTGAATGAGA 2013
 Db |||||
 1748 CCAGCAGACTTGAATATTAGGCGCAGATGAGAACGACTGAGGGGCCAGGGGGT 1807
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 QY 2014 CGCTCCATCATCTCTCT 2030
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 Db 1808 GGGAGAGCCAGCTCTCT 1824
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genomic survey sequence.

ACCESSION AY421215
VERSION AY421215.1 GI:39777172

KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarial, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
1 (bases 1 to 1497)
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE

AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarial, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
1 (bases 1 to 1497)
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT

This sequence as made by sequencing genomic exons and ordering them
based on alignment.

FEATURES

Location/Qualifiers

1..1497

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>1497

/gene="SLC2A4"

/locus_tag="HMC7483"

ORIGIN

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Best Local Similarity 75.6%; Pred. No. 4,3e-189;
Matches 1132; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

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DB 1 GATGGGAACCCCTCAGCAGAGTGAAGTGGGACATGGTCTTGTGTTATTCAGCT 60

QY 561 GTGCTTGGCTCCCTCAGTGGCTATTAACATTGGAGTCAACGCCGCCACAGAAAGT 620
DB 61 GTGCTTGGCTCCCTCAGTGGCTATTAACATTGGAGTCAACGCCGCCACAGAAAGT 120

QY 621 ATTGAACAGAGTACAATGCACTTGGCTGGTGGTGGGAGGCTCTGGGGACCGACTCC 680
DB 121 ATTGAACAGAGTACAATGCACTTGGCTGGTGGTGGGAGGCTCTGGGGACCGACTCC 180

QY 681 ATCCACAGGACCCCTCACTACCCCTTTGGGCTCTCCGCTGGGCACTTCTCTGTGGT 740
DB 181 ATCCCTCAGGACCCCTCACTACCCCTTTGGGCTCTCCGCTGGGCACTTCTCTGTGGT 240

QY 741 GGCATGATTCCTCTTCTCATTTGGCATCTTCTCAATGGTGGGAGGAAAGGGCT 800
DB 241 GGCATGATTCCTCTTCTCATTTGGCATCTTCTCAATGGTGGGAGGAAAGGGCT 300

QY 801 ATGCTGGGCAACATGCTTGGCTGGTGGGAGGAGGCTCTGGGGCTAGCCAAATGCC 860
DB 301 ATGCTGGTCAACATGCTTGGCTGGTGGGAGGAGGCTCTGGGGCTAGCCAAATGCC 360

QY 861 GCGGCTCTATGAGATCACTATTCGGAAGGTTCTCATTTGGGCTCTATCGAGGCTA 920
DB 361 GCTGCTCTATGAAATGCTATCTTGGAGCATCTCTCAATGGCTCTATCGAGGCTG 420

QY 921 ACATCAGGCTGGTGGCTATGATGAGGAGAAATCGCCCACTCATCTTCGGGGTGC 980
DB 421 ACATCAGGCTGGTGGCTATGATGAGGAGAAATGCTCTCCCACTCATCTTCGGGGTGC 480

RESULT 4

CD014068

LOCUS

DEFINITION

CD014068 1814 bp mRNA linear EST 21-OCT-2003
90134560 single gene library Homo sapiens cDNA, mRNA sequence.

QY 981 TTGGGAACACTCAACCAATTGGCCATCGTCAATTGGCAATTCGTGGTCCCGAGGTGGGT 1040
DB 481 CTGGGAGCGCTCAACCAACTGGCCATTGTTATCGGCATTCGTGATCGCCAGGTGGGC 540

QY 1041 TTGGAGTCTATGCTGGGCACAGCTACCTGTGGCCATTCGTCTTGGCTATCACAGTACTC 1100
DB 541 TTGGAGTCCCTCTCTGGGCACAGCTACCTGTGGCCATTCGTCTTGGCTATCACAGTACTC 600

QY 1101 CCTGCTCTCTGAGCTGCTTCTGTCCTTCTGTCCTGAGAGCCCGGACCTCTCTAC 1160
DB 601 CCTGCTCTCTGAGCTGCTTCTGTCCTTCTGTCCTGAGAGCCCGGACCTCTCTAC 660

QY 1161 ATCATCCGGAACCTGGAGGGGCTGCGCCGAAAGAGTCTAAAGCGCTGACAGGCTGGGT 1220
DB 661 ATCATCCAGATCTCGAGGGGCTGCGCCGAAAGAGTCTGAAAGCGCTGACAGGCTGGGC 720

QY 1221 GATGCTCTGATGCACTGGCTGAGCTGAAGATGAGAAACGGAAGTTGGAAGAGAGCT 1280
DB 721 GATGCTCTGAGTGTCTGGCTGAGCTGAAGATGAGAAAGCGGAGCTGAGCGCTGAGCGG 780

QY 1281 CCAGTCTCTGCTGAGCTCTGGGCGAGCGCCACCGGAGCTCTGATTTATTTGCA 1340
DB 781 CCAGTCTCTGCTGAGCTCTGGGCGAGCGCTCTGATTTATTTGCA 840

QY 1341 GTGCTGCTGAGCTGAGCGAGCTCTCAGGCTCAATGCTGTTTCTACTATTCAACC 1400
DB 841 GTGCTGCTGAGCTGAGCGAGCTCTCAGGCTCAATGCTGTTTCTACTATTCAACC 900

QY 1401 AGCATCTTGTAGTGTGGGTGGAACAGCGAGCTTACGCAACCATAGGAGCTGGTGTG 1460
DB 901 AGCATCTTGTAGTGTGGGTGGAACAGCGAGCTTACGCAACCATAGGAGCTGGTGTG 960

QY 1461 GTCAATACCGTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1520
DB 961 GTCAATACCGTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020

QY 1521 CTCATCTCTGGGCTGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
DB 1021 CTCATCTCTGGGCTGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080

QY 1581 CTGCTGCTGAGCGGGTTCATCATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1640
DB 1081 CTGCTGCTGAGCGGGTTCATCATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

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DB 1141 GTGCTCTCTTGTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200

QY 1701 AGCCAGGGCCCCCGCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1760
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QY 1761 TTCACTGCTGGCATGGGTTCAGTATGTTGCGGATGCTATGGTCCCTACGCTCTCTCT 1820
DB 1261 TTCACTGCTGGCATGGGTTCAGTATGTTGCGGATGCTATGGTCCCTACGCTCTCTCT 1320

QY 1821 CTATTTCCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1880
DB 1321 CTATTTCCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

QY 1881 AGAGCCGAGCATTTGACAGATCTCGGCCACCTTCCGAGCGGACACCTTCTCTTAGAG 1940
DB 1381 AGAGCCGAGCATTTGACAGATCTCGGCCACCTTCCGAGCGGACACCTTCTCTTAGAG 1440

QY 1941 CAGAGGTGAAACCCAGTACAGAACTTGAATACTTAGGGCCAGATGAGAAAGACTAA 1997
DB 1441 CAGAGGTGAAACCCAGTACAGAACTTGAATACTTAGGGCCAGATGAGAAAGACTAA 1497

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ACCESSION      CD014068
VERSION         CD014068.1  GI:37777598
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE           1 (bases 1 to 1814)
                Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
                PCR isolation and cloning of novel splice variant mRNAs from known
                drug target genes
                Unpublished (2003)
JOURNAL         Contact: Jin, P.
COMMENT         Incyte Corporation
                3160 Porter Drive, Palo Alto, CA 94304, USA
                Tel: 650 621 8639
                Fax: 650 621 8965
                Email: pj@incyte.com
FEATURES        Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="Single gene library"
                /notes="Vector: pDrive Cloning Vector; RT-PCR was performed
                using gene-specific primers flanking the open-reading
                frame. PCR products were subcloned into pDrive Cloning
                Vector and sequenced completely using M13 forward and
                reverse primers. Sequencing gaps were closed by
                re-sequencing using primers flanking the gapped areas."
ORIGIN
Query Match      42.7%; Score 1018.8; DB 14; Length 1814;
Best Local Similarity 80.1%; Pred. No. 6.4e-186;
Matches 1263; Conservative 0; Mismatches 197; Indels 116; Gaps 1;

QY 455 CTTATTAAGCAACATTAATGTCCTAAATTCACAGAGATCGGCTCTGAAGATGGGAAACCCCC 514
DB 115 CTTCTAAGACGAGATCGGTCGGGCTTCCACAGATAGGCTCCGAAGATGGGAAACCCCC 174
QY 515 TCAGGACGAGTCACTGGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
DB 175 TCAGGACGAGTCACTGGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 234
QY 575 TCAGTTTGGCTATAAACAATTGGAGTCACTCAACGCCGCCACAGAAAGTGAATTGAACAGAGCTA 634
DB 235 GCAGTTTGGGTACAAACATTTGGGGTCACTCATGCCCCCTCAGAAGGTGAATTGAACAGAGCTA 294
QY 635 CAATGCAACTTGGCTGGGTAGGACAGGCTCTCGGGGACCGGACTCCATCCCAAGGCAC 694
DB 295 CAATGAGACGTGGCTGGGAGGACGAGGCTGAGGGACCCAGCTCCATCCCTCCAGGCAC 354
QY 695 CTTCACTACCCCTTGGGCTCTCTCGTGGCCATCTTCTGCTGGGTGGCATGATTTCCCTC 754
DB 355 CTTCAACACCCCTTGGGCTCTCTCGTGGCCATCTTCTGCTGGGTGGCATGATTTCCCTC 414
QY 755 CTTTCTCATTTGGCATATTCTCAATGTTGGGAAGGAAAGGCTATGCTGGCCCAACAA 814
DB 415 CTTTCTCATTTGGTATCATCTCTCAGTGGCTTGAAGGAAGGCAATGCTGGTCAACAA 474
QY 815 TGTCTTGGCTGTGCTGGGGGCGCCCTCATGGGCTAGCCCAATGCGCGGCTCTCTATGA 874
DB 475 TGTCTTGGGCTGTGCTGGGGGCGAGCTCATGGGCTGGCCCAACGCTGCTGCTCTATGA 534
QY 875 GATACATCTCTCGAGGTTCTCTCATTTGGGCTACTCAGGCTAACATCAGGTTGGT 934
DB 535 AATGCTCATCTTGGACGATTCCTCATTTGGGCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 572
QY 935 GCCTATGATGTGGAGAAATGCCCCCACTCATCTCTGGGGTGCCTTGGGAACACTCAA 994
DB 573 ----- 572

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RESULT 5	AY421216	1497 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	Pan troglodytes SLC2A4 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION	AY421216				
ACCESSION	AY421216	GI:39777173			
VERSION	AY421216.1				
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.				
AUTHORS	1 (bases 1 to 1497) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Gargill, M.				
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1497) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Gargill, M.				
AUTHORS	Direct Submission				
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
JOURNAL	This sequence as made by sequencing genomic exons and ordering them based on alignment.				
COMMENT	Location/Qualifiers				
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gene					
ORIGIN					
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				Gaps	0;
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Qy	681	ATCCCAAGGACACCTCACTACCTTTGGGCTCTCTCCGTGGCCATCTTCTCTGTGGT	740		
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Qy	801	ATGCTGGCCCAACAATGTCTGGCTGTCTGGGGGGCGCCCTCATGGGCCCTAGCCAATGCC	860		
Db	301	ATGCTGGTCACAAATGTCTGGCGGTCTGGGGGGGAGCCCTCATGGGCCCTGGCCAACGCT	360		
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Qy	981	TTGGGAACACTCAACCAATTGGCCATCGTCATTGGCATCTCGTTGGCCCAAGGTGTTGGGT	1040		
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Db	661	NN	720		
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Db	721	GATGTTTCTGCANTCTGCTGNNNTGAGNNNNNAAGCGAAGCTGGAGCGTGAGCGG	780		
Qy	1281	CCACTGTCTGTCTGAGCTCTTGGGCGCGGCACCCACCGGAGCTCTGATTATTGCA	1340		
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Qy	1341	GTGTGTCTGAGCTGAGCCAGCAGCTCTCAGGCGATCAATCTGTTTCTACTATTCAACC	1400		
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Qy	1461	GTCAATACCTCTTCACTGTTGCTCGGTCTCTTAGTAGAGCGAGCTGGGCGACCGACA	1520		
Db	961	GTCAACACAGCTTTCACCTTGGTCTCGGTGTTGTTGGTGGAGGGGGGGCGCGGACG	1020		
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LOCUS
DEFINITION
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cDNA clone G42 similar to glucose transporter 4 (GLUT4), mRNA
sequence.
CB814984
CB814984.1 GI:29941278
EST.
Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
REFERENCE
1 (bases 1 to 857)
Navarrete-Santos, A., Kietz, S., Augustin, R. and Fischer, B.
Expression of glucose transporters in rabbit preimplantation
embryos (2003)
Unpublished (2003)
Contact: Kietz S
Department of Anatomy and Cell Biology
Martin Luther University Halle-Wittenberg, Medical Faculty
Grosse Steinstrasse 52, D-06097 Halle, GERMANY
Email: silke.kietz@mx.de
Seq primer: T7 Forward
High quality sequence stop: 857
POLYA=No.
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QY 734 TGTGGGTGGCATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 793
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QY 794 AAGGCTATCTGGCCCAACATGCTTGGCTGTGCTGGGGGGGCGCCCTCATGGGCTAGC 853
DB 181 GAGGCGCATCTGGCCCAACATGCTTGGCTGTGCTGGGGGGGACCCCTCATGGGCTGGC 240
QY 854 CAATCGCGCGCTCTCTATGAGATACCTCACTCTCGGACGGTCTCTCAATGGCGCTACTC 913
DB 241 CAAGCTGCTGCTCTCTATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 914 AAGGCTAAATCATAGGTTGGTGGCTATGATGTGGGAGAAATCGCCCGCATCATCTTCG 973
DB 301 AAGGCTGACATCAGGCTTGTGCCATGTACGTGGGGGAGATGGCCCGCATCACCTTCG 360
QY 974 GGTGGCTTGGGAACACTCAACCATTTGGCATCGTCAATTTGGCATTTCTGTGGCCAGGT 1033
DB 361 AGGTGGCTTGGGACGCTCAACAGCTGGCCATGCTCAATTTGGCATTTCTGTGGCCAGGT 420
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DB 721 CATTCGCTGGTCTGCTGAGCTGAGCAGAGCTCTGAGGATCAATGCTGCTGCTGCTGCT 780
QY 1394 TTCAACAGCATCTTTGAGTTAGCTGGGTGGAAACAGCCAGCTTACGCCACCATAGGAGC 1453
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QY 1454 TGGTGGTCAATACCG 1470
DB 841 TGGAGTGGTCAACACAG 857
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mRNA sequence.
ACCESSION
BI152694
VERSION
BI152694.1 GI:14612695
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 813)
NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1185 row: b column: 02
High quality sequence stop: 782.
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Stem cell origin."
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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ORIGIN
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Matches	736; Conservative 0; Mismatches 41; Indels 4; Gaps 4;
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QY	1387 TCTACTATTCAACAGACATCTTTGAGTTAGTGTGGGTGGAAACAGCAGCCTACGCCACCA 1446
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QY	1926 CTTTCTCTCTTAGAGCAGAGG-TGAAACCCAGTACAGAAC-TTGAATCTTAGGGCCAG 1983
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QY	1984 A 1984
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DEFINITION	BY740650 RIKEN full-length enriched, 17 days embryo heart Mus musculus cDNA clone I920091F09 5', mRNA sequence.
ACCESSION	BY740650
VERSION	BY740650.1 GI:27165065
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	
AUTHORS	1 (bases 1 to 688) Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brusci, V., Catholia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyszewski, B., Yanagisawa, M., Yang, I., Yang, D., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 22354683 12466851
JOURNAL MEDLINE PUBMED	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp/ URL: http://genome.gsc.riken.go.jp/ Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
COMMENT	Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES	Location/Qualifiers 1..688 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J"

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Matches 654; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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892 GGTTCCTCATTTGGGCTACTCAGGCTAAACATCAGGGTGTGCTCTATGATGGAG 951
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Db 362 AATGCGCCCATCATCTTGGGGTGGCTTGGGAACATCAACCAATGGCCATGCTCA 421
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1132 TCTGCTCTGAGAGCCCGGATACCTCTACATATCCGGAACCTGGAGGGGCTGCCGAA 1191
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ACCESSION BO992119
VERSION BO992119.1 GI:22284133
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (bases 1 to 883)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgabbs@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, Ph.D.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13880 row: f column: 10
High quality sequence stop: 571.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_129"
/notes="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
Query Match 26.6%; Score 634.6; DB 13; Length 883;
Best Local Similarity 94.6%; Pred. No. 6.9e-112;
Matches 699; Conservative 0; Mismatches 36; Indels 4; Gaps 4;
QY 789 AGAAAGGGCTATGCTGGCAACAATGCTTGGCTGTGCTGGGGGGCGGCTCATGGCC 848
Db 42 AGAAAGGGCTATGCTGGCAACAATGCTTGGCGGTGTGGGGGGCGGCTCATGGCC 101
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Db 102 CTAGCAATGCGCGGCTCTCTATGAGATCACTATCTCGAGCGTTCCTCATTTGGCGCC 161
QY 909 TACTAGGGCTAAACATCAGGGTGTGCTTATGATGAGAAATCGCCCCACATCAT 968
Db 162 TACTAGGGCTAAACATCAGGGTGTGCTTATGATGAGAAATCGCCCCACATCAT 221
QY 969 CTTGGGGTGGCTTGGGAACATCAACCAATGGCCATCGTCAATGGCATCTGTTGCC 1028
Db 222 CTTGGGGTGGCTTGGGAACATCAACCAATGGCCATCGTCAATGGCATCTGTTGCC 281
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QY 1209 ACAGGCTGGCTGATGCTGCTGATGCTGAGCTGAGCTGAAGGATGAGAAACGGAAGT 1268
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BI153345
 LOCUS 834 bp mRNA linear EST 05-JUL-2001
 DEFINITION 602918617F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5068708 5',
 mRNA sequence.

ACCESSION BI153345

VERSION BI153345.1 GI:146113346

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHM1185 row: b column: 05

High quality sequence stop: 798.

FEATURES

source

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 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 24.4%; Score 581.6; DB 12; Length 834;
 Best Local Similarity 91.3%; Pred. No. 1.1e-101;
 Matches 716; Conservative 0; Mismatches 59; Indels 9; Gaps 9;

QY 1209 ACAGCTGGCTGATGCTGCTGATCATCTGCTGAGCTGAAGGATGAGAAACGGAAGTTG 1268
 Db 1 ACCGGCTGGCTGATGCTGCTGACGCATCTAGCTGAGGATGAGAAACGGAAGTTG 60

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 QY 1444 CCATAGAGCTGGTGGTCAATACCGTCTTCACTGTTGGTCTCGTGTCTTTAGTAGAGC 1503
 Db 241 CCATAGAGCTGGTGGTCAATACCGTCTTCACTGTTGGTCTCGTGTCTTTAGTAGAAC 300
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 LOCUS 1461 bp DNA linear GSS 16-DEC-2003
 DEFINITION Mus musculus SLC2A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY411068

VERSION AY411068.1 GI:39767036

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

PUBMED

AUTHORS

TITLE

Infering nonneutral evolution from human-chimp-mouse orthologous

gene trees

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 1461)

Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Query Match 24.2%; Score 577.4; DB 29; Length 1461;
Best Local Similarity 57.5%; Pred. No. 6.1e-101;
Matches 804; Conservative 0; Mismatches 582; Indels 12; Gaps 1;
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QY 585 TATAACATGGAGTCATCAAGCCACACAGAAAGTATTGAACAGAGCTACATGCAACT 644
DB 64 TATAACATGGTGTATCAACAGCCGCCACAGAGGTTATTGAGAGTCTTACAATCAACA 123
QY 645 TGCTGGGTAGGAGGCTCTGGGGACCGGATCCATCCACAGGACCCCTCACTACC 704
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QY 705 CTTTGGGCTCTCCGTTGGCCATCTTCTCTGTGGGTGGCATGATTTCTCTTTCTCAT 764
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ACCESSION BX389357
VERSION BX389357.1 GI:30462744
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 854)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8888.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDBAF002ZG06_AF00144_1&cluster=8888.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSDBAF002ZG06_AF00144_1.
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AUTHORS			

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Job time : 3711.57 secs

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1983	GATGAGAAATGAC	1994
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RESULT 3

US-09-643-597-135
; Sequence 135, Application US/096433597

; sequence 133, Apprio
; Patent No. 6426072
; GENERAL INFORMATION:

APPLICANT: Wang. Tongtong

APPLICANT: wang, Tongtong
APPLICANT: Fan, Lijun

APPLICANT: Fan, Liqun
APPLICANT: Kalos Michael D

APPLICANT: Kalos, Michael

APPLICANT: Bangor, Chaitan

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A

APPLICANT: Henderson, Robe

APPLICANT: McNeill, Patricia

Db 1010 GCTGACGTGTCCACGACGTGTGTGGCATCAACGCTGTCTTATTACTCCAGAGCAT 1069
QY 1406 CTTTGAGTTAGCTGGGTGGAAACAGCCAGCCTAGCCACCATAGAGCTGTGTGGTCAA 1465
Db 1070 CTTTCGAAAGGCGGGGTGCAGACGCTGTGTATGCCACCATTTGGCTCCGGTATCGTCAA 1129
QY 1466 TACCGTCTTTACGTTGGTCTCGGTGTCTTTAGTAGAGCGAGCTGGCGACGACACTCCA 1525
Db 1130 CACGGCTTTCACTGCTGTGCTGTGTTGTGTGGAGCGAGCGCGCGACCTTCCA 1189
QY 1526 TCTCTGGGCTGGCAGGATGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 1585
Db 1190 CCTCATAGGCTCGCTGGCATGGCGGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 1249
QY 1586 GCTGGAGCGGTTCATCATGAGTATGTGTGCTATGTGCTATGTGCTATGTGCTATGTGCT 1645
Db 1250 GCTGGAGCGGTTCATCATGAGTATGTGTGCTATGTGCTATGTGCTATGTGCTATGTGCT 1309
QY 1646 CTTCTTTGAGATTGGTCTGGGCTTCATCATGAGTATGTGTGCTATGTGCTATGTGCTATGTGCT 1705
Db 1310 CTTCTTTGAGATTGGTCTGGGCTTCATCATGAGTATGTGTGCTATGTGCTATGTGCTATGTGCT 1369
QY 1706 GGGCCCCCGCCAGCAGCATGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 1765
Db 1370 GGGTCCAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429
QY 1766 CTTTGGCATGGTTCAGTATGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 1825
Db 1430 TGTGGCATGTGCTTCCAGTATGTGGCAACTGTGTGGCTGTGGCTGTGGCTGTGGCT 1489
QY 1826 TGGCGTCTCTGCTGTGGCTTCTTCACTTCTTCACTTCTTCACTTCTTCACTTCTTCACT 1885
Db 1490 CACTGTGCTCTGCTGTGGCTTCTTCACTTCTTCACTTCTTCACTTCTTCACTTCTTCACT 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTCGACGG 1922
Db 1550 CCGGACATTTGACAGATCTCGGCCACCTTCGACGG 1586

RESULT 4

US-09-480-884A-135

; Sequence 135, Application US/09480884A

; Patent No. 6482597

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE REFERENCE: 210121.455C6

; CURRENT APPLICATION NUMBER: US/09/480,884A

; NUMBER OF SEQ ID NOS: 330

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 135

; LENGTH: 2856

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-480-884A-135

Query Match 28.5%; Score 679; DB 4; Length 2856;

Best Local Similarity 68.1%; Pred. No. 2.5e-178;

Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY 506 GGAAACCCCTCAGCAGCGAGTGACGTGGGACACTGTGCTCTGTATTTCTCAGCTGTGCT 565

Db 182 GGAGCCAGCAGCAAGAGCTGACGGTGGCTCATGCTGTGGAGGAGCAGTGTCT 241

QY 566 TGGCTCCCTTGTGGCTATTAACATTTGGAGTGTATCAACGCCGCCACAGAAAGTGTATGA 625

Db 242 TGGCTCCCTTGTGGCTATTAACATTTGGAGTGTATCAACGCCGCCACAGAAAGTGTATGA 301

QY 626 ACAGAGCTACAATGCAACTTGGCTGGGTAGGACAGGCTCTTGGGGACCGGACTCCATCC 685
Db 302 GGAGTTCTTACAACAGACATGGGTCCACCGTATGG-----GGAGAGCATCTT 349
QY 686 ACAAGGACCCCTCACTACCTTTGGGCTCTCTCGTGGCCATCTTCTGTGGGTGGCAT 745
Db 350 GCCCACCACGCTACACCGCTCTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGCAT 409
QY 746 GATTTCTCTCTTCTCATTTGGCATCATTTCTCAATGTTTGGGAAGAAAAGGCTATGCT 805
Db 410 GATTTGGCTCTCTTCTGTGGGCTTTTGGTTAAACCGCTTTTGGCCGGCGGAATTCATGCT 469
QY 806 GGCCAAACAATGTCTTGGCTGTGGGGGGGGCCCTCATGCGGCTTAGCAATGCGCGCGC 865
Db 470 GATGATGAACTGTCTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 529
QY 866 CTCCTATGAGATCACTCATTTCTGGACCGTTCTCATTTGGCGCCCTACTCAGGGCTAACATC 925
Db 530 GTCTTTGAGATGCTGATCTGGGCGCTTCTCATCGTGTGTACTGTGGGCTTGACCAAC 589
QY 926 AGGTTGGTGGCTATGATGTGGGAGAAATCGCCCCCACTCATCTTCCGGGTGCTTGGG 985
Db 590 AGGCTTGTGGCTATGATGTGGGAGAAATCGCCCCCACTCATCTTCCGGGTGCTTGGG 649
QY 986 AACACTCAACCAATTTGGCCATCGTCAATTTGGCATTTGGTTCGCCAGGTGTGGGTTTGGA 1045
Db 650 CACCTGCAACAGCTGGGATCGTGTGGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 709
QY 1046 GTCTATGCTGGGACAGCTACCTGTGGCCATTTCTTGTGCTATCACAGTACTCCCTGC 1105
Db 710 CTCCTATCATGGGCAACAGGACCTGTGGGCTGTGGCTGTGGCTGTGGCTGTGGCT 769
QY 1106 TCTCTGACGTGTCTTGTGGCTTCTGTGCTGTGGAGCCCCCGATACCTCTATCATAT 1165
Db 770 CTTGCTGACGTGTCTTGTGGCTTCTGTGCTGTGGAGTCCCGCTTCTGCTCTCATCAA 829
QY 1166 CCGGACCTGTGGGGGCTGCGGCAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGT 1225
Db 830 CCGGACAGGAGNACCGGCGCAAGAGTGTCTAAAGAGCTGCGCGGACAGCTGACGT 889
QY 1226 GTCTGATGCACTGGCTGAGCTGAAAGATAGAAAACGGAAGTTGGAAAGAGAGCTCCAT 1285
Db 890 GACCATGACCTGACGAGATGAAAGAGAGAGTGGGAGATGATGCGGAGAGAGAGT 949
QY 1286 GTCTTGTGCTGCTGCTGGGACGCGCACCCCGCGAGCTCTGATTTATGCAAGTGT 1345
Db 950 CACCATCTGGAGCTGTTCGCTCCCGGCTACCGCGAGCCCATCTCTCATCGCTGTGT 1009
QY 1346 GCTGACGTGAGCCAGCAGCTCTCAGGCATCAATGCTGTTTCTACTATTCAACAGCAT 1405
Db 1010 GCTGACGTGTCCAGCAGCTGTCTGGCATCAACGCTGTCTTATTTACTCCACGAGCAT 1069
QY 1406 CTTTGAAGTTAGTGGGTGGAAACAGCAGCTCTAGCCACCATAGAGCTGTGTGGTCAA 1465
Db 1070 CTTTGAAGTTAGTGGGTGGAAACAGCAGCTCTAGCCACCATAGAGCTGTGTGGTCAA 1129
QY 1466 TACGCTCTTACGTTGTCTGCTGCTTGTAGTAGCGAGCTGGGCGACGACACTCCA 1525
Db 1130 CAGGCTCTTACGTTGTGCTGCTGTTGTGGTGGAGCGAGCGGCGGCGGACCTGCA 1189
QY 1526 TCTCTGGGCTGGCAGGCTATGTGGCTGTGGCTCTTGTATGACGGTGGCTCTGCTGT 1585
Db 1190 CTTATAGGCTCGCTGGCATGGCGGTGTGGCATACTACTATGACCATCGCGCTAGCAT 1249
QY 1586 GCTGGAGCGGTTCATCCATGAGTTATGTGTCCATCGTGCCCATATTTGGCTTTGTGGC 1645
Db 1250 GCTGGAGCAGTACCTCGATGTCTTATGTGAGCATCGTGCCCATCTTTGGCTTTGTGGC 1309
QY 1646 CTTCTTTGAGTTGGTCTCGGCCCATCCCTGCTTCAATTTGCGCGAGCTTTCAGCCA 1705
Db 1310 CTTCTTTGAGTTGGTCTCGGCCCATCCCATGTTTCAATGTTGCTGCTGAACTTTCAGCCA 1369

QY 1706 GGGCCCCCGCCAGCAGCCATGGCTGTAGCTGGTTTCTCAACTGGACCTGTAACTTCAT 1765
DB 1370 GGGTCCAGCTCCAGCTGCCATTGCCGTTGCGAGCTTCTCCAACTGGACCTCAAAATTCAT 1429
QY 1766 CGTTGGCATGGGTTCCAGATATGTCGGATGCTATGGGTCCTCAGTCTTCTCTTATT 1825
DB 1430 TGTGGGATGCTTTCAGTATGTGGAGCACTGTGTGGTCCCTAGCTCTTTCATCTT 1489
QY 1826 TGGCGTCTCTCTGTTGGCTTCTTCATCTTTCACCTTCAAGAGTGCCTGAAACAGAGG 1885
DB 1490 CACTGTGCTCTGTTCTTCTTCTTCTTCACTTCACTACTTCAAAAGTTCCTGAGACTAAAGG 1549
QY 1886 CCGGACATTTGACAGATCTGGCCACCTTCCGACGG 1922
DB 1550 CCGGACCTTCGATGAGATGCTTCCGGCTTCCGGCAG 1586

RESULT 5

US-09-542-615A-135
; Sequence 135, Application US/09542615A

; Patent No. 6518256

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C8

; CURRENT APPLICATION NUMBER: US/09/542.615A

; CURRENT FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 350

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 135

; LENGTH: 2856

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-542-615A-135

Query Match 28.5%; Score 679; DB 4; Length 2856;

Best Local Similarity 68.1%; Pred. No. 2.5e-178;

Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY 506 GGAACCCCTCAGCAGCGAGTGAATGGACACTGGTCTTGTGTTCTCAGCTGTGCT 565
DB 182 GGAGCCAGCAGCAGAGAGTGAACGGTCCCTCATGCTGTGGGAGGAGAGTGTCT 241
QY 566 TGGCTCCCTTCAGTTGGCTATAACATTTGGAGTCAACACGCCCCACAGAAAGTGA 625
DB 242 TGGCTCCCTTCAGTTGGCTATAACACTGGAGTCAATGTCCCCCAGAAAGTGA 301
QY 626 ACAGAGTCAATGCAACTTGGCTGGGTAGGAGGGTCTGGGGGACCGACTCCATCCC 685
DB 302 GGAAGTTCTACAAACAGACATGGGTCCACCGCTATGG-----GGAGAGCATCCT 349
QY 686 ACAAGGACCCCTCACTACCTTTGGGCTCTCGTGGCCATCTTCTCTGTGGTGGCAT 745
DB 350 GCCACACAGCTCACCAGCTTGTGTCCTCTAGTGGCCATCTTTCTGTGGGGCAT 409
QY 746 GATTTCCTCTCTCATTTGGCATCAFTTCTCAATGGTTGGGAAGGAAAGGCTATGCT 805
DB 410 GATTGGCTCTCTCTGTGGCCCTTTTTCGTTAAACCGCTTTGGCCGGCGGAATTCATGCT 469
QY 806 GGGCAACAATGTCTTGGCTGTGGGGGGCGGCTCATGGGCTAGCCATGCGGGG 865
DB 470 GATGATGAACCTGTGGGCTTCGTGTCCCGCGTCTCATGGGCTTCTCGAAACTGGGCAA 529
QY 866 CTCTATGAGATCACTATTCTCGACGGTTCTCATTTGGGCGCTACTCAGGGCTTAACATC 925
DB 530 GTCTTTGAGATGCTGATCTCTGGGCGGCTTTCATCATCGGTGTGTACTGCGGCTGACCAC 589

RESULT 6

US-09-606-421B-135

; Sequence 135, Application US/09606421B

; Patent No. 6591315

QY 926 AGGGTTGGTGGCTATATATGTGGGAAGAAATGCGCCCCCATCATCTTCTCGGGGGTGCCTTGGG 985
DB 590 AGGCTTCGTGGCCCATATATGTGGTGAAGTGTCAACACAGACCTTTTCGTGGGGCCCTGGG 649
QY 986 AACACTCAACCAATGGCCCATGTCTATTTGGCAATCTCTGGTTGCCAGAGTGTGGGTTGGA 1045
DB 650 CACCTTGCACCAAGCTGGGATCGTGTGGGATCTCTCATCGCCAGGTTTCGGGCTTGGGA 709
QY 1046 GTCTATGTCTGGGCACAGCTACCTGTGGGCATTTGCTTCTGGCTATCACAGTACTTCCCTGC 1105
DB 710 CTCATCATGGGCAACAAGGACCTGTGGCCCTGCTGTGAGCATCATCTTCACTCCCGGC 769
QY 1106 TCTCTGAGCTGCTTCTGTGTGCTTCTGTCTGTGAGAGCCCGCATACCTCTTACATCAT 1165
DB 770 CTTGTGTCAGTGTATGCTGTGCTGCTTCTGCCCCGAGAGTCCCGCTTCTGCTCATCAA 829
QY 1166 CCGGAACCTGGAGGGGCTGCCGGAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGT 1225
DB 830 CCGCAACGAGGAGAAACCGGCGCAAGAGTGTCTAAAGAGCTGCGCGGGAACAGTGAAGT 889
QY 1226 GTCTGATGCATCTGGCTGAGCTGAAGGATGAGAAACGGAAGTTTGGAAAGAGAGGCTCCACT 1285
DB 890 GACCCATGACCTGCAGAGATGAAGAGAGAGTTCGCGAGATGATCGCGGAGAGAGGT 949
QY 1286 GTCTTGTGTCAGCTCCTGGGAGCGGACCCACCGGAGGCTCTGATTAATTCAGTGTGT 1345
DB 950 CACCATCTGGAGCTGTTCGCTCCCGCTTACCGGACGACCATCTCATCGCTGTGTGT 1009
QY 1346 GCTGAGCTGAGCCAGCAGCTCTCAGGATCATGCTGTTTCTACTATTCAACACGAGCAT 1405
DB 1010 GCTGAGCTGTCCAGAGCTGTCTGGCATCAACGCTGTCTTATTAATTCACAGAGCAT 1069
QY 1406 CTTTGAAGTTAGCTGGGGTGGAAACAGCAGCTACTACGCCACCATAGGAGCTGGTGTGTC 1465
DB 1070 CTTGAGAGAGGCGGGGTGCAGCAGCTGTGTATGCCACCATTTGGCTCCGGTATGTC 1129
QY 1466 TACCGTCTTCACTGTGCTGTGCTCTTGTGTGAGAGCGAGCTGGGCGAGCGACATCCA 1525
DB 1130 CACGGCTTCACTGTGCTGTGCTGTTTGTGTGTGAGCGAGCAGGCGCGGACCCCTGCA 1189
QY 1526 TCTCTGGGCTGGGAGGATGCTGGCTGTGCTGCTTGTGATGATGACGCTGGCTGTGCTGCT 1585
DB 1190 CTTATAGGCTTGGTGGCATGGGGTGTGCTCATCTATGACCATCGGCTTAGCACT 1249
QY 1586 GCTGAGCGGGTTTCCATCCATGAGTTATGTGTCCATCGTGGCCATATTTGGCTTTGTGGC 1645
DB 1250 GCTGAGCAGCTACCTGGATGCTCTATCTGAGCATCGTGGCCATCTTTGGCTTTGTGGC 1309
QY 1646 CTTCTTTGAGATTGGTCTCGGCCCATTCCTGTTTCAATTTGTGGCGAGCTCTTTCAGCCA 1705
DB 1310 CTTCTTTGAAGTGGTCTCGGCCCATTCCTCATGTTTCTCATGTTGCTGAACTCTTTCAGCCA 1369
QY 1706 GGGCCCCCGCCAGCAGCATGCTGTAGTGGTTCCTCAACTGGACCTGTAACTTCAT 1765
DB 1370 GGGTCACGTCGAGCTGGCATTCCTGTTGAGGCTTCTCCAACTGGACCTCAAAATTCAT 1429
QY 1766 CGTTGATCATGGGTTTCCAGTATTTGGGATGCTATGGGTCCTTACGCTTCTTCTTATT 1825
DB 1430 TGTGGGATGCTGTCTCCAGTATGTGGGCAACTGTGTGGTCCCTACGCTTCTCATCATCTT 1489
QY 1826 TGGGCTCTCTGCTGGCTTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 1885
DB 1490 CACTGTGCTCTGGTGTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1549
QY 1886 CCGGACATTTGACAGATCTCGGCGACCTTCCGACGG 1922
DB 1550 CCGGACCTTCGATGAGATGCTTCCGGCTTCCGGCAG 1586

QY 506 GGAACCCCTCAGCAGGAGTGAATGGACACTGGTCTTGTCTGTATTTCTCAGCTGTGCT 565
DB 182 GGAGCCAGCAGCAAGAGTGAATGGTCTTGTCTGTATTTCTCAGCTGTGCTGTGCTGTGCT 241
QY 566 TGCTCTCCTCAGTGTGCTGTATTAACATTTGAGTATCAATGAGTATCAATGAGTATCAATGAGTATCA 625
DB 242 TGCTCTCCTCAGTGTGCTGTATTAACATTTGAGTATCAATGAGTATCAATGAGTATCAATGAGTATCA 301
QY 626 ACAGAGTACAATGCAATTTGGCTGTGGTATGAGGAGTCTTGGGGGACCGAGTCCATCC 685
DB 302 GGAGTCTTACAACAGACATGGTCCAGCGCTATGG-----GGAGAGCATCCT 349
QY 686 AAGAGCAGCCTCAGTACCTTTGGGCTCTCTGGTGGGCTATTTCTGTGTGGTGGCAT 745
DB 350 GCCCAGCAGCCTCAGCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 409
QY 746 GATTTCTCCTTCTCATTGGCATCATTTCTCAATGTTGGGAGGAAAGGCTATGCT 805
DB 410 GATTTCTCCTTCTCATTGGCATCATTTCTCAATGTTGGGAGGAAAGGCTATGCT 805
QY 806 GGCCAAACAATGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 865
DB 470 GATGATGACCTGCT 529
QY 866 CTCCTATGAGATCACTCATTTCTCGGACGGTTCCTCATTTGGGCGCTACTCAGGGCTAAACATC 925
DB 530 GTCTTTGAGATGCTGATCTGCGGCGCTTTCATCATCGGTGTGCTGCTGCGGCTGAGCCAC 589
QY 926 AGGTTGGTCCCTATGATGTGGGAGAAATCGCCCACTCATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 985
DB 590 AGGTTGGTCCCTATGATGTGGGAGAAATCGCCCACTCATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
QY 986 AACACTCAACAATGCGCATCTGCTCATTTGGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045
DB 650 CACCTGACAGCTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
QY 1046 GTCTATGTGGGACAGTACCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
DB 710 CTCATCATGGGCAACAAGAGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
QY 1106 TCTCTGCGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
DB 770 CTTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
QY 1166 CCGGAACCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225
DB 830 CCGCAAGAGGAGAAACCGGCGCAAGAGTGTGCTTAAGAGCTGCGCGGAGACAGTACGT 889
QY 1226 GTCTGATGCACTGGCTGAGCTGAAGATGAAGAAACCGGAGTGTGGAAGAGAGCGTCCACT 1285
DB 890 GACCCATGACCTGAGGAGATGAAGAGAGAGTGTGCGAGATGATGCGGAGAGAGGT 949
QY 1286 GTCTTGTGCT 1345
DB 950 CACCATCTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
QY 1346 GCTGAGCTGAGCAGCTCTCAGGCACTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405
DB 1010 GCTGAGCTGTCCAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069
QY 1406 CTTTGAATGAGTGGGTGAAACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465
DB 1070 CTTTGAATGAGTGGGTGAAACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1129
QY 1466 TACCGTCTTCACTGCT 1525
DB 1130 CACGGCTTCACTGCT 1189
QY 1526 TCTCTGGGCTGCGCAGCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1585
DB 1190 CTTATAGGCT 1249
QY 1586 GCTGGAGCGGGTTCCATCCATGAGTTATGTGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1645

DB 1250 GCTGGAGCAGCTACCCCTGATGCTCTATCTGAGCATCGTGGCCATCTTTGGCTTTGTGGC 1309
QY 1646 CTTCTTTGAGATTTGGTCTGCTGGCCCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1705
DB 1310 CTTCTTTGAGTGGTCTGCTGGCCCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369
QY 1706 GGGCCCCCAGC 1765
DB 1370 GGGTCCAGCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429
QY 1766 CTTTGCATGCT 1825
DB 1430 TGTGGCAGTGTGCTTCCAGTATGTGAGCAACTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1489
QY 1826 TGCCTGCTCCTGCT 1885
DB 1490 CACTGTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTCGAGCG 1922
DB 1550 CCGGACCTTCGATGAGATCGCTTCGCGCTTCGCGCAG 1586

RESULT 8

US-09-023-655-1104
; Sequence 1104, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREWITH
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/023,655
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3915 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g183684
; US-09-023-655-1104

496 TTATATTTGCTGGAGAGCATATCAGGACTATATTTGTGGGCTAAATTTTACGGCTGGTTC 555
937 CTATGTATGTGGAGAAATCGCCCACTCATCTTCCGGGTGCTTGGGAACTCAAC 996
556 CTAATGATATCGGTGAATTTGCTCAACCGCTCTCAGGGGAGCACTTGGCACTTTTTCATC 615
997 AATTGGCCATCGTCATTTGGCTATCTGGTTCGCCAGGTGTTGGGTTCGAGTCTATGCTGG 1056
616 AGCTGGCCATCGTCACGGCAATTTCTTATTAGTCAGATTTATGGCTTTGAATTTATCTCTGG 675
1057 GCACAGCTACCTCTGTCGCTATGCTCTGCTGCTACAGTACTCCCTGCTCTCTGCGAGC 1116
676 GCATATATGATCTGTGGCAATCTTGTCTGGCTGCTGTGGTGGAGGCACTCTTCACT 735
1117 TGCTTCTGTTGCTCTGCTGCTGAGAGCCCGGATACCTCTACATCATCCGGAACCTGG 1176
736 CTCTGCTACTCTTTTCTGCTCCAGAAAGCCAGATACCTTTTACATCAAGTTAGATGAGG 795
1177 AGGGGCTCGCCGAAGAGTCTAAAGCGCTGACAGCTGGGTGATGTCTGTATGTCAC 1236
796 AAGTCAAGCAAAACAAAGCTTGAAAGAGCTCAGAGGATATGATGTCAACCAAGATA 855
1237 TGGCTGAGCTGAAGATGAGAAACGGAAGTTGGAAGAGAGCGTCCACTGCTCTCTGCTGC 1296
856 TTAATGAATGAGAAAGAGAGAGCATGAGTGAAGAGAGTCTCTATATTC 915
1297 AGCTCTGCGGAGCGCCACCGGAGGCTCTGATTTATGAGTGTGCTGCTGAGCTGA 1356
916 AGCTCTTCCAAATTCAGCTACCGAGCAGCTTATCTAGTGGCACTGATGCTGATGTTG 975
1357 GCAGAGCTCTCAGGATCAATGCTGTTTTCTACTATTTCAACGAGCATCTTTGAGTTAG 1416
976 CTCAGCAATTTTCCGAATCAATGGCAATTTTACTACTCAACGAGCATTTTTCAGACGG 1035
1417 CTGGGTGGAACAGCAGCTACGCCACATAGAGCTGTGTGCTCAATACCGTCTTCA 1476
1036 CTGGTATCAGAAACCTGTTATGCAACCATGAGTGGCTGTAAACATGGTTTTCA 1095
1477 CGTGTGCTCGGTCTCTTAGTAGAGCGAGCTGGGCGAGCACTCCATCTCTCTGGGCC 1536
1096 CTGCTGTCTCTGATTTCTTGTGGAAGAGCGAGGCGAGCTTCTCTCTTCTAATTGAA 1155
1537 TGGAGGCAATGTGGCTGCTGCTATGATGAGGCTGTGCTGCTGCTGCTGAGGCGGG 1596
1156 TGAGTGGGATGTTTGTGTCATCTTCAATGTCAGTGGGACTTGTGCTGCTGCAATAAGT 1215
1597 TTCCAT--CCATGAGTTATGTCCTCGTGGCCATATTTGGCTTTGTGGCTTCTTTGA 1654
1216 TCTCTGGACTGAGTTACTGTGAGCATGATGAGCCATCTTCTCTTTGTGAGCTTCTTTGA 1275
1655 GATTGTCTCTGGCCCATCCCTGGTTTCAATGTGGCCGAGCTCTTTCAGCCAGGCGCCCGG 1714
1276 AATTGGGCGAGCCCGATCCCTGTTTCAATGTTGGCTGAGTCTTTCAGTCAAGGACAG 1335
1715 CCAGAGCAGCATGGCTGTAGCTGTTTCTCAATGAGCCTGTAACTTCACTGCTGGCAT 1774
1336 TCTGCTGCTTTAGCAATAGCTGATTTAGCAATTTGAGCCTGCAATTTCAATGTAGCTCT 1395
1775 GGGTTTCCAGTATGTTGGGATGCTATGGGTCCCTAGTCTTCTTCTTATTTGCGCTCT 1834
1396 GTGTTTCCAGTATGTCGAGCTTCTGTGAGCTTATGTTGTTTTTCTCTTCTGCTGAGT 1455
1835 CTGCTTGGCTTCTTCACTTTCACCTTCTTAAGAGTGCCTGAAACAGAGCGCGGACATT 1894
1456 GCTCTGGCTTTTACCTGTTTACATTTTAAAGTTCCAGAAACCAAGAGGAGTCTTT 1515
1895 TGACCCAGATCTGGGCCACCTTTCGAGCGGACACCTTCTCTCTTATAGAGGAGGTGAACC 1954
1516 TGAGGAAATTTGCTGCAATTTCCAAAAGA---AGAGTGGCTCAGCCACAGGCGCAAAAGC 1572
1955 CAGTACAGACTTGTACTTGGCCGAGATGAGATGACTAA 1997
1573 TGCTGTAGAAATGAAATTCCTAGGAGCTACAGAGCTGTGTAA 1615

RESULT 10 - 392-1
US-09-031-392-1
; Sequence 1, Application US/09031392
; Patent No. 5942398
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Weng, Xun
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,392
; FILING DATE: 26-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 73...1761
US-09-031-392-1

Query Match 10.4%; Score 248.4; DB 2; Length 2343;
Best Local Similarity 50.8%; Pred. No. 1.3e-58;
Matches 622; Conservative 0; Mismatches 596; Indels 6; Gaps 1;
QY 687 CRAAGGCACCTCACTACCTTTGGGCTCTCGTGGCCATCTTCTGTGGGTGGCATG 746
DB 379 CAGACACTCTGACTCTGCTCTGCTGTGACTGTGTCATATTCGCCATCGGTGACTT 438
QY 747 ATTTCTCTCTTCTCAATGSCATCAATTTCTCAATGTTGGGAGGAAAGGCTATGCTG 806
DB 439 GTGGGACGTTAATTTCTGAAGATGATTGGAAAGGTTCTTGGGAGGAGACACATTTGCTG 498
QY 807 GCCAACAAATGCTTGTGCTGTGGGGGGGGCCCTCATGGGCGCTAGCCAAATGCGGCGCC 866
DB 499 GCCAAATATGGGTTTCAATTTCTGTGCTGATGTCGCTGCTGCTCCAGGCGAGGA 558
QY 867 TCCTATGAGATCACTCAATTTCTCGGACGGTTCCTCAATTTGGGCGCTTACTCAGGCTTAAACATCA 926
DB 559 GCCTTTGAATATGCTCAATTTGGGACCGCTTCAATGAGGCAATAGATGAGGCGTGCCTC 618
QY 927 GGGTTGGTGCCTATGATGTTGGGAGAAATGCGCCCACTCATCTTCCGGGTGCTTGGGA 986
DB 619 AGTGTGCTCCCAATGTACCTCAGTGAGATCTCACCCAAAGGAGATCCGTGGCTCTCTGGGG 678
QY 987 ACATCAACCAATTTGGCCATCGCTGATTTGGTTCGCCAGGTTGTTGGTTGGAG 1046

Db 679 CAGGTGACTGCGCACTTTATCTGCAATTGGCGTGTCTCACTGGGCGAGCTTCTGGGCGTCC 738
Qy 1047 TCTATGCTGGGCACAGCTACCTGTGGCCATTGCTTCTGGCTATCACAGTACTCCCTGCT 1106
Db 739 GAGCTGCTGGGAAAGAGAGTACCTGGCCATACCTGTTGGAGTATGTTGGTCCCTGCC 798
Qy 1107 CTCCTGCACTGCTTCTGTGTCCTTCTGTCTGAGAGCCCCCGATACCTCTACATCATC 1166
Db 799 GTTGTCCAGCTGCTGAGCTTCCCTTTCTCCGGACAGCCCACTGCTCTCTGGAG 858
Qy 1167 CGGAACCTGGAGGCGCTGCGGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGTG 1226
Db 859 AAGCAACAAGGAGAGCTGTGAAAGCTTCCAAAGCTTCTTGGGTAAGACAGAGCTT 918
Qy 1227 TCTGATGCACTGCTGAGCTGAGATGAGATGAGAAAGGAGTTGGAAGAGAGCGTCCACTG 1286
Db 919 TCCCAAGAGGTAGAGAGTCTGCTGAGAGCCACGCTGAGAGAGATCCGCTCGGTG 978
Qy 1287 TCTTGTGCTGAGCTCTCTGGGAGCGCCACCCAGCGGAGCTCTGATTAATTGCAAGTGGT 1346
Db 979 TCCGTGCTGGAGCTCTGAGAGCTCCCTACGCTCGCTGGCAGGTGGTCACTGATTTGTC 1038
Qy 1347 CTGCACTGAGCGCAGCTCTCAGGATCAATGCTGTTTCTACTATTAACACAGCATC 1406
Db 1039 ACCATGGCTGCTACCACTCTGTGGCTCAATGCAATTTGGTCTATPACCAACAGCATC 1098
Qy 1407 TTTGAGTTAGCTGGGT-----GGAACAGCAGCTACGCCACCATAGGAGCTGGTGTG 1460
Db 1099 TTTGAAAGCTGGGATCCCTCCGCAAGATCCCATACGTCACCTTGAGTACAGGGGGC 1158
Qy 1461 GTCAATACCGTCTTCACTGCTGCTCGGTGCTCTTAGTAGAGAGCTGGGCGAGGACA 1520
Db 1159 ATCGAGACTTTGGCTGCGCTCTCTCTGTTTGGTCAATTGAGCACTGGGACGGAGACC 1218
Qy 1521 CTCATCTCTGGGCTGGAGGATGCTGGCTGTGCTGCTGATGAGAGCTGGCTGCTG 1580
Db 1219 CTCCTCATTTGGTGGCTTTGGGCTCATGGGCTCTCTTTGGGACCCCTCACCATCAGCGT 1278
Qy 1581 CTGCTGCTGGAGCGGTTCCATCCATGATGATGCTCCATCGTGGCCATATTGGCTTT 1640
Db 1279 ACCCTGGAGGACCGCCCTGGGTCCCTACCTGAGTATCGTGGGATTCGTGGCCATC 1338
Qy 1641 GTGGCTCTTTTGAATGCTCTGGCCCTCCATCCCTCGTTTCAATTGGCGAGCTCTTC 1700
Db 1339 ATCGCTCTTCTGAGTGGGCGAGGTGGCATCCGTTCACTTGAAGTGGTCTCTTC 1398
Qy 1701 AGCAGGCGCCCGCCAGAGCCATGCTGAGCTGTTTCTCCTCACTGAGACCTGTAAAC 1760
Db 1399 CAGCAATCTCAGCGGCGGCTGCTCTCATCATTTGAGGACCGCTCACTGGCTCTCCAAC 1458
Qy 1761 TTTATGCTGGCATGGGTTTCCAGTATGTTGGGATGCTAGGCTCCCTAGCTCTCTCTT 1820
Db 1459 TTTGCTGTTGGCTCTCTTCTCCATTCATCAGAAAGCTGGAACACCTACTGTCTTCTTA 1518
Qy 1821 CTATTGCGCTCTCTGCTGCTTCTTCTATCTTCACTTCTTCAAGAGTCCCTGAAACC 1880
Db 1519 GTCTTTGTACAAATTGATACAGGTGCTATCTACCTGATTTTGTGCTGCTGAGACC 1578
Qy 1881 AGAGCGGAGCAATTGACAGATC 1904
Db 1579 AAAAAACAGAACCTATGCAAAATC 1602

RESULT 11

US-09-299-549-1
; Sequence 1, Application US/09299549
; Patent No. 6136547
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: GLUTEX AND USES THEREOF
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,549
; FILING DATE: 26-APR-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/031,392
; FILING DATE: 26-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/072002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 73...1761
; US-09-299-549-1

Query Match 10.4%; Score 248.4; DB 3; Length 2343;
Best Local Similarity 50.8%; Pred. No. 1.3e-58;
Matches 622; Conservative 0; Mismatches 596; Indels 6; Gaps 1;

Qy 687 CAAGGCACTCTCACTACCTTTGGGCTCTCTCCGTGGCCATCTTCTCTGTGGTGGCATG 746
Db 379 CCAGACACTCTGACTCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438
Qy 747 ATTTCTCTCTTCTCATTTGGCATCTTCTCAATGTTGGAGAGAAAGGGCTATGCTG 806
Db 439 GTGGGAGCTTAATTGTGAAGATGATTGGAAAGGTTCTTTGGAGGAGACACACTTTGCTG 498
Qy 807 GCCAACAAATGTTTGGCTGTGCTGGGGGGCGCCCTCATGGGCCCTAGCCAAATGCCCGGCC 866
Db 499 GCCAAATGAGTTTGGCAATTTCTGCTGATGCTGATGGCTGCTGCTGCTGCTGCTGCTG 558
Qy 867 TCCTATGAGATACCTCACTTCTGGACGGTTCCTCATTTGGCGCTACTCAGGGGTAAACATCA 926
Db 559 GCCTTTGAAATGCTCACTTGTGGGAGCTTCATCATTTGGGATAGATGAGGGCTGCGCCCTC 618
Qy 927 GGGTGTGCTATGATGTTGGGAGAAATCGCCCCCACTCATCTTCGGGGTCCCTTGGGA 986
Db 619 AGTGTGCTCCCACTGATACCTCAGTGAGATCTCACCAAGGAGATCCCGGGCTCTCTGGGG 678
Qy 987 ACCTCAACAAATTTGGCATCTGTTGGCAATTTCTGTTGCCAGGTGTTGGTGTGGAG 1046
Db 679 CAGGTGACTGCTTCTTATCTGATTTGGCTGTTCATGAGGAGCTTCTGGGCTGCCCC 738
Qy 1047 TCTATGCTGGGACAGTACCTCTGGCCATTTCTTCTGCTATCAGAGTACTCCCTGCT 1106
Db 739 GAGCTGCTGGGAAAGAGAGTACCTGCGCATACCTGTTGGAGTATTTGGTCTGCTGCTG 798
Qy 1107 CTCCTGAGCTGCTTCTGTTGCCCTTCTGCTCTGAGAGCCCCCGCATCTCTACATCATC 1166
Db 799 GTTGTCCAGCTGCTGAGCCTTCCCTTTCTCCCGACAGCCCAACGCTACCTGCTCTTGGAG 858

QY 1287 TCCTGCTGACGCTCTGCGCAGCGCCACCCAGCGAGCTCTGATTTATTGCACTGGTG 1346
DB 979 TCCGTGCTGGAGCTGCTGAGAGCTCCCTACGTCCGCTGCGAGGTGGTCAACGCTGATGTC 1038
QY 1347 CTGCACTGAGCCAGCAGCTCTCAGGCATCAATGCTGTTTCTACTATTTCAACAGCATC 1406
DB 1039 ACCATGGCCTGTACCAGCTCTGTGGCTCAATGCAATTTGGTTCTATACCACAGCATC 1098
QY 1407 TTTGATTTAGCTGGGT-----GGAACAGCAGCCTAGCCACCATAGGAGCTGGTG 1460
DB 1099 TTTGGAAGAGCTGGGATCCCTCCGCAAGATCCCATACGTCACTTGGTACAGGGGC 1158
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DB 1159 ATCGAGACTTTGGCTGCGCTCTTCTCTGTTTGGTCAATGAGCAGCTGGGACGAGACCC 1218
QY 1521 CTCATCTCTCTGGGCTGCGCAGGCATGTGTGGCTGTGCCATCTTGAAGACGGTGGCTCTG 1580
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DB 1579 AAAACAGAACCTATGCAGAAATC 1602

RESULT 13

US-09-620-312D-574

Sequence 574, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2H
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_fl_genes Version 1.0
SEQ ID NO 574
LENGTH: 2842
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (345)..(1571)
FEATURE: misc feature
LOCATION: (1)..(2842)
OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-574

Query Match 9.3%; Score 222.2; DB 4; Length 2842;

Best Local Similarity 50.6%; Pred. No. 2.8e-51;
Matches 567; Conservative 0; Mismatches 548; Indels 6; Gaps 1;

QY 790 GGAAGAGGGCTATGCTGCGCAACAATGCTTTGGCTGTGCTGCGGGCGCCCTCATGGGCC 849
DB 358 GGAAGCACACTTTGCTGCGCAATAATGGGTTTGCAATTTCTGCTGCAATTTGCTGATGGCCT 417
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DB 418 GCTCGCTCCAGGACGAGCGCTTTGAAATGCTCATCTGCGGACGCTTCATCATGGGCATAG 477
QY 910 ACTCAGGGCTAAACATCAGGGTTGCTGCTATGATGCGGAGAAATCGCCCCACTCATC 969
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QY 1090 TCACAGTACTCCCTGCTCTCTGCGAGCTGCTTCTGTTGGCCCTCTGCTGAGAGCCCC 1149
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QY 1150 GATACCTCTACATCATCCGAACTGAGGGGCTGCGCCGAAAGAGTCTAAAGCGCCTGA 1209
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QY 1210 CAGGCTGGGCTGATGCTCTGATGCACTGGCTGAGCTGAAGATGAGAAACGGAAGTTGG 1269
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Qy	834	GGGGCCCTCATGGCCCTAGCCCAATGCCGGGGCTCCTATGAGATATCATTCATTCGGGACGG	893
Db	80	GGTTGCCCTTATGGGATTCTCAGACAAGCTGAGTTGGTTGAAATGCTGATTCCTGGGGCCAC	139
Qy	894	TTCTCTATTCGGCGCTACTCAGGGCTAAACATCAGGGTTTGGTGCCTATGTATGTGGGAGAA	953
Db	140	TAGATTACTGGCTTGTAATCGGGAAGCTGCGACAAGTTTGTGCCCCATGTACATGTGGAGAG	199
Qy	954	ATCGCCGCCCACTCATCTTCGGGGTGCTTGGGAACTCAACCAATTTGGGCCATGTCATTT	1013

Db	200	ATCTCGCCTACTCCCCCTTTGGGGTACCTTTAGTGTCTCAACCAAGCTGG---ACGTGCTT	256
Qy	1014	GGCATTCTGGTTGCCAGGTGTGGGTTTGGAGTCTATGCTGGGCACAGCTACCCCTGTGG	1073
Db	257	GGTATTCTGGAGATCCAGATCTTTGGTCTGGAGTTTCATCTTGGGGTCTGAAGAGCTATGC	316
Qy	1074	CCATTGCTTCTGGCTATCAGATCTCCCTGTCTCCTGCGAGCTGCTTCTGTTGCCCTTC	1133
Db	317	CCAGNGATACTGGGCTTTACCATCCTTCAGCTGTCTTAAAGTGNAGCCCTTCCATTT	376
Qy	1134	TGTCCTGAGAGCCCCCGATACCTCTACATCATCCGGACCTGGAG	1178
Db	377	TGCCCTGGAAGTCGTAAGTTTTTGCTCATTAACAGAAAGGAG	421

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Job time : 111.588 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
17041.041 Million cell updates/sec

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Perfect score: 2386
Sequence: 1 tcgactctagagatccctcctt.....ctggactttcttcagttg 2386

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA.*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
 - 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
 - 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
 - 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2386	100.0	2386	15	US-10-067-449-10 Sequence 10, Appl
2	1528.2	64.0	2506	16	US-10-191-803-36 Sequence 36, Appl
3	1490.4	62.5	2338	15	US-10-067-449-12 Sequence 12, Appl
4	1488.8	62.4	2338	15	US-10-067-449-13 Sequence 13, Appl
5	1485.6	62.3	2338	15	US-10-067-449-14 Sequence 14, Appl
6	1229	51.5	7828	15	US-10-067-449-9 Sequence 9, Appl
7	1066.4	44.7	2592	9	US-09-894-927A-8 Sequence 8, Appl
8	679	28.5	2856	9	US-09-735-705-135 Sequence 135, Appl
9	679	28.5	2856	9	US-09-850-716A-135 Sequence 135, Appl
10	679	28.5	2856	9	US-09-880-107-2128 Sequence 128, Appl
11	679	28.5	2856	9	US-09-897-778-135 Sequence 135, Appl
12	679	28.5	2856	10	US-09-466-396A-135 Sequence 135, Appl
13	679	28.5	2856	13	US-10-342-887-1394 Sequence 1294, Appl
14	679	28.5	2856	13	US-10-007-700-135 Sequence 135, Appl

15	679	28.5	2856	13	US-10-172-118-1294	Sequence 1294, Ap
16	679	28.5	2856	13	US-10-170-385-220	Sequence 220, App
17	679	28.5	2856	13	US-10-117-982-135	Sequence 135, App
18	679	28.5	2856	16	US-10-295-027-1031	Sequence 1031, Ap
19	679	28.5	2856	16	US-10-313-986-135	Sequence 135, App
20	679	28.5	2856	16	US-10-159-563-235	Sequence 235, App
21	679	28.5	3366	15	US-10-101-510-473	Sequence 473, App
22	679	28.5	7777	15	US-10-067-449-11	Sequence 11, Appl
23	678.2	28.1	2778	15	US-10-176-847-75	Sequence 75, Appl
24	670.2	28.4	2613	9	US-09-778-927A-7	Sequence 7, Appl
25	667.4	28.0	2683	9	US-09-778-927A-6	Sequence 6, Appl
26	663	27.8	2349	9	US-09-822-849A-381	Sequence 381, App
27	639.2	26.8	2319	9	US-09-778-927A-8	Sequence 8, Appl
28	637.6	26.7	2860	9	US-09-778-927A-9	Sequence 9, Appl
29	589	24.7	3046	9	US-09-778-927A-10	Sequence 10, Appl
30	542.8	22.7	3915	9	US-09-954-456-507	Sequence 507, App
31	542.8	22.7	3915	13	US-10-342-887-1341	Sequence 1341, Ap
32	542.8	22.7	3915	13	US-10-172-118-1341	Sequence 1341, Ap
33	542.8	22.7	3915	13	US-10-170-385-248	Sequence 248, App
34	542.8	22.7	3915	16	US-10-341-434-88	Sequence 88, Appl
35	542.8	22.7	3915	17	US-10-641-643-1104	Sequence 1104, Ap
36	510.8	21.4	1852	13	US-10-257-021-27	Sequence 27, Appl
37	456.2	19.1	3168	9	US-09-880-107-2099	Sequence 2099, Ap
38	456.2	19.1	3168	13	US-10-403-161-33	Sequence 33, Appl
39	456.2	19.1	3168	16	US-10-099-322-33	Sequence 33, Appl
40	456.2	19.1	3168	16	US-10-044-564-33	Sequence 33, Appl
41	454.8	19.1	2573	12	US-10-152-319A-1558	Sequence 1558, Ap
42	454.4	19.0	1587	13	US-10-403-161-37	Sequence 37, Appl
43	453	19.0	1664	13	US-10-403-161-39	Sequence 39, Appl
44	453	19.0	5228	10	US-09-919-039-216	Sequence 216, App
45	452.8	19.0	1587	13	US-10-403-161-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-10-067-449-10
; Sequence 10, Application US/10067449
; Publication No. US20030166258A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wiczorke, Roman
; APPLICANT: Dlugai, Silke
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; TITLE OF INVENTION: GLUT Promoter
; FILE REFERENCE: DEAV2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: DE 101 06 718.6
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2386
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-067-449-10

Query Match	100.0%	Score 2386;	DB 15;	Length 2386;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2386;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	121	GTGGCTCTCCACCTGTTTTCATCATTTAGATTTTCGCAAGCCATCGCTGCTTTC	180	Db	1201	AGCGCTGACAGGCTGGGCTGATGCTGATGCACTGGCTGAGCTGAAGATGAGAAC	1260
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Db	181	GTTTTTGGGATGGCAACGAGGGCTGGAAAAATTAAACGGTACGCGCTAAACGATAGTAA	240	QY	1321	GGCAGCCTCTGATTTATTTGCAAGTGGTGTGCAAGCCAGCAGCTCTCAGGCATCAATG	1380
QY	241	TAGGCGACGCAACTGGCTGGAGCAACAATAAGTCCGCTATTTTATGTTTTCAAAA	300	Db	1321	GGCAGCCTCTGATTTATTTGCAAGTGGTGTGCAAGCCAGCAGCTCTCAGGCATCAATG	1380
Db	241	TAGGCGACGCAACTGGCTGGAGCAACAATAAGTCCGCTATTTTATGTTTTCAAAA	300	QY	1381	CTGTTTTCTACTATTCAACAGCAGCATCTTTGAGTTAGCTGGGGTGGAAACGCGAGCTAGC	1440
QY	301	CCTAGCAACCCACCAAACTTGTCATGTTCCGGATTCAAAATGATATAAAAGCGA	360	Db	1381	CTGTTTTCTACTATTCAACAGCAGCATCTTTGAGTTAGCTGGGGTGGAAACGCGAGCTAGC	1440
Db	301	CCTAGCAACCCACCAAACTTGTCATGTTCCGGATTCAAAATGATATAAAAGCGA	360	QY	1441	CCACATAGAGAGCTGGTGTGCTCAATACCGTCTTCAAGTTCGCTCGGTCTCTTAGTAG	1500
QY	361	TTACAATTCTACATTTCAACCAAGTTTGAGATTTCTCTCTCAATTTCTCTTATATTA	420	Db	1441	CCACATAGAGAGCTGGTGTGCTCAATACCGTCTTCAAGTTCGCTCGGTCTCTTAGTAG	1500
Db	361	TTACAATTCTACATTTCAACCAAGTTTGAGATTTCTCTCTCAATTTCTCTTATATTA	420	QY	1501	AGCAGCTGGGCGACGACACTCCATCTCTGGGCTGGCAGGCAATGTGGCTGCGCA	1560
QY	421	GATTTATAGAACACAAATTAATTAACAAAAGACTTATAAGCAACATAATGCTGAAT	480	Db	1501	AGCAGCTGGGCGACGACACTCCATCTCTGGGCTGGCAGGCAATGTGGCTGCGCA	1560
Db	421	GATTTATAGAACACAAATTAATTAACAAAAGACTTATAAGCAACATAATGCTGAAT	480	QY	1561	TCCTGATGACGGTGGCTCTGCTGCTGAGCGGGTTCCATCCATGAGTTATGTGTCCA	1620
QY	481	TCAGCAGATCGGCTCTGAAGATGGGAAACCCCTCAGCAGGAGTGAATCGGACACTGG	540	Db	1561	TCCTGATGACGGTGGCTCTGCTGCTGAGCGGGTTCCATCCATGAGTTATGTGTCCA	1620
Db	481	TCAGCAGATCGGCTCTGAAGATGGGAAACCCCTCAGCAGGAGTGAATCGGACACTGG	540	QY	1621	TCGTTGGCCATATTTGGCTTTTGCGCTCTTTGAGATTGGTCTCTGGGCCCATCCCTGGT	1680
QY	541	TCCTTGTCTATTTCTCAGCTGTGCTGGCTCCCTTCAGTTTGGCTATAAACAATGGAGTCA	600	Db	1621	TCGTTGGCCATATTTGGCTTTTGCGCTCTTTGAGATTGGTCTCTGGGCCCATCCCTGGT	1680
Db	541	TCCTTGTCTATTTCTCAGCTGTGCTGGCTCCCTTCAGTTTGGCTATAAACAATGGAGTCA	600	QY	1681	TCATTTGGCGGAGCTCTTCAGCCAGGCGCCCGCCAGCAGCCATGCTGAGCTGGTT	1740
QY	601	TCAGCGCCCAAGAGATGTAACAGAGCTACATGCAACTTGGCTGGGTGAGGACG	660	Db	1681	TCATTTGGCGGAGCTCTTCAGCCAGGCGCCCGCCAGCAGCCATGCTGAGCTGGTT	1740
Db	601	TCAGCGCCCAAGAGATGTAACAGAGCTACATGCAACTTGGCTGGGTGAGGACG	660	QY	1741	TCTCCAACTGGACCTGTAACTTCACTGTTGGCATGGGTTTCCAGTATGTTGGGATGCTA	1800
QY	661	GTCTGGGGGACCGGACTTCATCCCAAGGCAACCTCCTACCTTTGGGCTCTCTCCG	720	Db	1741	TCTCCAACTGGACCTGTAACTTCACTGTTGGCATGGGTTTCCAGTATGTTGGGATGCTA	1800
Db	661	GTCTGGGGGACCGGACTTCATCCCAAGGCAACCTCCTACCTTTGGGCTCTCTCCG	720	QY	1801	TGGTCCCTACGCTTCTCTTCAATTTGGCGTCTCTCTGCTGGGTTCTTCACTTCACT	1860
QY	721	TGGCCATCTTCTCTGGGTGGCATGATTTCTCTCTCTCAATTTGGCATATTTCTCAAT	780	Db	1801	TGGTCCCTACGCTTCTCTTCAATTTGGCGTCTCTCTGCTGGGTTCTTCACTTCACT	1860
Db	721	TGGCCATCTTCTCTGGGTGGCATGATTTCTCTCTCTCAATTTGGCATATTTCTCAAT	780	QY	1861	TCCTAAGATGCTGAAACAGAGCGCGGACATTTGACAGATCTCGGCGACCTTCCGAC	1920
QY	781	GGTTGGGAAGAAAGGCTATGCTGGCCCAACATGCTTGGCTGTGCTGGGGGGCGCC	840	Db	1861	TCCTAAGATGCTGAAACAGAGCGCGGACATTTGACAGATCTCGGCGACCTTCCGAC	1920
Db	781	GGTTGGGAAGAAAGGCTATGCTGGCCCAACATGCTTGGCTGTGCTGGGGGGCGCC	840	QY	1921	GGACACCTTCTCTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATACTTAGGGC	1980
QY	841	TCAATGGGCTAGCCAAATGCGGGGCTCTCTATGATATCAATTCGAGCGGTTCTCTCA	900	Db	1921	GGACACCTTCTCTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATACTTAGGGC	1980
Db	841	TCAATGGGCTAGCCAAATGCGGGGCTCTCTATGATATCAATTCGAGCGGTTCTCTCA	900	QY	1981	CAGATGAGATGACTAATCGATTTGAAAGTGAAGCGTCCATCATCTCTTAAATTTTCA	2040
QY	901	TTGGGCGCTTACTCAGGGCTTAACATCAGGGTTGGTGGCTTATGATGTGGGAGAAATCGCC	960	Db	1981	CAGATGAGATGACTAATCGATTTGAAAGTGAAGCGTCCATCATCTCTTAAATTTTCA	2040
Db	901	TTGGGCGCTTACTCAGGGCTTAACATCAGGGTTGGTGGCTTATGATGTGGGAGAAATCGCC	960	QY	2041	TGACTGACGTTTTTCTTCAATTTTAAATTTATCATAGTATTTGTTGAAAAAATAAAAAA	2100
QY	961	CACTCATCTTCGGGGTGGGAAACACTCAACCAATTTGGCCATCGTCAATGGCATTC	1020	Db	2041	TGACTGACGTTTTTCTTCAATTTTAAATTTATCATAGTATTTGTTGAAAAAATAAAAAA	2100
Db	961	CACTCATCTTCGGGGTGGGAAACACTCAACCAATTTGGCCATCGTCAATGGCATTC	1020	QY	2101	AATTTCCCTTATCAATGATATCTTACGATTTATAAATTTCTTACCTTAACCTATTAT	2160
QY	1021	TGGTTGCCAGGTGTTGGGTTGGAGTCTATGCTGGGCAAGCTACCTGTGGCCATTCG	1080	Db	2101	AATTTCCCTTATCAATGATATCTTACGATTTATAAATTTCTTACCTTAACCTATTAT	2160
Db	1021	TGGTTGCCAGGTGTTGGGTTGGAGTCTATGCTGGGCAAGCTACCTGTGGCCATTCG	1080	QY	2161	TGTTACATATACAGATTTATATACATATTAACCTTTTCTTAAACAGGAAAAA	2220
QY	1081	TTCTGGCTATACAGTACTCCTCTCTGAGCTGCTCTCTGAGCTGCTCTGTTGGCTG	1140	Db	2161	TGTTACATATACAGATTTATATACATATTAACCTTTTCTTAAACAGGAAAAA	2220
Db	1081	TTCTGGCTATACAGTACTCCTCTCTGAGCTGCTCTCTGAGCTGCTCTGTTGGCTG	1140	QY	2221	AAAAAGAAACGATAACATGCTCTGCCATCTCTGTTTCAACGAGCAAAATTAACACGCAA	2280
QY	1141	AGAGCCCCGATACCTCTACATCATCCGGAACCTTGGAGGGGCTCCCGGAAGAGTCTAA	1200	Db	2221	AAAAAGAAACGATAACATGCTCTGCCATCTCTGTTTCAACGAGCAAAATTAACACGCAA	2280
Db	1141	AGAGCCCCGATACCTCTACATCATCCGGAACCTTGGAGGGGCTCCCGGAAGAGTCTAA	1200	QY	2281	AATGAATGTCCCTATGAAATTTATTAAGGAGCAACATCACAGACTTATCTCTGGGGGT	2340
QY	1201	AGCGCTGACAGGCTGGGCTGATGCTGATGCACTGGCTGAGCTGAAGGATGAGAAAC	1260				

Db 916 CCACAGCTCTTCGTGGAGCCCTTGGGACCCCTGCACACAGCTGGGCATCGTGTGGGATCC 975
Qy 1021 TGGTTGCCAGGTGTTGGGTTGGAGTCTATGCTGGGCACAGCTACCCGTGGCCATTCG 1080
Db 976 TTAATGGCCAGGTGTTGGCTTAGACTCATCATGGGCAATGCAGACTTGTGGCTCTAC 1035
Qy 1081 TTCTGGCTATACAGTACTCCCTGCTCTCTCTGCTGAGCTGCTTCTGTGTGCCCTTCTGTCCG 1140
Db 1036 TGCTCAGTGTCTATCTTCATCCAGCCCTGTACAGTGTATCTGTGTGCCCTTCTGCCCTG 1095
Qy 1141 AGAGCCCCGATACCTCTACATCATCCGAACCTGGAGGGGCTGCGCCGAAGAGTCTAA 1200
Db 1096 AGAGCCCCGCTTCTGTCTCATCAATCGTAACGAGGAGAACCGGGCCAAAGAGTGTGCTGA 1155
Qy 1201 AGCGCTGACAGGCTGGCTGATGTCTGTATGCACTGGCTGAGCTGAAGATGAGAAAC 1260
Db 1156 AAAGCTTCGAGGGACAGCCGATGTGACCCGAGACCTCGAGGATGATGAAGAGGGTC 1215
Qy 1261 GGAAGTTGGAAGAGAGGGTCCACTGTCTTGTCTGCACTCTCTGGCAGCGCCACCCACC 1320
Db 1216 GGCAGATGATCGGGAGGAAGGTCAACATCTTGGAGCTGTTCCGCTCACCGCTACC 1275
Qy 1321 GGCAGCTCTGATTAATGTCAGTGTGCTGCACTGAGCCAGCAGCTCTCAGGCATCAATG 1380
Db 1276 GCGAGCCCATCTCATCGCGGTGTGCTGCACTGTCCAGCAGCTGTGCGGCATCAATG 1335
Qy 1381 CTGTTTCTACTATTCAACACGACATCTTGTGATGCTGGGTGGAACAGCAGCCTACG 1440
Db 1336 CTGTGTCTACTACTCAACAGACATCTTCGAGAAGCAGGTGTGAGCAGCCTGTGTATG 1395
Qy 1441 CCACCATAGGAGCTGTGTGTGTCATACCGTCTTCACTGTGTCTCGGTGCTCTTAGTAG 1500
Db 1396 CCACCATCGCTCGGTATCGTCAACAGGCTTCACTGTGTGTGCTGTGCTGTG 1455
Qy 1501 AGCAGCTGGGCGAGCAGCATCTCATCTCTGGCGCTGGCAGGCAATGTGTGCTGTGCGCA 1560
Db 1456 AGCAGCTGGCGCTGGGACCTCTCATTTGTGCTGTGCTGGCATGGCGGCTGTGCTG 1515
Qy 1561 TCTTGATGACGTGTCTGTCTGTCTGGAGCGGTTCCATCATGATGATGTGTCCA 1620
Db 1516 TGCTATGACCATCGCCCTGGCCCTGTGGAGCAGCTGCCCTGGATGTCCTATCTGAGTA 1575
Qy 1621 TGTGGCCCATATTTGGCTTTTGGCTCTCTTTGAGATTTGGTCTCTGGCCCATCCCTGGT 1680
Db 1576 TGTGGCCCATCTTTGGCTTTTGGCTCTCTTTGAAGTAGGCCCTGGTCTCTATCCATGT 1635
Qy 1681 TCATTGTGCCAGCTCTTCAGCCAGGCGCCCGCCAGCAGCAGCAGCAGCTGTAGCTGTT 1740
Db 1636 TCATTGTGCCAGCTGTTTCAGCCAGGCGCCCGCCAGCCTGTCTGTGTGCTGTGCTG 1695
Qy 1741 TCTCCAACCTGGACCTGTAACCTTCATCGTTGGCATGGGTTCCAGTATGTTGCGGATGCTA 1800
Db 1696 TCTTAACCTGGACCTCAAACTTCATCGTGGGATGTGCTTCCAATATGGAGCACTGT 1755
Qy 1801 TGGGTCCTTACGTCTCTCTTATTTGGCGTCTCTCTCTTGGCTTCTTCACTCTTCACT 1860
Db 1756 GTGGCCCTTACGTCTCTCATCTTTCAGGTGTCTGTGTCTCTTCTTCTTCTTCACT 1815
Qy 1861 TCCTAAGAGTGTCTGAACACGAGCGCGGCAATTTGACCAAGATCTCGGCGCACTTCGAC 1920
Db 1816 ACTTCAAAGTTCTTGAGACCAAAGCCGAGCCTTCGATGAGATGCTTTCGCGCTTCGCG 1875
Qy 1921 GGACACCTTCTCTTTAGAGCAGGAGGTGAACCCAGTACAGAACTTGAATACTTAGGG 1980
Db 1876 AGGGGGTGC---CAGCCAGCGCAAGACACCTGAGGAGCTCTTCAACCTCTGGGG 1932
Qy 1981 CAGATGAGAATGACTAATCGATTGAAGTGAAGCCTCCATCATCTCTCTTAATTTTCA 2040
Db 1933 CTGACTCCCAAGTGAATCGATTGAAGTGAAGCCTCCATCATCTCTCTTAATTTTCA 1992
Qy 2041 TCACTGACGTTTTTCTTCAATTTAATTAATCATAGTATTTGTTGAAAAAAGAAAAA 2100
Db 1993 TGACTGACGTTTTTCTTCAATTTAATTAATCATAGTATTTGTTGAAAAAAGAAAAA 2052

Qy 2101 AATTTCCCTTATCAATGATATCCTTAGCATATATAATTCCTTACCTAAACCTATTAT 2160
Db 2053 AATTTCCCTTATCAATGATATCCTTAGCATATATAATTCCTTACCTAAACCTATTAT 2112
Qy 2161 TGTGTACATATATCAGAGTATTATTAATATATATACCTTTTCTCTAAACAGGAAAAA 2220
Db 2113 TGTGTACATATATCAGAGTATTATTAATATATATACCTTTTCTCTAAACAGGAAAAA 2172
Qy 2221 AAAAGAAAACGATACATGCTCTGCCATCCTTTGTTACCCGAGCAAAATTAAGAACGCA 2280
Db 2173 AAAAGAAAACGATACATGCTCTGCCATCCTTTGTTACCCGAGCAAAATTAAGAACGCA 2232
Qy 2281 AATGAATTTGCTCCCTATGAAATTTAAGAGCACCATCACAGACTTATCTCTGGGGGT 2340
Db 2233 AATGAATTTGCTCCCTATGAAATTTAAGAGCACCATCACAGACTTATCTCTGGGGGT 2292
Qy 2341 CCTCTAGAAAATAGTCAGGTACTTGGCTGGACTTTCTTCAGTTG 2386
Db 2293 CCTCTAGAAAATAGTCAGGTACTTGGCTGGACTTTCTTCAGTTG 2338

RESULT 5
US-10-067-449-14
; Sequence 14, Application US/10067449
; Publication No. US20030166258A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wiczorke, Roman
; APPLICANT: Diugai, Silke
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; FILE REFERENCE: DEAV2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: DE 101 06 718.6
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-067-449-14

Query Match 62.3%; Score 1485.6; DB 15; Length 2338;
Best Local Similarity 77.7%; Pred. No. 0;
Matches 1854; Conservative 0; Mismatches 484; Indels 48; Gaps 3;
Qy 1 TCGACTCTAGAGGATCCCTTAAGCTAATCCTTATGATCCGGAGAAAAGCGGGTCTTT 60
Db 1 TCGACTCTAGAGGATCCCTTAAGCTAATCCTTATGATCCGGAGAAAAGCGGGTCTTT 60
Qy 61 TAACCTCAATAAAATTTTCGAAATCCTTTTCTTACGCTTTTCTTCGGGAACCTAGATAG 120
Db 61 TAACCTCAATAAAATTTTCGAAATCCTTTTCTTACGCTTTTCTTCGGGAACCTAGATAG 120
Qy 121 GTGGCTCTTCCACCTGTTTTTCCATCATTTTATGTTTTTTCGAAAGCAGTCGCTTTTC 180
Db 121 GTGGCTCTTCCACCTGTTTTTCCATCATTTTATGTTTTTTCGAAAGCAGTCGCTTTTC 180
Qy 181 GTTTTTCCGATGGCGAAGCGGCTGGAAATTAACGGTACGCGCTTAACGATAGTAA 240
Db 181 GTTTTTCCGATGGCGAAGCGGCTGGAAATTAACGGTACGCGCTTAACGATAGTAA 240
Qy 241 TAGGCCACGCAACTGGCGTGGACGACCAATAGTCGCCCAATTTTTTATGTTTTCAAA 300
Db 241 TAGGCCACGCAACTGGCGTGGACGACCAATAGTCGCCCAATTTTTTATGTTTTCAAA 300
Qy 301 CTTAGAACCCCAACCAAACTTGTCTCGGATTTCAGATGATATATAAGCGA 360

301 CCTAGCAACCCCAACAACTTGTCTCATCGTTCCGGATTACAAATGATATAAAAGCGA 360
361 TTACAATTTCTACATTTCAACAGATTGAGATTTCCTTTCTCAATTCCTCTTATATTA 420
361 TTACAATTTCTACATTTCAACAGATTGAGATTTCCTTTCTCAATTCCTCTTATATTA 420
421 GATTATAGAACAAACAAATTTAAATTACAAAGAACTTATAAGCAACATAATCTCTGAAT 480
421 GATTATAGAACAAACAAATTTAAATTACAAAGAACTTATAAGCAACATAATCTCTGAAT 480
481 TCCAGCAGATCGGCTCTGAAGATGGGGAACCCCTCAGCAGCAGTGACTGGGACACTGG 540
481 TCAGCAGA-----AGGTGAAGGGCGGCTTAA 507
541 TCCTTGTCTGATTTCTCAGCTGTGCTTGGTCCCTTCAGTTTGGCTATAAATGGAGTCA 600
508 TGTGGCCGTGGGAGGGCAGTGTCTCGATCCCTGCGAGTTTCGGCTATAACACCGGTTCA 567
601 TCAACGCCCCACAGAAAGTGAATGAACAGAGCTACAAATGCAACTTGGCTGGGTAGGAGG 660
568 TCAACGCCCCCCAGAAAGTGAATGAAGAGTTCTACAAATCAAAATGGAACACCGCTATG 627
661 GTCTTGGGGACCGGACTCCATCCCAAGGACCCCTCACTACCCTTTGGGCTCTCTCCG 720
628 G-----AGAGTCCATCCCATCCACACACTCACACACTCTGGTCTCTCTCCG 675
721 TGGCCATCTTCTCTGTGGGTGGCATGATTTTCTCTCTTCTCAATGGCATCAATTTCTCAAT 780
676 TGATGATCTTCTGTCTGGGGGATGATGGTTTCTCTCTGTGGGCTCTTTGTTAATC 735
781 GGTGGGAAGAAAGGGCTATGCTGGCCCAAAATGTTTGGCTGTGCTGGGGGGGCC 840
736 GCTTTGGCAGCGGAACCTCCATGCTGATGATGAACCTGTTGGGCTTTGTCTGCGCGTGC 795
841 TCATGGCCCTAGCAATGCGCGGCTCTCTATGATGATCTCAATTCGAGCGTTCCTCA 900
796 TTATGGGTTTCTCAAACTGGGCAAGTCTTTGAGATGCTGATCTCTGGGCGCTTCAATCA 855
901 TTGGCGCTACTCAGGCTAACATCAGGGTGTGGCTATGATGATGGGAGAAATCGCCC 960
856 TTGGAGTGTACTGTGGCTGACCAACCGCTTTGTGCCATGATGTGGGGAGGTGTAC 915
961 CCACTCATCTTGGGGTGTCTGGGAACAACCAACAAATGGCCATGCTCAATTTGGGATTC 1020
916 CCAAGCTCTTCTGGAGCCCTGGGCAACCCCTGCAACAGCTGGGCACTCGTGTGGATCC 975
1021 TGGTTCGCCAGGTGTGGGTGGAGTCTATGCTGGGCAAGCTACCTCTGGGCCATTC 1080
976 TTATGGCCAGGTGTGGGCTTGAATCTTCAATCATGGGCAATGAGACTTGTGGCCCTAC 1035
1081 TTCTGGCTATCAGATCTCCTGCTCTCTGAGCTGTCTTCTTGGCCCTTCTGTCTG 1140
1036 TGCTCAGTGTATCTTCAATCCAGCCCTGTCAAGTGTATCTTGTGGCCCTTCTGGCCCTG 1095
1141 AGAGCCCGGATACCTCTCATCATCCGGAACCTGGAGGGGCTGTGCCGAAGAGTCTAA 1200
1096 AGAGCCCGGCTTCTCTCTCATCAATCGTAAAGGAGAACCCGGGCCCAAGAGTGTCTGA 1155
1201 AGCGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTGAAGGATGAGAAC 1260
1156 AAAAGCTTCGAGGAGACGCGATGTGACCCCGAGACCTTCAGGAGATGAAAGAGAGGGTC 1215
1261 GGAAGTTGGAAGAGAGCGTCCAATGCTTGTGTGAGCTCTCTGGGAGCGCGCACCCACC 1320
1216 GGCAGATGATGGGGAAGAGGTACCATCTTGGAGCTGTTCCGCTCACCCGCTACC 1275
1321 GGCAGCTCTGATTTATGCAAGTGTGTGCTGAGTGAAGCCAGAGCTCTCAGGCATCAATG 1380
1276 GGCAGCCCATCTCATCGCGTGTGTGCTGAGTGTCTCCAGAGCTGTCCGGGCATCAATG 1335
1381 CTGTTTCTACTATTGAACAGCATCTTTGAGTTAGCTGGGTGGGAACAGCCGCTACG 1440
1336 CTGTGTTCTACTACTCAACAGCATCTTTCAGAAAGGCGAGGTGTGCAGCAGCCTGTGTATG 1395

QY 1441 CCACCATAGAGCTGTGTGGTCAATACCGTCTTCAAGTTGGTCTCGGTGCTCTTAGTAG 1500
Db 1396 CCACCATCGGCTCGGATATCGTCAACACGCGCTTCACTGTGGTGTGCTGTCTTGGTGG 1455
QY 1501 AGCGAGCTGGGCGAGCAGACATCTCTCTGGGCTTGGCAGCAGTGTGGGTGTGGCCA 1560
Db 1456 AGCGAGCTGGGCTGGGACCTCGATCTCATTTGGTCTGGCTGGCAGTGGCGGCTGTGCTG 1515
QY 1561 TCTTGATGAGCGGTGGTCTGTCTGTCTGGAGCGGTTCCATCCATGAGTATGTGTGCTCA 1620
Db 1516 TGCTCATGACCATCGCCTGGCCCTGCTGGAGCAGTGCCTGGATGTCTCTAATCTAGTA 1575
QY 1621 TGTGGCCATATTTGGCTTTTGGCCCTTCTTTGAGATTTGGTCTGTGGCCCATCCCTGGT 1680
Db 1576 TGTGGCCATCTTTGGCTTTTGGCCCTTCTTTGAAGTAGGCCCTGTCTTATTTCCATGGT 1635
QY 1681 TCATTTGGCGGAGCTTTCAGCCAGGCGCCCGCCAGCAGCATGCTGTGTGTGGCTGGT 1740
Db 1636 TCATTTGGCGGAGCTTTCAGCCAGGCGCCCGCCAGCAGCTGTGTGTGTGGCTGGT 1695
QY 1741 TCTCCAACTGGAGCTCTAACTTCATCGTTGGGATGGGTTTCCAGTATGTTGGCGATGCTA 1800
Db 1696 TCTCTAACTGGAGCTCAAACTTCATCGTTGGGATGCTTCCAAATGTGGAGCACTGT 1755
QY 1801 TGGGTCCCTACGCTTCTTCTTATTTGGCCCTCTCTGTGTGGCTTCTTCACTTCACT 1860
Db 1756 GTGGCCCTACGCTTCTTCTCATCTTTCACGCTGTCTGTGGTACTTCTTCTTCACTTCACT 1815
QY 1861 TCTTAGAGTGTCTGAAACAGGAGCGCGGACATTTGACAGATCTCGGCCACCTTCCGAC 1920
Db 1816 ACTTCAAGTGTCTGAGACCAAGGCGGACCTTTCATGAGATCGGCTTCCGGCTCCGGC 1875
QY 1921 GGAACCTTCTCTCTTAGAGCAGGAGTGAACCCAGTACAGAACTTGAATCTTAGGGC 1980
Db 1876 AGGGGGGTGC--CAGCCAGAGGACAGACACTGAGGAGCTTCCACCTCTGGGG 1932
QY 1981 CAGATGAGAAATGATTAATCGATTGAAGTGAGAGCTCCATCACTCTCTTAAATTTTCA 2040
Db 1933 CTGACTCCCAAGTGAATCGATTGAAGTGAGAGCTCCATCATCTCTCTTAAATTTTCA 1992
QY 2041 TGAAGTCAAGTGTCTTCTTCAATTTAATATCATAGTATTTGTTGAAAGGAGGAGGAGG 2100
Db 1993 TGAAGTCAAGTGTCTTCTTCAATTTAATATCATAGTATTTGTTGAAAGGAGGAGGAGG 2052
QY 2101 AATTTCCCTTATCAATGATATCTTACGATTTAATAATTTCTTACCTAAACCTTATTT 2160
Db 2053 AATTTCCCTTATCAATGATATCTTACGATTTAATAATTTCTTACCTAAACCTTATTT 2112
QY 2161 TGTGTACATATATCAGAGTATTTATACATATATAACCTTTTCTTAAAGCAGGAGGAGG 2220
Db 2113 TGTGTACATATATCAGAGTATTTATACATATATAACCTTTTCTTAAAGCAGGAGGAGG 2172
QY 2221 AAAAGAAAGGAGTAAACATGCTGTGCCATCTTGTTCACGAGAGGAGGAGGAGGAGG 2280
Db 2173 AAAAGAAAGGAGTAAACATGCTGTGCCATCTTGTTCACGAGAGGAGGAGGAGGAGG 2232
QY 2281 AATGAATTTGCTTATGAATTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
Db 2233 AATGAATTTGCTTATGAATTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2292
QY 2341 CCTTGAAGAAATAGTCAGGACTTCTGCTGGAGCTTCTTCCAGTTG 2386
Db 2293 CCTTGAAGAAATAGTCAGGACTTCTGCTGGAGCTTCTTCCAGTTG 2338

RESULT 6

US-10-067-449-9

; Sequence 9, Application US/10067449

; Publication No. US20030166258A1

; GENERAL INFORMATION:

; APPLICANT: Muller, Gunter

; APPLICANT: Koller, Klaus-Peter

APPLICANT: Boles, Eckhard
APPLICANT: Wiczorke, Roman
APPLICANT: Dlugai, Slike
TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
TITLE OF INVENTION: GLUT Promoter
FILE REFERENCE: DEAV2001/00002
CURRENT APPLICATION NUMBER: US/10/067,449
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: DE 101 06 718.6
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 7828
TYPE: DNA
ORGANISM: Homo sapiens
US-10-067-449-9

Query Match 51.5%; Score 1229; DB 15; Length 7828;
Best Local Similarity 85.8%; Pred. No. 7,3e-301;
Matches 1364; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 468 ATAAATGCTGAATTCACAGAGATCGGCTCTGAAGATGGGAAACCCCTCAGCAGCGAGTG 527
DB 1 ATCCCGTCGGGCTCCAAACAGATAGGCTCCGAAGATGGGAAACCCCTCAGCAGCGAGTG 60

QY 528 ACTGGGACACTGGCTCTGCTGCTATTCTCAGCTGTGCTTGGCTCCCTTCAGTTGGCTAT 587
DB 61 ACTGGGACCTGGTCTGCTGTGCTGTGCTGCGGTGCTTGGCTCCCTGCACTTTGGGTAC 120

QY 588 AACATTGAGTGCATCAAGCGCCCAAGAAAGTGAATGAACAGAGCTACAATGCCAATTGG 647
DB 121 AACATTGGGGTGCATCAATGCCCTCAGAAAGTGAATGAACAGAGCTACAATGAGACGTGG 180

QY 648 CTGGGAGCAGGGCTCTGGGGACCGGACTCCATCCCAAGGACCCCTCACTACCCCT 707
DB 181 CTGGGAGCAGGGCTCTGGGGACCGGACTCCATCCCTCCAGGCAACCCCTCAACACCCCTC 240

QY 708 TGGGCTCTCTCGTGGCCATCTTCTCTGCTGGGTGCGATGATTTCTCTCTCTCTCTCTCTCT 767
DB 241 TGGGCTCTCTCGTGGCCATCTTTCTCTGCTGGGTGCGATGATTTCTCTCTCTCTCTCTCTCT 300

QY 768 ATCAATTTCTCAATGGTTGGGAAGAAAGGGCTATGCTGGGCAACAATGCTCTGGCTGTG 827
DB 301 ATCAATCTCAATGGTTGGGAAGAAAGGGCTATGCTGGGCAACAATGCTCTGGCTGTG 360

QY 828 CTGGGGGGGGCCCTCATAGGCGCTACGCAATGCGCGGCTCTCTATGAGATACCTATCTC 887
DB 361 CTGGGGGGGGCCCTCATAGGCGCTACGCAATGCGCGGCTCTCTATGAGATACCTATCTC 420

QY 888 GGACGGTTCCTCATTTGGCGGCTTCTCAGGGCTTAACATCAGGGTGGTGGCTATGATGTG 947
DB 421 GGACGATTCCTCATTTGGCGGCTTCTCAGGGCTTAACATCAGGGTGGTGGCTATGATGTG 480

QY 948 GGAGAAATCGCCCACTCATCTCGGGGTGCTTGGGAAACACTCAACAAATGGCCATC 1007
DB 481 GGAGAGATTCCTCCCACTCATCTCGGGGTGCTTGGGAAACACTCAACAAATGGCCATC 540

QY 1008 GTCAATGGCAATCTGGTTGGCCAGGTGTGGGTTGGAGTCTATGCTGGGCAAGCTTACC 1067
DB 541 GTTATCGGCATTCATGATCGCCAGGTGTGGGTTGGAGTCTATGCTGGGCAAGCTTACC 600

QY 1068 CTGTGGCAATCTGCTTGGCTATCAGATCTACCTGCTCTCTGCTCTCTGCTCTCTGCTGTTG 1127
DB 601 CTGTGGCAATCTGCTTGGCTATCAGATCTACCTGCTCTCTGCTCTCTGCTCTCTGCTGTTG 660

QY 1128 CCCTTCTGCTGAGAGCCCGGCTACCTCTACATCATCCGGAACCTCGAGGGGCGCTGCC 1187
DB 661 CCCTTCTGCTGAGAGCCCGGCTACCTCTACATCATCCGGAACCTCGAGGGGCGCTGCC 720

QY 1188 CGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTG 1247
DB 721 AGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTG 780

QY 1248 AAGGATCAGAAACCGAAAGTTGGAAGAGAGCGTCCACTGTCTCTGTGCTCAGCTCCTGGGC 1307
DB 781 AAGGATCAGAAACCGAAAGTTGGAAGAGCGTCCACTGTCTCTGTGCTCAGCTCCTGGGC 840

QY 1308 AGCGCACCCACCGGACGCTCTGATTTATGCACTGTGCTGCACTGAGCAGCAGCTC 1367
DB 841 AGCGGTACCCACCGGACGCTCTGATCATTTGCGGTGCTGCACTGAGCAGCAGCTC 900

QY 1368 TCAGGCATCAATGCTGTTTCTACTATTTCAACACAGCATCTTTGAGTTAGCTGGGCTGGA 1427
DB 901 TCTGGCATCAATGCTGTTTCTATTTATTCGACAGCATCTTCGAGACAGCGGGTAGGC 960

QY 1428 CAGCCAGCTACGCCACCATAGGAGCTGGTGTGCTCAATACCGTCTTCAAGCTGTGCTCG 1487
DB 961 CAGCTGCTATGCCACCATAGGAGCTGGTGTGCTCAACAGATCTTCACTTGTGCTCG 1020

QY 1488 GTGCTCTTAGTAGCAGCTGGGCGAGCGGACATCTCCATCTCTCTGGGCTGGCAGCATG 1547
DB 1021 GTGTTGTGGTGGAGCGGGGCGCGGACGCTCCATCTCTCTGGGCTGGCAGCATG 1080

QY 1548 TGTGGCTGTGCCATCTTGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1607
DB 1081 TGTGGCTGTGCCATCTTGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

QY 1608 AGTTATGCTGCCATCTGCTGGCCATATTTGGCTTTTGTGGCTTTCTTTGAGATTTGCTG 1667
DB 1141 AGCTAGCTCTCATTTGTGGCCATCTTTGGCTTTTGTGGCTTTTGTGGCTTTTGTGGCT 1200

QY 1668 CCCATCCCTGTTTCTATTTGTGGCGAGCTTTTCAAGCAGGCGCCCGCCAGCAGCATG 1727
DB 1201 CCCATCTCTGTTTCTATCTGCTGGCGAGCTTTTCAAGCAGGCGCCCGCCAGCAGCATG 1260

QY 1728 GCTGAGCTGTTTCTCAACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1787
DB 1261 GCTGAGCTGTTTCTCAACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1320

QY 1788 GTTGGGATGCTATGGGTCCCTAGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1847
DB 1321 GTTGGGATGCTATGGGTCCCTAGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380

QY 1848 TTCACTTCACT 1907
DB 1381 TTCACTTCACT 1440

QY 1908 GCCACCTTCCGACCGGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1967
DB 1441 GCTGCTTCCACCGGACCT 1500

QY 1968 GAATCTTAGGGCCAGATGAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2027
DB 1501 GAGTATTTAGGGCCAGATGAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1560

QY 2028 TCTTAAATTTTCTAGTACTGAGCTTTTTC 2056
DB 1561 ATGTAATTAGTTATGTCAAGCTTACATTC 1589

RESULT 7
US-09-894-927A-8
; Sequence 8, Application US/09894927A
; Patent No. US20020052012A1
; GENERAL INFORMATION:
; APPLICANT: Bogan, Jonathan S.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Method of Measuring Plasma Membrane
; TITLE OF INVENTION: Targeting of GLUT4
; FILE REFERENCE: 0399.1210-004
; CURRENT APPLICATION NUMBER: US/09/894, 927A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/591, 025
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/154, 078

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; PRIOR FILLING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/138,237
; PRIOR FILLING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified GLUT4 containing myc tag sequences
US-09-894-927A-8

Query Match      44.7%; Score 1066.4; DB 9; Length 2592;
Best Local Similarity 87.5%; Pred. No. 7.4e-260;
Matches 1166; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 663 CTTGGGGGACCGGACTCCATCCACAAAGGACACCTCACTACCTTTGGGGCTCTCCGTCG 722
DB 511 CTTAAGGGACCAAGCTCCATCCCTCCAGGACACCTCACACCTCTGGGGCCCTCTCCGTCG 570
QY 723 GCATCTCTCTGTGGGTGGCATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAATGG 782
DB 571 GCATCTCTCTGTGGGTGGCATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAATGG 630
QY 783 TTGGGAAGAAAGGCTATGTCTGGCCAAATGTCTTGGCTGTCTGGGGGGGGCCCTC 842
DB 631 CTTGGGAAGAAAGGCTATGTCTGGCCAAATGTCTTGGCTGTCTGGGGGGGGCCCTC 690
QY 843 ATGGGCTAGCCATGCGGGGCTCTATGATATCTATCTCTCGGAGGTTCTCTCATT 902
DB 691 ATGGGCTAGCCATGCGGGGCTCTATGATATCTATCTCTCGGAGGTTCTCTCATT 750
QY 903 GGGCCCTACTCAGGGCTAAATCAGGGTGGTGGCTATGATGTGGGAGAAATCGCCCC 962
DB 751 GGGCCCTACTCAGGGCTAAATCAGGGTGGTGGCTATGATGTGGGAGAAATCGCCCC 810
QY 963 ACTCATCTTCGGGGTGCCTTGGGAACACTCAACAAATGGCCATCGTCATTTGGCATTTG 1022
DB 811 ACTCATCTTCGGGGTGCCTTGGGAACACTCAACAAATGGCCATCGTCATTTGGCATTTG 870
QY 1023 GTTGGCCAGGTGTGGGTGGGATCTATGCTGGGACACTACCTGTGGCCATTTGCTT 1082
DB 871 ATGCCCCAGGTGTGGGTGGGATCTATGCTGGGACACTACCTGTGGCCATTTGCTT 930
QY 1083 CTGGCTATCAGTACTCCCTGCTCTCTGAGTGTCTCTGTGGCTCTCTGTCTCTGAG 1142
DB 931 CTGGCTATCAGTACTCCCTGCTCTCTGAGTGTCTCTGTGGCTCTCTGTCTCTGAG 990
QY 1143 AGCCCCCGATACCTCTACATCATCCGGAACCTGGAGGGGCTCCCGAAAGAGTCTAAAG 1202
DB 991 AGCCCCCGATACCTCTACATCATCCGGAACCTGGAGGGGCTCCCGAAAGAGTCTAAAG 1050
QY 1203 CGCTGACAGGCTGGGCTGATGTCTGATGCTAGCTGGCTAGCTGAAGATGAAACGG 1262
DB 1051 CGCTGACAGGCTGGGCTGATGTCTGATGCTAGCTGGCTAGCTGAAGATGAAACGG 1110
QY 1263 AAGTTGGAAGAGAGCGTCCACTGTCTCTGCTGAGCTCTGGGAGCCGACCCACCGG 1322
DB 1111 AAGTTGGAAGAGAGCGTCCACTGTCTCTGCTGAGCTCTGGGAGCCGACCCACCGG 1170
QY 1323 CAGCCTCTGATTTATGAGTGGTGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1382
DB 1171 CAGCCTCTGATTTATGAGTGGTGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1230
QY 1383 GTTTTCTACTATTCAACAGCATCTTTGAGTGGTGGTGGGAGTGGGAGTGGGAGTGGGAG 1442
DB 1231 GTTTTCTACTATTCAACAGCATCTTTGAGTGGTGGTGGGAGTGGGAGTGGGAGTGGGAG 1290
QY 1443 ACCATAGGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1502
DB 1291 ACCATAGGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1350

RESULT 8
US-09-735-705-135
; Sequence 135, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-735-705-135

Query Match      28.5%; Score 679; DB 9; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY 506 GGAACCCCTCAGCAGGAGTGAACCTGGGACACTGGCTTGTGTTATCTCAGCTGTGCT 565
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Db 182 GGAGCCAGCAGCAAGAGCTGACGGGTGCGCTCATCTGCTGGCTGTGGAGGAGCAGTGTCT 241
Qy 566 TGGCTCCCTTCACTTGGCTTAAATGAGTATCAATCAACGCCCCACAGAAAGTATGA 625
Db 242 TGGCTCCCTTGGCTTAAATGAGTATCAATCAACGCCCCACAGAAAGTATGA 301
Qy 626 ACAGAGCTACAAATGCAACTTGGCTGGGTAGGAGGAGTCTGGGAGCCGAGCTCCATCCC 685
Db 302 GGAGTCTACACACAGACATGGTCCACCGTATGG-----GGAGAGCATCCT 349
Qy 686 ACAGAGCCCTCACTACCTTTGGGCTCTCCGTTGGCCATCTTCTCTGTGGGTGGCAT 745
Db 350 GGGCCACAGCTCAGCAGCTCTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGGAT 409
Qy 746 GATTTCTCTCTCTCATTTGGCATCTTCTCAATGGTTGGAGGAAAGGGCTATGCT 805
Db 410 GATTTGGCTCTCTCTCTGTGGGCTTTTCTGTTAACCGCTTTGGCGGGGGAATTCATGCT 469
Qy 806 GGCCAAACAAATGCTTGGCTGTGGGGGGGCGCTCATGGGCTTAGCCAAATGCGCGGC 865
Db 470 GATGATGAACCTGCTGGCTTGGTCCGCGTGTCTCATGGCTTCTGAAACTGGGCA 529
Qy 866 CTCCTATGAGACTCACTTCTGGAACGGTTCCTCATTTGGCGCCCTACTCAGGGCTAAATC 925
Db 530 GTCTTTGAGATGCTGATCTGGGCGGCTTCTCATCGGTGTGACTGCGGCTGACCA 589
Qy 926 AGGTTGGTGTATGATGGGAGAAATCGCCCACTCATCTTGGGGTGTCTGGG 985
Db 590 AGGCTTGTGGCCATGATGGGGAAGTGTCAACCAAGCTTTGTGGGGGCTTGG 649
Qy 986 AACACTCAACAAATGGGCATCGTCAATGGGCATCTGGTGTCCAGGTTGGGTTTGA 1045
Db 650 CACCTGACACAGCTGGGATGCTGTGGCATCTCATGCCCAAGTGTGGGCTTGA 709
Qy 1046 GTCTATGTGGGCAAGCTACCTGTGGCAATGCTTCTGGCTATCACAGTACTCCCTGC 1105
Db 710 CTCCTATGAGCAACAGGACCTGTGGGCGCTGTGCTGAGCATCATCTTCAATCCGGC 769
Qy 1106 TCTCTGAGCTGCTTCTGTGGCTTCTGTGGCTTCTGTGGAGCGCCGATACCTTACATCAT 1165
Db 770 CTGCTGAGTGCATGCTGTGGCTTCTGTGGCGAGAGTCCCGCTTCTGTCTCATCAA 829
Qy 1166 CCGGAACCTGAGGGGCTTGGCCGAAAGAGTCTAAGCGCTGACAGGCTGGGCTGTATGT 1225
Db 830 CGCAACGAGGAGACCGGCCAAGAGTGTCTAAGAGCTGCGCGGACAGTGCAT 889
Qy 1226 GTCTGATGACCTGAGCTGAGGATGAGAAACGGAAGTTGAAAGAGAGCTTCACT 1285
Db 890 GACCCATGACCTGACGAGATGAGGAAGAGAGTGGCAGATGATGCGGGAGAGAAAGT 949
Qy 1286 GTCTTGTGAGCTTCTGGGAGCGCCGACCCAGCGGAGCTCTGATTTATTCAGTGTGT 1345
Db 950 CACCATCTTGGAGCTTCTGGCTTCCCGCTTACCGCAGCCCATCTCATCTGTGTGT 1009
Qy 1346 GCTGAGCTGAGCCAGCAGCTCTCAGGATCAATGCTGTTTCTACTATTCAAACAGCAT 1405
Db 1010 GCTGAGCTGTCCAGCAGCTGTCTGGCATCAAACGCTGTCTTCTATCTCAAGCAT 1069
Qy 1406 CTTTGAGTTAGCTGGGTGGAACAGCCAGCCTTACGCCACATAGAGAGTGTGTGGTCAA 1465
Db 1070 CTTTGAGAAAGGGGGGTGACAGAGCTGTGTATGCCACCATTTGGCTCCGGTATCGTCAA 1129
Qy 1466 TACCTCTTCACTGTTGCTCGGTCTCTTAGTAGAGGAGCTGGGAGGAGCACTTCA 1525
Db 1130 CACGGCTTCACTGCTGTGTGTGTGTGGTGGAGGAGGAGCGCGGCGGACCTTGCA 1189
Qy 1526 TCTCTTGGGCTTGGAGGAGTGTGGCTGTGGCTCTTGTAGCGGTGGCTCTGTGCT 1585
Db 1190 CTTATGAGCTTGGTGGATGGCGGGTGTGGCATACTCATGACCATCGGCTAGCAT 1249
Qy 1586 GCTGAGCGGGTTCCATCCATGAGTTATGTGTCCATGTGGCCATATTTGGCTTTTGGC 1645
Db 1250 GCTGGAGCAGCTTACCTGATGTCTCTATCTGAGCATCTGTGGCCATCTTTTGGCTTTTGGC 1309
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RESULT 9
US-09-850-716A-135
; Sequence 135, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-850-716A-135

Query Match 28.5%; Score 679; DB 9; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.4e-161;
Matches 968; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

Qy 506 GGAACCCCTCAGCAGCAGTGTGAGTGGGACACTGGTCTTCTGTCTGATTTCTCAGCTGTGTCT 565
Db 182 GGAGCCAGCAGCAAGAAAGCTGACGGGTGGCTCTCATGCTGTGGGAGGAGCAGTGTCT 241
Qy 566 TGGCTCCCTTCACTTGGCTTAAATGAGTATCAATCAACGCCCCACAGAAAGTATGA 625
Db 242 TGGCTCCCTTGGCTTAAATGAGTATCAATCAACGCCCCACAGAAAGTATGA 301
Qy 626 ACAGAGCTACAAATGCAACTTGGCTGGGTAGGAGGAGTCTGGGAGCCGAGCTCCATCCC 685
Db 302 GGAGTCTACACACAGACATGGTCCACCGTATGG-----GGAGAGCATCCT 349
Qy 686 ACAGAGCCCTCACTACCTTTGGGCTCTCCGTTGGCCATCTTCTCTGTGGGTGGCAT 745
Db 350 GGGCCACAGCTCAGCAGCTCTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGGAT 409
Qy 746 GATTTCTCTCTCTCATTTGGCATCTTCTCAATGGTTGGAGGAAAGGGCTATGCT 805
Db 410 GATTTGGCTCTCTCTCTGTGGGCTTTTCTGTTAACCGCTTTGGCGGGGGAATTCATGCT 469
Qy 806 GGCCAAACAAATGCTTGGCTGTGGGGGGGCGCTCATGGGCTTAGCCAAATGCGCGGC 865
Db 470 GATGATGAACCTGCTGGCTTGGTCCGCGTGTCTCATGGCTTCTGAAACTGGGCA 529
Qy 866 CTCCTATGAGACTCACTTCTGGAACGGTTCCTCATTTGGCGCCCTACTCAGGGCTAAATC 925

Db 530 GTCTTTGAGATGCTGATCTGGGCGCTTCATCATCGGTGTACTGTGGCGCTGACCAC 589
Qy 926 AGGTTGGTCCCTATGATGTGGAGAAATCGCCCCACTCATCTTCGGGGTCCCTTGGG 985
Db 590 AGGCTTGTGTCCTCCATGATGTGGTGAAGTGTACCCACACAGCTTTCTGTGGGCGCTGGG 649
Qy 986 AACACTCAACCAATTTGGCCATGCTCATTTGGCATTTCTGGTTCGCCAGGTGTGGGTTTGA 1045
Db 650 CACCTTGCACAGCTGGCATGCTGTGCGCATCTCATCGCCAGGTGTTCGGGCTTGA 709
Qy 1046 GTCTATGTGGGACAGCTACCTGTGGCCATTTCTTGGCTATCACAGTACTCCCTGC 1105
Db 710 CTCATCATGGGACACAGAGCTGTGGCCCTGTCTGTGAGCATCATCTTCATCCGGC 769
Qy 1106 TCTCTGCAGCTGCTTCTGTGGCTTCTGTCTGTGAGAGCCCGCATACCTCTACATCAT 1165
Db 770 CTTGCTGCAGTGCATGCTGTGCTGCTTCTGCCCCGAGAGTCCCGCTTCTGCTCATCAA 829
Qy 1166 CCGGAACCTGGAGGGGCTCCCGAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGT 1225
Db 830 CCGCAACGAGGAGAACCGGGCCCAAGAGTGTCTTAAAGAGCTGCGGGGACAGCTGACGT 889
Qy 1226 GTCTGATGCACTGCTGAGCTGAAGATGAGAAACGGAAGTTCGAAAGAGAGCGTCCACT 1285
Db 890 GACCCATGACCTGAGAGATGAAGAGAGAGTTCGAGATGATGCGGGAGAGAGGT 949
Qy 1286 GTCTTTGCTGACGCTCTCTGGGACGCGCACCCAGCGAGCTCTGATTTATTCAGTGT 1345
Db 950 CACCATCTGGAGCTGTTCGCTCCCGCGCTACCGCCAGCCCATCTCATGCTGTGT 1009
Qy 1346 GCTGAGCTGAGGACAGCTCTCAGGCATCAATGCTGTGTTTCTACTATTTCAACAGCAT 1405
Db 1010 GCTGAGCTGTCTCCAGCAGCTGTCTGCGCATCAACGCTGTCTTCTATTTACTCTCCAGCAT 1069
Qy 1406 CTTTGAAGTGTAGCTGGGTGAAACAGCAGCTACGCCACCATAGGAGCTGTGTGTCAA 1465
Db 1070 CTTGAGAGCGGGGTGAGCAGCTGTGTATGCCACCATTTGGCTCGGTATGTCGTA 1129
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Db 1130 CACGGCTTTCACGTGCTGTGCTGTTTGTGGTGGAGCAGCAGCGCGGCGGACCTGCA 1189
Qy 1526 TCTCTGGGCTGGCAGGATGTGTGGCTGTGCGCATTTGATGACGGTGGCTCTGTGCT 1585
Db 1190 CTTATAGGCTGCTGGCATGGCGGTGTGCGCATCTCATGACCATCGCGCTAGCAT 1249
Qy 1586 GCTGGAGCGGTTCCATCCATGATGATGTGTCATCGTGCCCATATTTGGCTTTGTGGC 1645
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Db 1310 CTTCTTTGAGTGGTCTGCTGGCCCCCATCCCATGTTTCATGCTGCTGAACTCTTCAGCCA 1369
Qy 1706 GGGCCCCCGCCAGAGCCATGAGTGTGAGTGTGTTTCTCAACTGACACCTGTAATTCAT 1765
Db 1370 GGGTCCACGCTCCAGCTGCAATGCGGTGCGAGCTTCTCCAACTGGACCTCAAAATTCAT 1429
Qy 1766 CGTTGGCATGGGTTTCCAGTATGTGCGGATGATGGGTCCCTACGCTCTCTCTATTT 1825
Db 1430 TGTGGGATGCTGCTTCAGTATGTGGAGCAACTGTGTGGTTCCTTACGCTTTCATATCTT 1489
Qy 1826 TGCCTGCTCCTGCTGGCTTCTTTCATCTTTCACCTTCCCTTCAAGAGTGCCTGAAACAGAGG 1885
Db 1490 CACTGTGCTCTGTTCTGTTCTTCTCATCTTTCACCTTCTCAAGTTCCTGAGACTAAGG 1549
Qy 1886 CCGGACATTTGACAGATCTGCGCCACCTTTCGACGG 1922
Db 1550 CCGGACCTTCGATGAGATGCTTTCGGGCTTTCGGGCGAG 1586

RESULT 10

US-09-880-107-2128

; Sequence 2128, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherif, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2128
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 K03195
; US-09-880-107-2128

Query Match 28.5%; Score 679; DB 9; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2,4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

Qy 506 GGNACCCCTCAGCAGCGAGTGAATGGGACATGGTCTTGTGCTTATCTCAGCTGTGCT 565
Db 182 GGAGCCACGACGACGAAGCTGACGGTGCCTCATGCTGGTGTGGAGGAGCGTGT 241
Qy 566 TGCTCTCCCTTCACTTTGGCTTATAAATTTGAGTTCATCAACGCCCCACAGAAAGTGA 625
Db 242 TGCTCTCCCTGAGTTTGGCTTACAACTGGAGTTCATCAATGCCCCACAGAGTGTG 301
Qy 626 ACAGAGCTCAATGCAACTTTGGCTAGGAGGTTCCTGGGGACCGGACTCCATCCC 685
Db 302 GGAGTTCTACACAGACATGGGTCCACCGCTATGG-----GGAGAGCATCCT 349
Qy 686 ACAGAGCAGCTTACCTTGGGCTCTCCGTTGGCCATCTTCTGTGGGTGGCAT 745
Db 350 GCCACACGCTCACACGCTCTGTGCTCTCAGTGGCCATCTTTCTGTGGGGCAT 409
Qy 746 GATTCTCTCTTCTCATTTGGCATCTTCTCAATGTTGGGAAGGAAAGGCTATGCT 805
Db 410 GATTGCTCTTCTCTGTGGGCTTTTGTAAACCGCTTTGGCCGGGGAATTCATGCT 469
Qy 806 GGCACAAATGTCTTGGCTGTGCTGGGGGCGCCCTCATGGGCTTACCCAAATGCCGCGC 865
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Qy 866 CTCCTATGAGATCACTCATTTCTGGACGGTTCCTCATTTGGCGCTACTCAGGCTTACATC 925
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Db 590 AGGTTCTGTCGCCATGATGTGGGTGAGTGTACCCACAGCCCTTGTGGGCGCTTGGG 649
Qy 986 AACACTCAACCAATTTGGCCATGCTCATTTGGCATTTCTGGTTGGCCAGGTGTGGGTTTGA 1045
Db 650 CACCTTGCACAGCTGGGCATGCTGTGCGCATCTCATCGCCACAGGTGTTCGGGCTTGA 709
Qy 1046 GTCTATGTGGGACAGCTACCTGTGGCCATTTGCTTGGCTATCACAGTACTCCCTGC 1105
Db 710 CTCATCATGGGCAACAGAGACCTGTGGGCGCTTGTGCTGAGCATCATCTTTCATCCGGC 769
Qy 1106 TCTCTGCGAGCTGCTTCTGTGCTGCTTCTGCTGAGAGCCCGCATACCTCTTACATCAT 1165
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QY 1166 CCGGAACCTGAGGGGCTGCCGGAAGAGTCTAAAGCCCTGACAGGCTGGGTGATGT 1225
DB 1167 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 830 CCGCAACGAGGAGAACCGGGCCCAAGAGTGTCTAAAGAAAGCTGCGCGGACAGCTGACGT 889
QY 1226 GTCTGATGACATGGCTGAGCTGAAGGATGAGAAACGGAAGTTGGAAGAGAGCTCCACT 1285
DB 1227 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 890 GACCCATGACCTGCAGGAGATGAAGAAAGAGAGTGGCAGATGATGCGGGAGAAAGGT 949
QY 1286 GTCTTGTGTCAGCTCCTGGGCGAGCGCACCCACCGGAGCTCTGATTATTGAGTGGT 1345
DB 1287 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 950 CACCATCTCTGGAGCTGTTCCGCTCCCCCGCTACCGCCAGCCCATCTCATCGTGTGGT 1009
QY 1346 GCTGAGCTGAGCCAGCAGCTCTCAGGCATCAATGCTGTTTCTACTATTCAACACAGCAT 1405
DB 1347 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1010 GCTGAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCTTCTATTACTCCAGCAT 1069
QY 1406 CTTTGAGTTAGTGGGTGGAAACAGCCAGCTTACGCCACCATAGAGCTGGTGTGGTCAA 1465
DB 1407 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1070 CTTTGAGAAAGGCGGGGTGCAGCAGCTGTGTATGCCACCATTTGGCTCCGGTATCGTCAA 1129
QY 1466 TACCGTCTTCACTGTTGGTCTCGGTGCTCTTAGTAGAGCGAGTGGCGACGACACTCCA 1525
DB 1467 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1130 CACGGCTTCACTGCTGTGCTGCTGTTGTGGTGGAGCGAGCGCGCGGACCCCTGCA 1189
QY 1526 TCTCTGGGCTGGCAGGATGTGTGGCTGTGCCATCTTGATGACGGTGGCTCTGCTGCT 1585
DB 1527 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1190 CCTCATAGGCTCGCTGGCATGGCGGGTGTGCCATCTCATGACCATCGCGCTAGCACT 1249
QY 1586 GCTGAGCGGGTTCATCCATGAGTATGTGTCCATGTCATGTCGCGCATATTGCTTTGGC 1645
DB 1587 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1250 GCTGAGCAGCTACCTCGATGTCTATCTGAGCATCGTGGCCATCTTTGGCTTTTGGC 1309
QY 1646 CTTCTTTGAGATTGCTGTGGCCCATCCCTGGTTCATTGTGGCGGAGCTCTTCAGCCA 1705
DB 1647 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1310 CTTCTTTGAGTGGTCTGTGGCCCATCCCATGGTTCATCGTGGTGAACCTCTTCAGCCA 1369
QY 1706 GGGCCCCCGCCAGCAGCATGGCTGTAGCTGTGTTCTTCCAACTGGACCTGTAACTTCAT 1765
DB 1707 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1370 GGGTCCAGCTCCAGTGCATGCGTGGAGCAACTGTGTGTGTCCTTACGCTTCATCATCTT 1429
QY 1766 CTTTGGATGTTTCCAGTATGTTGGGAGTCTATGGTCCCTTACGCTTCTTCTTCTATT 1825
DB 1767 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1430 TGTGGGCACTGTCTTCCAGTATGTGGAGCAACTGTGTGTGTCCTTACGCTTCTTCACTCATCTT 1489
QY 1826 TSCCGTCTCTGCTTGGCTTCTTCACTTCCACTTCTAGAGTGTCTGAAACGAGG 1885
DB 1827 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1490 CACTGTGCTCTGCTTGTGTTCTTCTTCACTTCACTTCACTTCAAGTTCCTGAGACTAAGG 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTCCGACGG 1922
DB 1887 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1550 CCGGACCTTCGATGAGATCGCTTCCGGCTTCCGGCAG 1586
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RESULT 11

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US-09-897-778-135
; Sequence 135, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-135
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Query Match 28.5%; Score 679; DB 9; Length 2856;
Best Local Similarity 68.18; Pred. No. 2.4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;
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QY 506 GGAACCCCTCAGCAGCAGTGACTGGGACACTGGTCTCTGTATTTCTCAGCTGTGCT 565
DB 507 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 182 GGAGCCCGCAGCAAGAAGCTGACGGGTGCGCTCATGCTGTGGGAGGAGTGTCT 241
QY 566 TGGTCTCTTCACTTGGCTATTAACATTTGAGTGTATCAACGCCCCACAGAAAGTGTGA 625
DB 567 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 TGGTCTCTTCACTTGGCTATTAACATTTGAGTGTATCAACGCCCCACAGAAAGTGTGA 301
QY 626 ACAGAGCTACAATGCAACTTGGCTGGGTAGGACGGTCTCTGGGGACCGGACTCCATCCC 685
DB 627 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 302 GGAGTCTTACACAGACATGGGTCCACCGCTATGG-----GGAGAGCATCT 349
QY 686 ACAAGGACCCCTCACTACCTTTTGGGCTCTCTCCGTGGCCATTTCTCTGTGGGTGGCAT 745
DB 687 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 350 GCCCACCACGCTCACACGCTCTGTCCTCTCAGTGGCCATCTTTCTGTGGGGGCA 409
QY 746 GATTTCCTCTTCTCATTTGGCATCATTTCTCAATGTTGGGAGGAAAGGGCTATGCT 805
DB 747 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 410 GATTGGCTCTCTCTCTGTGGGCTTTTCTGTTAAACCGCTTTGGCGGGGGAATTCATGCT 469
QY 806 GGCCAAACAATGTCTTGGCTGTGGGGGGCGCTCATGGGCTTAGCCAAATGCCGCGGC 865
DB 807 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 470 GATGATGAACCTGTCTGGCTTCTGTCTCGCGCTGCTCATGGCTTCTCGAACTGGGCA 529
QY 866 CTCCTATGAGATCACTAATTCGGACGGTTCCTCATTTGGCGCTTACTCAGGGCTAAATC 925
DB 867 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 530 GTCTTTGAGATGTGATCTCTGGGCGCTTCTCATCGTGTGTACTGTGGGCTGACCAC 589
QY 926 AGGTTGGTGGTATGTATGGGAGAAATCGCCCGCACTCATCTTGGGGTGGCTTGGG 985
DB 927 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 590 AGGCTTCTGTCCTTCTGTGGGTGAAGTGTCAACCAAGCTTTCTGTGGGGCTTGGG 649
QY 986 AACACTCAACCAATTTGGCCATCGTCAATTGGCATTTCTGGTTCGCCAGGTGTGGGTTGA 1045
DB 987 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 650 CACCTGCAACAGCTGGGCACTGCTGTGGCATCTCATCGCCAGGTGTTCGGGCTGGA 709
QY 1046 GTCTATGCTGGGCAAGCTACCTGTGGCCATTTCTTGTGCTATCACAGTACTCCCTGC 1105
DB 1047 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 710 CTCCATCATGGGCAACAGGACCTGTGGCGCTCTGTCTGAGCATCATCTTCTATCCCGGC 769
QY 1106 TCTCTGAGCTGTCTTGTGGCTTCTGTCTGAGAGCCCGGATACCTTACATCAT 1165
DB 1107 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 770 CTTGCTGAGTGCATGCTGTGGCTTCTGTGGCGAGTCTTCTGCTTCTGCTCATCAA 829
QY 1166 CCGGAACCTGGAGGGGCTGCCGGAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGT 1225
DB 1167 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 830 CCGCAACGAGAGAACCGGGCCCAAGAGTGTCTTAAAGAGCTGCGCGGACAGCTGACGT 889
QY 1226 GTCTGATGCACTGGCTGAGTGAAGATGAGAAACGGAAGTTGGAAGAGAGCGTCCACT 1285
DB 1227 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 890 GACCCATGACCTGCAGGAGATGAAGAAAGAGAGTGGCAGATGATGCGGGAGAAAGGT 949
QY 1286 GTCTTGTCTGAGCTCTTGGGCGAGCGCACCCACCGGAGCTCTGATTATTGAGTGGT 1345
DB 1287 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 950 CACCATCTTGGAGCTGTTCCGCTCCCCCGCTACCGCCAGCCCATCTCATCGTGTGGT 1009
QY 1346 GCTGAGCTGAGCCAGCAGCTCTCAGGCATCAATGCTGTTTCTACTATTCAACACAGCAT 1405
DB 1347 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1010 GCTGAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCTTCTATTACTCCAGCAT 1069
QY 1406 CTTTGAGTTAGTGGGTGGAAACAGCAGCCTTACGCCACCATAGAGCTGTGTGCTCAA 1465
DB 1407 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 1070 CTTGAGAGGCGGGGTCAGCAGCCTGTGTATGCCACATTTGGCTCCGGTATCGTCAA 1129
QY 1466 TACCGCTTTCACGTTGGTCTCGGTGCTCTTAGTAGAGCAGCTGGGCGACGACACTCCA 1525
Db 1130 CACGGCTTTCACGTGCTGCTGCTGTTGTGGTGGAGCGAGCAGCGCGGACCTGCA 1189
QY 1526 TCTCTGGGCTGGCAGGACATGTGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1585
Db 1190 CTTATAGGCTCGCTGGCATGGCGGTTGTGCGCATCTCATGACCATCGCGTAGCACT 1249
QY 1586 GCTGGAGCGGTTCCATCCATGATGTATGTATGCTCATGCTGGCCATATTTGGCTTGGC 1645
Db 1250 GCTGGAGCAGTACCTCGGATGCTCATCTGAGCATCGTGGCCATCTTTGGCTTGGC 1309
QY 1646 CTTCTTTGAGATTGGTCTGGGCCCCATCCCTGTTTCAATTTGGCGGCTACTCTAGGCCA 1705
Db 1310 CTTCTTTGAGTGGTCTGGGCCCCATCCCATGTTTCAATTTGGCGGCTACTCTAGGCCA 1369
QY 1706 GGGCCCCCGCCAGCAGCAGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1765
Db 1370 GGGTCCACGTCAGCTGCCATTCGCTGTGCGGCTTCTCCAACTGGACCTCAAAATTCAT 1429
QY 1766 CHTTGGCATGGTTCAGTATGTGGGATGTATGGGTCCCTAGCTCTTCTCTATT 1825
Db 1430 TGTGGGATGTGCTTCAGTATGTGGAGCAACTGTGTGGTCCCTAGCTCTTCTCTATT 1489
QY 1826 TGGCGTCTCTGCTGGCTTCTTCTATCTTCACTTCACTTCAAGAGTGTCTGAAACACGAGG 1885
Db 1490 CACTGTGCTCTGCTGCTTCTTCTATCTTCACTTCACTTCAAGAGTGTCTGAAACACGAGG 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTTCGACGG 1922
Db 1550 CCGGACCTTCGATGATGCTTTCGGGCTTCGGGCGAG 1586

RESULT 12
US-09-466-396A-135
; Sequence 135, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-466-396A-135

Query Match 28.5%; Score 679; DB 10; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2,4e+161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY 506 GGAACCCCTTCAGCAGCGAGTGTGCTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCT 565
Db 182 GGAAGCCAGCAGCAAGAGCTGACGGGTGCGCTCATGCTGGCTGTGGGAGGAGCAGTGCT 241
QY 566 TGGCTCCCTTCAGTGTGGCTATACATTTGGAGTCAATCAACGCCGCCACAGAAAGTGTGA 625
Db 242 TGGCTCCCTTCAGTGTGGCTATACATTTGGAGTCAATCAATGCCCCCAGAAAGTGTGCA 301
QY 626 ACAGAGTCAATGCAATTTGGCTGGGTAGGCGGGTCTGGGGAGCCGAGCTCCATCCC 685
Db 302 GGAGTCTCAACACAGACATGGGTCCACCCGCTATGG-----GGAGAGCATCCT 349
QY 686 ACAAGGACCCCTCACTACCTTTGGGCTCTCTCGTGGCCATCTTCTCTGCTGGGTGGCAT 745
Db 350 GCCCACCACGCTCACCACGCTCTGGTCCCTCTCAGTGGCCATCTTTTCTGTTGGGGCAT 409
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QY 746 GATTTCTCTCTTTTCTCATTTGGCATCATTTCTCAATGTTGGGAAGGAAAGGCTATGCT 805
Db 410 GATTTGCTCTCTCTCTGTGGGCTTTTCTGTTAAACCGCTTTGGCGCGGAAATTCATGCT 469
QY 806 GGGCAACAATGTCTGGCTGTGCTGGGGGGCGCCCTCATGGGCTAGCCATATCCGCGGC 865
Db 470 GATGATGAACCTGCTGGGCTTCTGTTCCGCGCTGCTCATGGGCTTCTCGAAATCGGCAA 529
QY 866 CTCCTATGAGATACTCATTTCTGGACGGTTTCTCAATTTGGCGCTACTCTAGGGCTAAATC 925
Db 530 GTCTTTTGAATGCTGATCTGGGCGCTTCTCATCTGCTGTGCTGCTGCTGCTGCTGCTGCT 589
QY 926 AGGGTTGGTGCCTTATGTATGTGGGAGAAATCGCCCCCATCATCTTTGGGGTGCCTTGGG 985
Db 590 AGGCTTGTGGTCCCATGTATGTGGTGAAGTGTCAACCCACAGACCTTCTTGGGGCTTGGG 649
QY 986 AACACTCAACAAATGGCCATGTCTATTTGGCATCTGTGGTGTGGCCAGGTGTGGGTTTGA 1045
Db 650 CACCTTGCACAGCTGGGATCTGCTGCTGGCATCTCTCATCGCCAGGTGTTCGGGCTTGA 709
QY 1046 GTCTATGCTGGGCGACAGCTACCTGTGGCCATTTGCTTCTGGCTATCACAGTACTCCCTGC 1105
Db 710 CTCATCATGGGCAACAAGACCTGTGGGCTTCTGCTGAGCATCATCTTCTATCCCGGC 769
QY 1106 TCTCTGCTGAGCTGCTTCTGTGCTTCTGTCTGAGAGCCCCCGATACCTCTACATCAT 1165
Db 770 CTTGCTGCTGAGTGTCTGCTGCTTCTGCTGCTGAGAGTCTGCTGCTGCTGCTGCTGCTGCT 829
QY 1166 CCGGAACTGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225
Db 830 CCGCAACGAGGAGAACCGGCGCAAGAGTGTCTTAAAGAAAGCTGCGCGGAGCAGCTGACGT 889
QY 1226 GTCTGATGCACTGGCTGAGCTGAGGATGAGAAACGGAAGTTTGGAAAGAGAGCTCCACT 1285
Db 890 GACCCATGACCTGAGGAGATGAAGAGAGTGTGGGAGATGATGCGGGAGAGAGAGGT 949
QY 1286 GTCTTGTGCTGAGCTCTTGGGAGCGCGCACCCACCGCGGAGCTCTGATTTATTTGAGTGT 1345
Db 950 CACCATCTGGAGCTGTTCCGCTCTCCCGCTTACCGCGAGCCCATCTCTCATCTGCTGCTGCT 1009
QY 1346 GTGCTGAGTGGCAGCAGCTCTGAGCATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405
Db 1010 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069
QY 1406 CTTTGTGATGTGCTGGGCTGGAACAGCAGCAGCTTACGCCACCATAGGAGCTGCTGCTGCTGCT 1465
Db 1070 CTTGAGAAAGCGGGGCTGAGCAGCTGTGTATGCCACCATTTGGCTCCGGTATCGTCAA 1129
QY 1466 TACCGCTTTCACGTTGCTCTGCTGCTCTTAGTAGAGCAGCTGGGCGAGCAGCTCCCA 1525
Db 1130 CACGGCTTTCACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
QY 1526 TCTCTGGGCTGGCAGGATGTGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1585
Db 1190 CTTATAGGCTCGCTGGCATGGCGGTTGTGCGCATCTCATGACCATCGCGTAGCACT 1249
QY 1586 GCTGGAGCGGTTCCATCCATGATGTATGTGCTCATGCTGGGCGCATATTTGGCTTGGC 1645
Db 1250 GCTGGAGCAGTACCTCGGATGCTCTATCTGAGCATCGTGGCCATCTTTGGCTTGGC 1309
QY 1646 CTTCTTTTGAATTTGGTCTGGGCCCCATCCCTGTTTCAATTTGGCGGCTACTCTAGGCCA 1705
Db 1310 CTTCTTTTGAATTTGGTCTGGGCCCCATCCCATGTTTCAATTTGGCGGCTACTCTAGGCCA 1369
QY 1706 GGGCCCCCGCCAGCAGCAGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1765
Db 1370 GGGTCCACGTCAGCTGCCATTCGCTGTGCGGCTTCTCCAACTGGACCTCAAAATTCAT 1429
QY 1766 CHTTGGCATGGTTCAGTATGTGGGATGTATGGGTCCCTAGCTCTTCTCTATT 1825
Db 1430 TGTGGGATGTGCTTCCAGTATGTGGAGCAACTGTGTGGTCCCTAGCTCTTCTCTATT 1489
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Qy	1826	TGCGGTCTCTGCTTGGCTTCTTCATCTTCACCTTCCTCAAGAGTGCTCAAAACGAGG	1885
Db	1490	CACGTGCTCCTGGTCTTGTTCTTCATCTTCACCTACTCTCAAGTTCTCTGAGACTAAAG	1549
Qy	1886	CCGGACATTTGACGAGATCTCGGCCACCTTCCGACGG	1922
Db	1550	CCGGACCTTCGATGAGATCGCTTCCGGCTTCCGGCAG	1586

RESULT 13

US-10-342-887-1294
; Sequence 1294, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene

```

; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1294
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1294

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Query Match	28.5%	Score 679;	DB 13;	Length 2856;
Best Local Similarity	68.1%	Pred. No. 2.4e-161;		
Matches 965;	Conservative	0;	Mismatches 440;	Indels 12;
Gaps 1;				

506	QY	GGAA	CCCCCTCAGCAGCGAGTGA	CTGGGACAC	TGGTCTTGTGTATTTCTCAGCTGTGCT	565
182	Db	GGAG	CCCCACGACGACAGAGCTG	ACGGGTCCGCTCATGCTGGCTGTGGGAGGACGAGTGC	241	
566	QY	TGGCTCCCTTCAGTCTTGGCTATACATTTGGAGTGCATCA	CGCCCCACAGAAAGTCATTTGA	625		
242	Db	TGGCTCCCTTCAGTCTTGGCTATACACACTGGAGTGCATCA	ATGCCCCCAGAAAGTGATCGA	301		
626	QY	ACAGAGCTACAATGCAACTTGGCTGGGTAGGACGAGGTCT	TGGGGGACCGGACTCCATCCC	685		
302	Db	GGAGTCTACAACACGACATGGGTCCACCGCTATGG	-----GGAGAGCATCCT	349		
686	QY	ACAAGGACCCCTACTACCTTTTGGGCTCTCCGCTGGCCATCT	TCTCTGTGGGTGGCAT	745		
350	Db	GCCCCACACGCTCACCACGCTCTGTCCTCTCAGTGGCCATCT	TTCTTGTGGGGGCAT	409		
746	QY	GATTTCTCTCTTCTCATTTGGCATCATTTCTCAATGGTTGGAGGAAAGGGCTATGCT	805			
410	Db	GATTTGGCTCCTTCTCTGTGGGCCCTTTTCGTTAAACCGCTTTGGCCGCGGAAATTCATGCT	469			
806	QY	GGCCCAACAATGCTTGGCTGTGCTGGGGGGCGCCCTCATGGCCCTAGCCAA	TGCCCGCGG	865		
470	Db	GATGATGAACCTGTGTGGCTTCTGTGTC	CCGCGTGCTCATGGGCTTCTCGAAACTGGGCAA	529		
866	QY	CTCCTATGAGATACTCATTTCTCGGACGGTTTCCTCATTTGGCGCTACTCAGGGCTAAACATC	925			
530	Db	GTTCCTTTGAGATGCTGATCTCTGGGCCCGCTTCATCTC	GGTGTGTA	589		
926	QY	AGGGTTGGTGCCTATGTATGTGGAGAAATCGCCCCCACTCATCTT	TCGGGGTGCCTTGGG	985		

590	AGGCTTCGTGCCCATGTATGTGGGTGAAGTGTCA	CCCA	CAGCCTTTC	TCGTGGGGCCCTGGG	649
986	AAACACTCAAACCAATTGGCCCATCGTCA	TTTGGCCATTTCTGGTTGCCACAGGTGTGGGTTT	TGGA	1045	
650	CACCTTGCAACAGCTGGGCATCGTCGTGGGCATCTCATCGCC	CCAGGTGTTCGGCCTGGA	709		
1046	GTCTATGCTGGGCA	CAGCTACCTGTGGCCATTTGCTTCTGGGTATCA	CAGTACTCCCTGC	1105	
710	CTCCATCATGGGCAACAAGGACCTGTGGCCCTGCTGCTGAGCATCATTT	CATCCATCCCGGC	769		
1106	TCCTCTGCAGCTGCTTCTGTTCCTCTGTCCTGAGAGCC	CCCCCATCTCTACATCAT	1165		
770	CTGTCTGCAGTGATCGTGTCTGCCCTTCTGCCCGAGAGTCC	CCGCTTCCCTGCTCATCAA	829		
1166	CCGGAACCTTGGAGGGCCCTGCCCGCAAGAGTCTAAAGCGCCTG	CACAGGTGGGCTGATGT	1225		
830	CCGCAACGAGGAGAACCGGGCCAAAGAGTGTCTAAAGAGCTGC	CGCGGACAGCTGACGT	889		
1226	GTCTGATGACCTGGCTGAGCTGAAGGATGAGAAA	CGGAAGTTGGAAGAGAGGCTCCACT	1285		
890	GACCCATGACCTTGCAAGGAGATGAAGGAAGAGAGT	CGGCAGATGATGCGGAGAGAAGGT	949		
1286	GTCTCTGTCTGACGTCTCTGGGCAGCGCACCA	CCGCGAGCCTCTGATTTATTCAGTGT	1345		
950	CACCATCTTGGAGCTGTTCCGCTCCCGCCTACCGC	AGCCCATCTCTCATCTGCTGTGT	1009		
1346	GCTGCAGCTGAGCCAGCAGCTCTCAGGCATCAATGCTGTTTT	CTACTATTTCAACACGACAT	1405		
1010	GCTGCAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGCTT	CTATTACTCCACGAGCAT	1069		
1406	CTTTGAGTTAGCTGGGTGGAA	CAGCCAGCCTACGCCACCATAGGAGCTGGTGTGTTCAA	1465		
1070	CTTCGAGAAAGCGGGGGTSCAGACGCTGTGTATGCCACCA	TATTTGGCTCCGGTATCGTCAA	1129		
1466	TACCGTTCACGTTGCTCTCGTGTCTTACTAGAGCGAGCT	GGCGACGGACACTCCA	1525		
1130	CAGCGCTTCACTGTCTGTCTGCTTTGTGTGTGAGCGAG	CAGCGCCGACCTGCA	1189		
1526	TCTCTGGCCCTGGCAGGCATGTGGCTGTGCCATCTTTGAT	GACGGTGGCTCTGCTGTCT	1585		
1190	CCTCATAGCCCTCGCTGGCATGGCGGTTGTGCCATACTCAT	GATCCGCTAGCACT	1249		
1586	GCTGGAGCGGGTTCCATCCATGAGTTATGTGTCCATCGTGGCC	ATATTTGGCTTTTGGC	1645		
1250	GCTGGAGCAGTACCCCTGGATGCTCTATCTGAGCATCGTGG	CCATCTTTGGCTTTTGGC	1309		
1646	CTTCTTTGAGATTGCTCTGGGCCCATCCCTCTGGTTCA	TTTGGCGCAGCTCTTCAGCCA	1705		
1310	CTTCTTTGAAGTGGGTCTCTGGCCCATCCCATGGTTT	CATCGTGGCTGAACTCTTCAGCCA	1369		
1706	GGGCCCCGCCCAGCAGGCATGGCTGTAGCTGGTTTCTCAA	ACTGGA	CTGTAACTTCAT	1765	
1370	GGGTCCACGCTCCAGCTGCCATTTGCCGTTGACGGCTTCT	CCAACTGGACCTC	CAAAATTCAT	1429	
1766	CGTTGGCATGGGTTTCCAGTATGTTCCGATGCTATGGGTCC	CTAGTCTCTCTCTTCTATTT	1825		
1430	TGTGGGCATGTGCTTCCAGTATGTGGAGCAACTGTGTGGT	CCCTACGCTCTTCATCATCTT	1489		
1826	TGCGGTCTCTCTGCTTGGCTTCTTCATCTTTCACTTT	CACTTTCTTAAGATGCTCTTCAAGAC	CGAGG	1885	
1490	CACGTGCTCTCTGGTCTGTCTTCTTCTTCTTCACTACT	TTCAAGTTCCTGAGACT	AAAGG	1549	
1886	CCGGACATTTGACCAATCTCGGCCACCTTCCGACGG	1922			
1550	CCGGACCTTTCGATGAGATCGCTTCCGGGTTCCGGGAG	1586			

RESULT 14
US-10-007-700-135
; Sequence 135, Application US10007700
; Publication No. US20030064947A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckman, David W.
APPLICANT: Cai, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 135
LENGTH: 2856
TYPE: DNA
ORGANISM: Homo sapiens
US-10-007-700-135

Query Match 28.5%; Score 679; DB 13; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY 506 GGAAACCCCTCAGCAGCGAGTGGACACATGGCTTCTGTGTTATCTCAGCTGTGCT 565
DB 182 GGAGCCAGCAGCAAGAGCTGAGCGGTGCGCTCATGCTGCTGTGGAGGACAGTGTCT 241
QY 566 TGCTCCCTTCACTTTGGCTATCAATTTGGAGTCATCAACGCCGCCACAGAAAGTGA 625
DB 242 TGCTCCCTGCACTTTGGCTTACAACTGGAGTCATCAATGCCCCCAGAAAGTGA 301
QY 626 ACAGAGTCAATGCAACTTGGCTGGGTAGGAGGCTTGGGGGACCGACTCATCC 685
DB 302 GGAGTTCTACAAACAGACATGGGTCCACCGCTATGG-----GGAGAGCATCT 349
QY 686 ACAAGCACCCTCACTACCTTTGGGCTCTCCGTGGCCATCTCTCTGTGGGTGSCAT 745
DB 350 GCCACACGCTCACACGCTCTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGCAT 409
QY 746 GATTTCTCTCTCATTTGGCATCAATTTCTCAATGGTTGGGAAGAAAGGCTATGCT 805
DB 410 GATTTGCTCTCTCTGTGGGCTTTTCTGTTAACCGCTTTGGCGCGGAATTCATGCT 469
QY 806 GGCCAAACATGTCTGTGCTGTGGGGGGCGCCCTCATGGGCTAGCCATGCCGGGC 865
DB 470 GATGTAACCTGTGGGCTTCTGTGCGCGTGTCTCATGGGCTTCTCGAAACTGGGCA 529
QY 866 CTCCTATGATACATCTCTCGACGGTTTCTCATTTGGCGCTCTCAGGGCTAACATC 925
DB 530 GTCTTTGATGATGCTATCTGGGCGCTTCTCATCATCGGTGTGCTGCGGCTTGACCAC 589
QY 926 AGGGTTGGTCCCTATGTATGGGAGAAATCGCCCCCCTCATCTTCGGGGTGCCTTGGG 985
DB 590 AGGCTTCGTCCTATGTATGGTGAAGTGTACCCACAGCCCTTCGTGGGGCCCTGGG 649
QY 986 AACACTCAACATGGCCATCGTCATTTGGCATCTGGTTGCCAGGTGTGGGTTTGA 1045
DB 650 CACCTGACACAGTGGGCTCGTGTGGGCTCTCATCGCCAGGTGTTCGGGCTTGA 709
QY 1046 GTCTATGCTGGGACAGCTACCTGTCGGGCTTCTGCTGCTATCAGATCTCCCTGC 1105
DB 710 CTCATCATGGGCAACAGAGACCTGTGGGCGCTTCTGCTGATGATCATCTTCATCCGGC 769

QY 1106 TCTCTGCGAGCTGCTTCTGTGTCCTTCTGTCTGAGAGCCCGCATACCTCTACATCAT 1165
DB 770 CTTGCTGCGAGTGCATCGTGTGCTGCTGCTTCTGCCCCGAGAGTCCCGCTTCTGCTCATCA 829
QY 1166 CGGGAACCTGGAGGGGCTGCCCGAAGAGTCTTAAAGCGCTTACAGAGCTGAGGCTGATGT 1225
DB 830 CGCAACAGAGGAGAACCGGGCCAGAGTGTGCTTAAAGAGCTCGCGGGACAGCTGACGT 889
QY 1226 GTCTGATGCACTGGCTGAGCTGAAGGATGAGAAACGGAAGTTTGGAAAGAGAGGCTCCACT 1285
DB 890 GACCCATGACCTGCAGAGATGAAGGAGAGAGTTCGCGAGATGATCGCGGAGAAGGT 949
QY 1286 GTCTTGTGCGAGCTCTCGGCGAGCGCGACCCACCGCGAGCTCTCATTTATTCAGTGT 1345
DB 950 CACCATCTGAGCTGTTCGCTCCCGCTTACCGCGAGCCCATCTCATCTGCTGTGGT 1009
QY 1346 GCTGAGCTGAGCGAGCTCTCAGGCATCAATGCTGTTTCTACTATTATTAACACAGCAT 1405
DB 1010 GCTGAGCTGTCCAGAGCTGTTCGCGATCAAGCTGTCTTATTAATTCACAGAGCAT 1069
QY 1406 CTTTGAAGTTAGCTGGGGTGGAAACAGCCAGCTTACGCCACCATAGGAGCTGTGTGTGTC 1465
DB 1070 CTTGAGAGAGCGGGGTGCGAGCGCTGTGTATGCCACCATTTGGCTCCGCTATCGTCAA 1129
QY 1466 TACCGTCTTCACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1525
DB 1130 CACGGCTTCACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1189
QY 1526 TCTCTGGGCTGGCGAGGATGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1585
DB 1190 CTTATAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1249
QY 1586 GCTGAGCGGGTTCATCCATGAGTTATGTGTCCATCGTGGCCATATTTGGCTTTGTGGC 1645
DB 1250 GCTGAGAGCTACCTGGATGCTCTATCTGAGCATCGTGGCCATCTTTGGCTTTGTGGC 1309
QY 1646 CTTCTTTGAGATTGCTGCTGGCCCCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1705
DB 1310 CTTCTTTGAGTGGGTCTGCGGCCCATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369
QY 1706 GGCCCCCGCCAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1765
DB 1370 GGTCCACGCTCGAGCTGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429
QY 1766 CGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1825
DB 1430 TGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1489
QY 1826 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1885
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RESULT 15

US-10-172-118-1294
; Sequence 1294, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118

/ CURRENT FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/380,770
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 1294
/ LENGTH: 2856
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: NM 006516
/ DATABASE ENTRY DATE: 2001-06-18
/ us-10-172-118-1294

Query Match 28.5%; Score 679; DB 13; Length 2856;

Best Local Similarity 68.1%; Pred. No. 2,4e-161;

Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

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Qy	686	ACAAGGCAACCTCACTAC	CCCTTTGGGCTCTCTCGGTGGCCATCTTCTGTGGGTGGCAT	745
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Qy	986	AACACTCAACCAAT	TGGCCATCGTCAATTTGGCATTTCTGTTGCCAGGTGTTGGT	1045
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Qy	1046	GTCTATGCTGGGCAC	AGCTPACCTGTGGCCATTTGCTTGGCTATCACAGTACTCCCTGC	1105
Db	710	CTCCATCATGGGCA	CAAGGACCTGTGGCCCTGTCTGTGAGCATCATCTTTCATCCCGGC	769
Qy	1106	TCCTCTGAGCTGCT	TTCTGTGGCCCTTCTGTCTGAGAGCCCGATACCTCTACATCAT	1165
Db	770	CCTGTGTCAGTGC	ATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	829
Qy	1166	CCGGAACCTTGGAG	GGGCTTGGCCCAAGAGTCTAAAGCGCTGACAGGCTGGCTGTGAT	1225
Db	830	CCGCAACGAGGAG	AACCGGCCCAAGAGTGTGCTAAAGAGTGTGCGGGGACAGCTGACGT	889
Qy	1226	GTCTGATGCACTGG	CTGAGCTGAAGGATGAGAAACGGAAGTTGGAAGAGAGCGGTCCACT	1285
Db	890	GACCCATGACCTG	CAGGAGATCAAGAGAGAGTGGCAGATGATGCGGGAGAGAGGT	949
Qy	1286	GTCTTGTCTGAG	CTTCTGGGAGCGGCACCCACCGGAGGCTCTGATTTATTCAGTGGT	1345
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Job time : 644.395 secs

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Qy	1886	CCGGACATTTGAC	CCAGATCTCGGCCACCTTCCGACGG 1922	
Db	1550	CCGGACCTTCG	ATGAGATCGCTTCCGGCTTCCGGCAG 1586	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2004, 22:29:22 ; Search time 19566.2 Seconds
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Perfect score: 7828

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	6975.2	89.1	7777	6	AX573333	Sequence
3	5908	75.5	6360	6	AX573337	Sequence
C 4	4492.6	57.4	7209	6	AX006823	Sequence
C 5	4492.6	57.4	7209	6	AX417671	Sequence
C 6	4492.6	57.4	7209	6	BD223877	Evaluation
C 7	4492.6	57.4	8749	6	AX084712	Sequence
C 8	4492.6	57.4	8941	6	AX084714	Sequence
C 9	4492.6	57.4	9700	6	AX054976	Sequence
C 10	4492.6	57.4	9749	6	AX054977	Sequence
C 11	4492.6	57.4	10288	6	A58524	Sequence 28
C 12	4492.6	57.4	10288	6	AR432922	Sequence
C 13	4492.6	57.4	13414	6	A58523	Sequence 27
C 14	4492.6	57.4	13414	6	AR432921	Sequence
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C 16	3621	46.3	6849	12	PR5425	U03452 Yeast episo
C 17	3621	46.3	7168	12	AF174132	AF174132 Cloning v
C 18	3621	46.3	8182	12	AF174133	AF174133 Cloning v
C 19	3619.4	46.2	5616	12	PR5424	U03453 Yeast episo
C 20	3609	46.1	5797	12	PR5423	U03454 Yeast episo
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C 23	3591.2	45.9	9560	12	AY150810	AY150810 Cloning v
C 24	3578.6	45.7	6779	12	AF008932	AF008932 DNA-bindi
C 25	3578.6	45.7	6827	12	CVU57443	U57443 Cloning vec
C 26	3547.4	45.3	11912	6	BD249046	BD249046 Centrifug
C 27	3484	44.5	7933	12	AF359244	AF359244 Integrati
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C 29	3404.6	43.5	6631	12	AF063585	AF063585 Cloning v
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ALIGNMENTS

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DEFINITION	Sequence 9 from Patent WO02064784.					
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VERSION	AX573331.1	GI:26005217				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1					
AUTHORS	Mueller,G., Koller,K.P., Boles,E., Wiczorke,R. and Dlugai,S.					
TITLE	Yeast strain of saccharomyces cerevisiae with functional expression of a glut transporter					

JOURNAL Patent: WO 02064784-A 9 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
Source 1..7828
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 7828; DB 6; Length 7828;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB |||||
QY 61 ACTGGGACCCCTGCTCTGCTGTGTCTCTCGGCTGTGGCTCCCTGACGTTTGGGTAC 120
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QY 121 AACATTTGGGCTCATCAATGCCCTCAGAAAGTGATTGAACAGAGCTACAATGAGACGTGG 180
DB |||||
QY 121 AACATTTGGGCTCATCAATGCCCTCAGAAAGTGATTGAACAGAGCTACAATGAGACGTGG 180
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QY 301 ATCATCTCTCAGTGGCTTGAAGAAAGAGGCGATGCTGGTCAACATGCTCTGGCGGTG 360
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RESULT 2
AX573333 LOCUS AX573333 7777 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 11 from Patent WO02064784.
ACCESSION AX573333
VERSION AX573333.1 GI:26005219
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Mueller,G., Koller,K.P., Boles,E., Wieszorke,R. and Dlugai,S.
TITLE Yeast strain of saccharomyces cerevisiae with functional expression
of a glut transporter
JOURNAL Patent: WO 02064784-A 11 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
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ORGANISM	synthetic construct									
REFERENCE	1 ,									
AUTHORS	Mueller,G., Koller,K.P., Boles E., Wiczorke,R. and Dlugai,S.									
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JOURNAL	Patent: WO 02064784-A 15 22-AUG-2002;									
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DEFINITION Sequence 8 from Patent WO0001846.
ACCESSION AX006823
VERSION AX006823.1 GI:9994839
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mortier,K., Bogaert,T., Plaetinck,G. and Platteeuw,C.
TITLE Characterisation of gene function using double stranded rna inhibition
JOURNAL Patent: WO 0001846-A 8 13-JAN-2000;
MORTIER KATHERINE (BE); BOGAERT THIERRY (BE); DEVGEN N V (BE);
PLAETINCK GEERT (BE); PLATTEEUW CHRIST (BE)
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ORIGIN
Query Match 57.4%; Score 4492.6; DB 6; Length 7209;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

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Db	2495	GATCTCTGTTGAAAAATPAGCGCTCTCGCGTTGCAATTTTGTCTACAAAAATGAAGCA	2436	Db	1415	TACTCATATATCTTTTATAGATTTTAAACTTCATTTTAAATTTTAAAGGATCTAGGTG	1356
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Plattinck, G., Plattinck, C., Mortier, K. and Bogaert, T.
AUTHORS
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ACCESSION AX084712
VERSION AX084712.1 GI:13274966
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kaletta, T., Vangeel, A., Bogaert, T. and van de Craen, M.
TITLE pkd constructs and screening methods
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Devgen NV (BE)
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QY	3239	AATTTGGGACCTAAATGCTTCAACTAATCCAGTAAATCTCTGGTGGTAC-GAACATCCA	3297
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Db	4292	 GTGAAATTAATAACAGACATACTCCAAGCTGCCTTTGTGTGCTTAATCACGTATCTCAC	4233
QY	3358	GACTAGATGAGTAGCGACAGTTCCTTATATATGTAGCTTTTCGACATGATTTATTCCTGTT	3417
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QY	3418	TCCTGCAGGTTTTTGTGTCGTCAGTTGGGTTAAGAATACTGGGCAATTTTCATGTTCTTT	3477
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QY	3538	TCTGTTGGGAGATTACGGAATCAAAAAATTTCAAAGAAACCGAAATCAAAAAAAGAAT	3597
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QY	3598	AAAAAAAATGATGAATTGAATTTGAAGCTGTGTGTTAGTGTGCTCTCAGTACAACTCT	3657
Db	4023	 GCTTCTTATATATATATATATAGTAATGTGCTGATCTATGGTGCATCTCAGTACAACTCT	3964
QY	3658	GCTCTGATGCGCATAGTTAAGCAGCCCGCACACCGCCCAACACCGCTGACGCGCCCT	3717
Db	3963	 GCTCTGATGCGCATAGTTAAGCAGCCCGCACACCGCCCAACACCGCTGACGCGCCCT	3904
QY	3718	GACGGCTGTCTGCTCCCGGCATCCGTTTACAGACAAGCTGTGACCGTCTCCGGGAGCT	3777
Db	3903	 GACGGCTGTCTGCTCCCGGCATCCGTTTACAGACAAGCTGTGACCGTCTCCGGGAGCT	3844
QY	3778	GCATGTCTCAGAGGTTTTACCGTCTATCACCAGAACGCGCGAGACGAAAGGCGCTCGTGA	3837
Db	3843	 GCATGTCTCAGAGGTTTTACCGTCTATCACCAGAACGCGCGAGACGAAAGGCGCTCGTGA	3784
QY	3838	TACGCTATTTTATAGTTAATGTCAATGATAATATATGTTTCTTATAGTATGATCCAAAT	3897
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QY	3898	CAAGGAAATGATAGCATTTGAAGGATGAGACTAATCCAATTTGAGGAGTGGCAGCATATAG	3957
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QY	3958	AAACGCTAAAGGGTAGTCTGTAAGGAAGCATACGATACCCCGCATGGAATGGGATATAT	4017
Db	3663	 AAACGCTAAAGGGTAGTCTGTAAGGAAGCATACGATACCCCGCATGGAATGGGATATAT	3604
QY	4018	CACAGAGGTACTAGACTACCTTTTCACTCTACATAAATAGCCCATATATAGTACGATTT	4077
Db	3603	 CACAGAGGTACTAGACTACCTTTTCACTCTACATAAATAGCCCATATATAGTACGATTT	3544
QY	4078	AAGCATAAAACACGACTATCCGTTCTTCTCATGTATATATATATACAGGCAACACGCAG	4137
Db	3543	 AAGCATAAAACACGACTATCCGTTCTTCTCATGTATATATATATACAGGCAACACGCAG	3484
QY	4138	ATATAGGTGCGACGTGAAACAGTGAGCTGTATGTGCGGAGCTCGGGTTGCATTTTCGGAAG	4197
Db	3483	 ATATAGGTGCGACGTGAAACAGTGAGCTGTATGTGCGGAGCTCGGGTTGCATTTTCGGAAG	3424

QY	4198	CGTCGTTTTCCGAAACGCCTTTGAAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTA	4255
DB	3423	CGTCGTTTTTCGAAACGCCTTTGAAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTA	3364
QY	4258	TAGGAACCTTCAGAGCGCTTTGAAACCAAAAGCGCTCTGGAAGCGCATCTTTCAAAAAAC	4317
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QY	4318	CAAAAAACGACCCGGAAGCTGTAAACGAGCTACTTAAATAATTGCGAATACCGCTTCCACAAACA	4377
DB	3303	CAAAAAACGACCCGGAAGCTGTAAACGAGCTACTTAAATAATTGCGAATACCGCTTCCACAAACA	3244
QY	4378	TTGCTCAAAAGTATCTCTTTGCTATATATATCTCTGTGCTATATATCCCTATATAACCTACCCA	4437
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QY	4438	TCCACCTTTTCGCTCCCTTGAACTTGCACTTAAACTCGACCTCTACATTTTTTATGTTTTATC	4497
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QY	4498	TCTAGTATTACTCTTTTAGACAAAAAATGTAGTAAGAACTATTTCATAGAGTGAATCGAA	4557
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QY	4558	AACAATACGAAATGTAAACATTTCTCTATACGPGATATAGAGACAAAAATAGAAGAAC	4617
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QY	4618	CGTTCATATTTTCTGACCAATGGAAGATCATCAACGCTTATCACATTTCTGTTTCACAAAGT	4677
DB	3003	CGTTTCATATTTTCTGACCAATGGAAGATCATCAACGCTTATCACATTTCTGTTTCACAAAGT	2944
QY	4678	ATCGCAATCCACATCGGTATAGAAATAATCGGGATGCTTTTATCTTGAAAAAATGCA	4737
DB	2943	ATCGCAATCCACATCGGTATAGAAATAATCGGGATGCTTTTATCTTGAAAAAATGCA	2884
QY	4738	CCGCGAGCTTCGCTAGTAATCAGTAAACCGGGAAGTGGAGTCAGGCTTTTTTATGGA	4797
DB	2883	CCGCGAGCTTCGCTAGTAATCAGTAAACCGGGAAGTGGAGTCAGGCTTTTTTATGGA	2824
QY	4798	GAGAAATAGACACCAAAGTAGGCTTCTCTTAACCTTAAACGAGCTTACAGTGCAGAAAGT	4857
DB	2823	GAGAAATAGACACCAAAGTAGGCTTCTCTTAACCTTAAACGAGCTTACAGTGCAGAAAGT	2764
QY	4858	TATCAAGAGACTGCATTTATAGAGCGCACAAAGGAGAAAAAGTAACTCTAAGATGCTTTG	4917
DB	2763	TATCAAGAGACTGCATTTATAGAGCGCACAAAGGAGAAAAAGTAACTCTAAGATGCTTTG	2704
QY	4918	TTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCCT	4977
DB	2703	TTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCCT	2644
QY	4978	TGTTGTAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAAAAATGCAGCTCAGATTC	5037
DB	2643	TGTTGTAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAAAAATGCAGCTCAGATTC	2584
QY	5038	TTTTGTTGAAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAGCACAGA	5097
DB	2583	TTTTGTTGAAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAGCACAGA	2524
QY	5098	TTCTTCGTTGGTAAAAATAGCGCTTTTCGCTTGCAATTTCTGTTCTGTAAAAATGCAGCTCA	5157
DB	2523	TTCTTCGTTGGTAAAAATAGCGCTTTTCGCTTGCAATTTCTGTTCTGTAAAAATGCAGCTCA	2464
QY	5158	GATTCCTTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTGTGTTCTCAAAAATGAGCA	5217
DB	2463	GATTCCTTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTGTGTTCTCAAAAATGAGCA	2404
QY	5218	CAGATCGTTTCAGTGGCATTTTCGGGGAATGTCGGCGGAACCCCTATTTCTTTTA	5277
DB	2403	CAGATCGTTTCAGTGGCATTTTCGGGGAATGTCGGCGGAACCCCTATTTCTTTTA	2344
QY	5278	TTTTTCTAAATACATTTCAATATGATTCGCTCATGAGACAATTAACCTCTGATTAATGCTT	5337

Db	2343	 TTTTTCTAAATACAAATTCAATATATGATATCCCGCTCATGAGACAATAAACCCCTGATAAATGCCTT	2284
Qy	5338	CAATAAATATTGAAAAAGGAAGAGATGAGTATTCAACATATTTCCGTGTGCGCCCTTATTCCCT	5397
Db	2283	CAATAAATATTGAAAAAGGAAGAGATGAGTATTCAACATATTTCCGTGTGCGCCCTTATTCCCT	2224
Qy	5398	TTTTTTGGGGCAATTTTCCCTTCTCTGCTTTCCTCACCCAGAAACGCTGGTGAAAGTAAAA	5457
Db	2223	TTTTTTGGGGCAATTTTCCCTTCTCTGCTTTCCTCACCCAGAAACGCTGGTGAAAGTAAAA	2164
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Db	2103	AAGATCCTTGAGAGTTTTTCGGCCCGAAGAACGTTTTTCCAATGATGAGCACTTTTTAAAGTT	2044
Qy	5578	CTGCTATGTGGCGGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGCGC	5637
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Qy	5638	ATACACTATTCTCAGAATGACTTGGTTGAGTACTACACAGTCAAGAAAAAGCATCTTTACG	5697
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Qy	5698	GATGGCATGACAGTAAGAGAAATATGACAGTCTGSCCATTAACCATGAGTGATACACTGCG	5757
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Qy	5938	ACTGGCGAACTACTTACTCTAGCTTCCCGGCACAAATTAATAGACTGGATGGAGGCGGAT	5997
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Db	1443	AGACAGATCGCTGAGATGAGTGCCCTCACTGATTAAGCAATTTGGTAACTGTGAGACCAAGTT	1384
Qy	6238	TACTCATATATACTTTAGATTTGATTTAAACTTCATTTTTAAATTTAAAGATCTAGGTG	6297
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963	Db	ACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGCGCAGCGGTGGGCTGGAACGGGG	904
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903	Db	GGTTCTGTGCACACAGCCGAGCTTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAG	844
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VERSION	AX084714.1	GI:13274968			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1. .8941				
AUTHORS	Kaletha, T., Vangeel, A., Bogaert, T. and van de Craen, M.				
TITLE	Pkd constructs and screening methods				
JOURNAL	Patent: WO 0112796-A 6 22-FEB-2001;				
	Devgen NV (BE)				
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Qy	1619	AAAGGAGGAGGTAGACAACTGAAGTCTAGGTCCTATTTATTTTATATAGTTATGT	1678		
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Qy	1859	CGTCGTTTTACACGTCGTGACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCTTGC	1918		
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Qy	1919	AGCATATCCCTTTTCGCCAGTGTGCGTAATAGCGAAGCGCCGACCGATCGCCCTTC	1978		
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Qy	1979	CCAAAGTTGCGCAGCTGAATGGCGAATGGCGGACGCGCTGTAGCGGCGCATTAAG	2038		
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Db	5180	ACTCAACCTTATCTCGGCTCTATTCTTTTGAATTTAAGGGATTTTCCGATTTTCGGCCTTA	5121		
Qy	2399	TTGTTTAAAAAATGAGCTGATTTTAAACAAAATTTTAAACGCGAATTTTAAACAAATATTAAC	2458		
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RESULT 9

AX054976/c

LOCUS

AX054976

DEFINITION

Sequence 91 from Patent WO0073328.

ACCESSION

AX054976

VERSION

AX054976.1 GI:12228344

KEYWORDS

synthetic construct

SOURCE

synthetic construct

ORGANISM

artificial sequences.

REFERENCE

1

AUTHORS

van Criekeing, W., Roelens, I., Bogaert, T. and Verwaerde, P.

TITLE

Unc-5 constructs and screening methods

JOURNAL

Patent: WO 0073328-A 91 07-DEC-2000;

Devgen NV (BE)

FEATURES

Location/Qualifiers

1. .9700

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ORIGIN										
Query Match 57.4%; Score 4492.6; DB 6; Length 9700; Best Local Similarity 87.3%; Pred. No. 0; Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;										
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VERSION AX054977.1 GI:12228345
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Crielinge,W., Roelens,I., Bogaert,T. and Verwaerde,P.
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Devgen NV (BE)
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Db
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Db
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Db
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Db
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Db
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Db
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Db
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Db
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QY
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Db
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QY
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Db
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QY
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Db
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DB 5493 CCCGAGCTTCGCTAGTAAATCAGTAAACGCGGAAGTGGAGTCAAGGCTTTTTTATGGAA 5434
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TITLE PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE IN THE CONTROL OF CELL BEHAVIOUR
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COMMENT BOGAERT THIERRY (BE)
FEATURES Other publication AU 6123496 961218.
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Query Match 57.4%; Score 4492.6; DB 6; Length 10288;
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Db	6988	GTTT	ACAATTTCTGATGCGGTAATTTCTCTCTTTACGCACTCTGTGCGGTAATTTCAACACGC	6929
Qy	2519	ATAG	GGTAATAACCTGATATAATTAATTTGAAGCTCTAAATTTGTGAGTTTAGTATACATGC	2578
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Qy	2699	TCCT	CCAACTAATAATATGTCCAGATCTGTAGAGCACAATCATCCAGGTTCTATCTAGT	2758
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Qy	2759	TTGA	CCAAATGCGTCTCCCTTGTCTATCTAAACCCACACCGGGTGTCTATAATCAACCAATC	2818
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Db	6611	AG	TTTTCTGTGAAGCTGCATGAGTAGTAGTTGCGAGTCTTTTGGAAATACGAGTCTTTT	6552
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VERSION AR432922.1 GI:40195525
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10288)
AUTHORS Peng, J., Hirayama, L. and Lochetto, C.
TITLE Use of the maize X112 mutant has 2 gene and imidazolinone herbicides for selection of transgenic monocots, maize, rice and wheat plants resistant to the imidazolinone herbicides
JOURNAL Patent: US 6653529-A 28 25-NOV-2003;
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4018 CACAGGAGTACTAGACTACTCTTTCATCTACATAAATAGACGATATAAGTACGATTT 4077
5531 CACAGGAGTACTAGACTACTCTTTCATCTACATAAATAGACGATATAAGTACGATTT 5472
4078 AAGCATAAACACGCACTATCCGCTTCTCTCATCTATATATATACAGGCAACACGAG 4137
5471 AAGCATAAACACGCACTATCCGCTTCTCTCATCTATATATATATACAGGCAACACGAG 5412
4138 ATATAGTGTGCACTGAAACAGTGTATGTCGCGAGCTCGGCTGCAATTTTCGGAAG 4197
5411 ATATAGTGTGCACTGAAACAGTGTATGTCGCGAGCTCGGCTGCAATTTTCGGAAG 5352
4198 CGCTCGTTTTCGGAACCGTTTGAAGTTCCTTATTTCCGAAGTTCCTATTTCTCTAGAAAGTA 4257
5351 CGCTCGTTTTCGGAACCGTTTGAAGTTCCTTATTTCCGAAGTTCCTATTTCTCTAGAAAGTA 5292
4258 TAGGAAGCTTCAGAGCGCTTTTGAAGCCAAAGCGCTCTGAAGAGCGACTTTTCAAAAAAC 4317
5291 TAGGAAGCTTCAGAGCGCTTTTGAAGCCAAAGCGCTCTGAAGAGCGACTTTTCAAAAAAC 5232
4318 CAAAAACGCAACCGGACTGTAAACGAGCTACTAAAAATTTTGGAAATACCGCTTCCCAACA 4377
5231 CAAAAACGCAACCGGACTGTAAACGAGCTACTAAAAATTTTGGAAATACCGCTTCCCAACA 5172
4378 TTGCTCAAAAGTATCTCTTGTGCTATATATCTCTGCTATATATCTCTATATACCTTACCCA 4437

5171	TTGCTCAAAAGTATCTCTTTTGGCTATATATCTCTGTGCTATATCTCCCTATATATACCTTACCCA	5111
4438	TCACCTTTTCGCTCTCTTTGAACCTTGCATCTAAACTCGACCTCTACATCTTTTATATGTTTATC	4497
5111	TCACCTTTTCGCTCTCTTTGAACCTTGCATCTAAACTCGACCTCTACATCTTTTATATGTTTATC	5052
4498	TCTAGTATTACTCTTTTAGACAAAATAATTTGTAGTAGAAGCTATTTCATAGAGTGAATCGAA	4557
5051	TCTAGTATTACTCTTTTAGACAAAATAATTTGTAGTAGAAGCTATTTCATAGAGTGAATCGAA	4992
4558	AACAAATACGAAATGTAAACATTTCTTATAGTAGTAGTATATAGAGACAAAATAGAGAAAC	4617
4991	AACAAATACGAAATGTAAACATTTCTTATAGTAGTAGTATATAGAGACAAAATAGAGAAAC	4932
4618	CGTTCAATAATTTTTCGACCAATGAAGAAATCATCAACGCTATCACTTTCTCTGTTCACAAAGT	4677
4931	CGTTCAATAATTTTTCGACCAATGAAGAAATCATCAACGCTATCACTTTCTCTGTTCACAAAGT	4872
4678	ATGCGCAATCCACATTCGGTATAGAAATATAATTCGGGGATGCTTTATCTTGAAAAAATGCA	4737
4871	ATGCGCAATCCACATTCGGTATAGAAATATAATTCGGGGATGCTTTATCTTGAAAAAATGCA	4812
4738	CCCGCAGCTTCGCTAGTAAATCAGTAGAAGCGGGAGTGGAGTCAGGCTTTTTTTTATGCAA	4797
4811	CCCGCAGCTTCGCTAGTAAATCAGTAGAAGCGGGAGTGGAGTCAGGCTTTTTTTTATGCAA	4752
4798	GAGAAATAGACACAAAGTAGCCCTCTCTTAACTTAAACGGACCTACAGTCGCAAAAAGT	4857
4751	GAGAAATAGACACAAAGTAGCCCTCTCTTAACTTAAACGGACCTACAGTCGCAAAAAGT	4692
4858	TATCAAGAGACTGCAATTATAGAGCGCACAAGGAGAAAAAAGTAATCTAAGATGCTTTTG	4917
4691	TATCAAGAGACTGCAATTATAGAGCGCACAAGGAGAAAAAAGTAATCTAAGATGCTTTTG	4632
4918	TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCCT	4977
4631	TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCCT	4572
4978	TGTTGTTAAAAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAAAAATGCAGCTCAGATTC	5037
4571	TGTTGTTAAAAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAAAAATGCAGCTCAGATTC	4512
5038	TTTGTTTGAATAATTAGCGCTCTCGCGTTGCAATTTTGTTTTACAAAAATGAAGCACAGA	5097
4511	TTTGTTTGAATAATTAGCGCTCTCGCGTTGCAATTTTGTTTTACAAAAATGAAGCACAGA	4452
5098	TTCTTCGTTGGTAAAAATAGCGCTTTTCGCGTTGCAATTTCTGTTCTGTAAAAATGCAGCTCA	5157
4451	TTCTTCGTTGGTAAAAATAGCGCTTTTCGCGTTGCAATTTCTGTTCTGTAAAAATGCAGCTCA	4392
5158	GATTCCTTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTGTCTTACAAAAATGAAGCA	5217
4391	GATTCCTTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTGTCTTACAAAAATGAAGCA	4332
5218	CAGATGCTTCGTTTCAGGTGGCACTTTTTCGGGGAAATGTGCGCGGAAACCCCTATTGTTTA	5277
4331	CAGATGCTTCGTTTCAGGTGGCACTTTTTCGGGGAAATGTGCGCGGAAACCCCTATTGTTTA	4272
5278	TTTTTCTAAATAACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATTAATGCTTT	5337
4271	TTTTTCTAAATAACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATTAATGCTTT	4212
5338	CAATAATATTGAAAAAGGAGATACAGTATTTCAACATTTCCGTGTCCGCTTATTTCCC	5397
4211	CAATAATATTGAAAAAGGAGATACAGTATTTCAACATTTCCGTGTCCGCTTATTTCCC	4152
5398	TTTTTTTCGGCATTTTTCGCTTCTCTGTTTTCCTCACCACAGAAACCGCTGGTGAAGTAAAA	5457
4151	TTTTTTTCGGCATTTTTCGCTTCTCTGTTTTCCTCACCACAGAAACCGCTGGTGAAGTAAAA	4092
5458	GATCCTGAAGATCAGTTGGGTGCAAGATGGGTTTATATCGAACTGGATCTCAACAGCGGT	5517
4091	GATCCTGAAGATCAGTTGGGTGCAAGATGGGTTTATATCGAACTGGATCTCAACAGCGGT	4032

QY	5518	AAGATCCTTCGAGAGTTTTTCGCCCGAAGAAAGTTTTCCTCAATGATGAGCACTTTTAAAGTT	5577
DB	4031	AAGATCCTTCGAGAGTTTTTCGCCCGAAGAAAGTTTTCCTCAATGATGAGCACTTTTAAAGTT	3972
QY	5578	CTGCTATGTGCGCGGTATTTATCCCGTATTGACGCGCGGCAAGAGCAACTCGGTGCGCGC	5637
DB	3971	CTGCTATGTGCGCGGTATTTATCCCGTATTGACGCGCGGCAAGAGCAACTCGGTGCGCGC	3912
QY	5638	ATACACTATTCTCAGAATGACTTGGTTGAGTACTCACAGTCAAGAAAAAGCATCTTTACG	5697
DB	3911	ATACACTATTCTCAGAATGACTTGGTTGAGTACTCACAGTCAAGAAAAAGCATCTTTACG	3852
QY	5698	GATGGCATGACGTAAGAGAATTTATGACGTGCTGCCATAACATAGAGTGAATAACCTGCG	5757
DB	3851	GATGGCATGACGTAAGAGAATTTATGACGTGCTGCCATAACATAGAGTGAATAACCTGCG	3792
QY	5758	GCCAACTTACTCTGACAAAGATCGGAGGACCGAAGAGCTAACCGCTTTTTTGCACAAC	5817
DB	3791	GCCAACTTACTCTGACAAAGATCGGAGGACCGAAGAGCTAACCGCTTTTTTGCACAAC	3732
QY	5818	ATGGGGGATCATGTAACTCCGCTTGATCGTTTGGAAACCGAGCTGAAATGAAGCATACCA	5877
DB	3731	ATGGGGGATCATGTAACTCCGCTTGATCGTTTGGAAACCGAGCTGAAATGAAGCATACCA	3672
QY	5878	AACGACGAGCGTGACACACGATGCCCTGTAGCAATGGCAACAACGTTTGCACAACTATTA	5937
DB	3671	AACGACGAGCGTGACACACGATGCCCTGTAGCAATGGCAACAACGTTTGCACAACTATTA	3612
QY	5938	ACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGAT	5997
DB	3611	ACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGAT	3552
QY	5998	AAAGTTCGAGCAACACTTCTCGCTCGCTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATAAA	6057
DB	3551	AAAGTTCGAGCAACACTTCTCGCTCGCTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATAAA	3492
QY	6058	TCTGGAGCCCGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAG	6117
DB	3491	TCTGGAGCCCGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAG	3432
QY	6118	CCCTCCCGTATCGTAGTTATCTACACGCGGGAGTCAGGCAACTATGGAATGAACGAAAT	6177
DB	3431	CCCTCCCGTATCGTAGTTATCTACACGCGGGAGTCAGGCAACTATGGAATGAACGAAAT	3372
QY	6178	AGACAGATCCGTGAGATAGTGCCTCACTAATTAAGCATTTGTAACCTGTCAGACCCAGATT	6237
DB	3371	AGACAGATCCGTGAGATAGTGCCTCACTAATTAAGCATTTGTAACCTGTCAGACCCAGATT	3312
QY	6238	TACTCATATATCTTTAGATTGATTTAAAACTTCATTTTAAATTTAAAAAGATCTAGGTG	6297
DB	3311	TACTCATATATCTTTAGATTGATTTAAAACTTCATTTTAAATTTAAAAAGATCTAGGTG	3252
QY	6298	AAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTTGGTTCCACTGA	6357
DB	3251	AAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTTGGTTCCACTGA	3192
QY	6358	CGCTCAGACCCCGTAGAAAAAGATCAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTA	6417
DB	3191	CGCTCAGACCCCGTAGAAAAAGATCAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTA	3132
QY	6418	ATCTGCTGCTTGCAACAAAAAACACCGCTACACGCGGTGGTTTCTGTTTGGCGGATCAA	6477
DB	3131	ATCTGCTGCTTGCAACAAAAAACACCGCTACACGCGGTGGTTTCTGTTTGGCGGATCAA	3072
QY	6478	GAGCTACCAACTCTTTTTTCCGAAGTTAACTGGCTTTCAGCAGAGCGCAGATACCAAACTACT	6537
DB	3071	GAGCTACCAACTCTTTTTTCCGAAGTTAACTGGCTTTCAGCAGAGCGCAGATACCAAACTACT	3012
QY	6538	GTCCTTCTAGTGACCGTATGTTAGGCCACCACTTTCAAGAACTCTGTGAGCAACCGCTTACA	6597
DB	3011	GTCCTTCTAGTGACCGTATGTTAGGCCACCACTTTCAAGAACTCTGTGAGCAACCGCTTACA	2952

Db 8057 CGTTCATAATTTCTGACCAATGAAGAATCATCAACGCTATCATCTTTCTGTTCCAAAGT 7998
Qy 4678 ATGCGCAATCCACATCGGTATAGATATAATACGGGATGCCCTTATCTTTGAAAAATGCA 4737
Db 7997 ATGCGCAATCCACATCGGTATAGATATAATACGGGATGCCCTTATCTTTGAAAAATGCA 7938
Qy 4738 CCGCAGCTTCCTAGTATATCAATAGTAAGACGGGGAAGTGGAGTCAGCGCTTTTTTATGGAA 4797
Db 7937 CCGCAGCTTCCTAGTATATCAATAGTAAGACGGGGAAGTGGAGTCAGCGCTTTTTTATGGAA 7878
Qy 4798 GAGAAATAGACACCAAAAGTAGCTTCTTAAACCTTAAACGGACCTACAGTGCAAAAAGT 4857
Db 7877 GAGAAATAGACACCAAAAGTAGCTTCTTAAACCTTAAACGGACCTACAGTGCAAAAAGT 7818
Qy 4858 TATCAAGAGACTGCATTTATAGAGCCGACAAAGGAGAAAAAGTAATCTTAAGATGCTTTG 4917
Db 7817 TATCAAGAGACTGCATTTATAGAGCCGACAAAGGAGAAAAAGTAATCTTAAGATGCTTTG 7758
Qy 4918 TTAGAAAAATAGCGCTCTCGGATGCATTTTGTAGAACAAAAAGAAAGTATAGATTCCT 4977
Db 7757 TTAGAAAAATAGCGCTCTCGGATGCATTTTGTAGAACAAAAAGAAAGTATAGATTCCT 7698
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Db 7697 TGTGTAAAAATAGCGCTCTCGGATGCATTTCTGTTCTGTAAATAACAGCTCAGATTC 7638
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Db 7637 TTTGTTTGAATAATAGCGCTCTCGGATGCATTTTGTAGAACAAAAAGAAAGTATAGATTC 7578
Qy 5098 TTTCTTGTGTAAAAATAGCGCTCTCGGATGCATTTCTGTTCTGTAAATAACAGCTC 5157
Db 7577 TTTCTTGTGTAAAAATAGCGCTCTCGGATGCATTTCTGTTCTGTAAATAACAGCTC 7518
Qy 5158 GATTCCTTTGTTGAAAAATAGCGCTCTCGGATGCATTTTGTGTCTACAAATAAGAGCA 5217
Db 7517 GATTCCTTTGTTGAAAAATAGCGCTCTCGGATGCATTTTGTGTCTACAAATAAGAGCA 7458
Qy 5218 CAGATGCTTCGTTACAGTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTGTTTA 5277
Db 7457 CAGATGCTTCGTTACAGTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTGTTTA 7398
Qy 5278 TTTTCTTAATAACATTTCAATATGATCGCTCATGAGACAATAACCCCTGATTAATGCTT 5337
Db 7397 TTTTCTTAATAACATTTCAATATGATCGCTCATGAGACAATAACCCCTGATTAATGCTT 7338
Qy 5338 CAATAATATTGAAAAAGGAAGATAGATATCAACATTTCCGTTGTCGCCCTTATCCC 5397
Db 7337 CAATAATATTGAAAAAGGAAGATAGATATCAACATTTCCGTTGTCGCCCTTATCCC 7278
Qy 5398 TTTTTCGCGCATTTTGCCTTCTCTGTTTGTCTACCCAGAACCGCTGGTGAAGTAAAA 5457
Db 7277 TTTTTCGCGCATTTTGCCTTCTCTGTTTGTCTACCCAGAACCGCTGGTGAAGTAAAA 7218
Qy 5458 GATGCTGAAGATCAGTTGGGTGACAGAGTGGGTATACATCGAATCGATCTCAACAGCGGT 5517
Db 7217 GATGCTGAAGATCAGTTGGGTGACAGAGTGGGTATACATCGAATCGATCTCAACAGCGGT 7158
Qy 5518 AAGATCCTTTGAGAGTTTTCGCCCCGAAAGAGAGTTTCCAAATGATGAGACCTTTTAAAGTT 5577
Db 7157 AAGATCCTTTGAGAGTTTTCGCCCCGAAAGAGAGTTTCCAAATGATGAGACCTTTTAAAGTT 7098
Qy 5578 CTGCTATGTGGCGGTATATATCCGTTATGACGCGGGAAGAGCAACTCGGTGCGCGC 5637
Db 7097 CTGCTATGTGGCGGTATATATCCGTTATGACGCGGGAAGAGCAACTCGGTGCGCGC 7038
Qy 5638 ATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCACAGTCAACAAAAAGCATCTTACG 5697
Db 7037 ATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCACAGTCAACAAAAAGCATCTTACG 6978
Qy 5698 GATGGCATGACAGTAAGAGAAATTTGCGAGTGTGCTGCCATAACCATGAGTGAATAACCTGCG 5757
Db 6977 GATGGCATGACAGTAAGAGAAATTTGCGAGTGTGCTGCCATAACCATGAGTGAATAACCTGCG 6918

Qy 5758 GCCAACTTACTTCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTTGTGACAAAC 5817
Db 6917 GCCAACTTACTTCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTTGTGACAAAC 6858
Qy 5818 ATGGGGATCATGTAACTCGCTTGTATGCTTTGGGAAACCGGAGCTGAATGAAGCCATACCA 5877
Db 6857 ATGGGGATCATGTAACTCGCTTGTATGCTTTGGGAAACCGGAGCTGAATGAAGCCATACCA 6798
Qy 5878 AACACAGAGGTGACACCAACGATGCTGTAGCAATGGCAACAAACGTTGGGCAAACTATTTA 5937
Db 6797 AACACAGAGGTGACACCAACGATGCTGTAGCAATGGCAACAAACGTTGGGCAAACTATTTA 6738
Qy 5938 ACTGGCGAACTACTTACTTCTAGCTTCCGCGCAACAAATTAATAGACTGATGAGGCGGAT 5997
Db 6737 ACTGGCGAACTACTTACTTCTAGCTTCCGCGCAACAAATTAATAGACTGATGAGGCGGAT 6678
Qy 5998 AAAGTTGCAGACCACTTCTCGCTCGGCCCTTCCGCTGCTGCTTTTATTGCTGATAAA 6057
Db 6677 AAAGTTGCAGACCACTTCTCGCTCGGCCCTTCCGCTGCTGCTTTTATTGCTGATAAA 6618
Qy 6058 TCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCATTCAGACACTGCGGCGCAGATGGTAAG 6117
Db 6617 TCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCATTCAGACACTGCGGCGCAGATGGTAAG 6558
Qy 6118 CCCTCCCGTATCGTAGTATTCTACACGACGGGAGTCAGGCAACTATGATCAACGAAAT 6177
Db 6557 CCCTCCCGTATCGTAGTATTCTACACGACGGGAGTCAGGCAACTATGATCAACGAAAT 6498
Qy 6178 AGACAGATCGCTGAGATAGGTGCTCTACTGATTAAGCAATGGTAACTGTGACACCAAGTT 6237
Db 6497 AGACAGATCGCTGAGATAGGTGCTCTACTGATTAAGCAATGGTAACTGTGACACCAAGTT 6438
Qy 6238 TACTCATATATACATTTAGATTTTAAACCTCATTTTTTAAATTTTAAAGGATCTAGGTG 6297
Db 6437 TACTCATATATACATTTAGATTTTAAACCTCATTTTTTAAATTTTAAAGGATCTAGGTG 6378
Qy 6298 AAGATCCTTTTTGATTAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTTTCGTTCCACTCA 6357
Db 6377 AAGATCCTTTTTGATTAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTTTCGTTCCACTCA 6318
Qy 6358 GCCTCAGACCCCGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTA 6417
Db 6317 GCCTCAGACCCCGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTA 6258
Qy 6418 ATCTGCTCTGTCACAAACCAAAACCAACCGCTACAGCGGTGGTTTTGTTTTCGCGGATCAA 6477
Db 6257 ATCTGCTCTGTCACAAACCAAAACCAACCGCTACAGCGGTGGTTTTGTTTTCGCGGATCAA 6198
Qy 6478 GAGCTACCAACTCTTTTTCCGAAAGTAACTGGCTTTCAGCAGAGCGCAGATACCAATACT 6537
Db 6197 GAGCTACCAACTCTTTTTCCGAAAGTAACTGGCTTTCAGCAGAGCGCAGATACCAATACT 6138
Qy 6538 GTCCTTCTAGTGTAGCGGTAGTTAGGCCAACCACTTCAAGAACTCTGTAGCAGCGCTACA 6597
Db 6137 GTCCTTCTAGTGTAGCGGTAGTTAGGCCAACCACTTCAAGAACTCTGTAGCAGCGCTACA 6078
Qy 6598 TACCTCGCTCTGCTAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAGTCTGTCTT 6657
Db 6077 TACCTCGCTCTGCTAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAGTCTGTCTT 6018
Qy 6658 ACCGGGTTGGAATCAAGACGATAGTTTACCGGATTAAGCGCGCAGCGGTGCGGCTGAACCGGG 6717
Db 6017 ACCGGGTTGGAATCAAGACGATAGTTTACCGGATTAAGCGCGCAGCGGTGCGGCTGAACCGGG 5958
Qy 6718 GGTTCTGTCACACAGCCAGCTTGGAGCGAAACGACTTACACCGAACTGAGATACCTTACAG 6777
Db 5957 GGTTCTGTCACACAGCCAGCTTGGAGCGAAACGACTTACACCGAACTGAGATACCTTACAG 5898
Qy 6778 GGTGAGCTATGAGAAAGCGCCACCGCTTCCGGAAGGAGAAAGCGGACGAGTATCCGGTA 6837
Db 5897 GGTGAGCTATGAGAAAGCGCCACCGCTTCCGGAAGGAGAAAGCGGACGAGTATCCGGTA 5838

Qy	6838	AGCGCAGGGTCCGAACACAGAGAGCGCAAGAGGGAGCTTCCAGGGGGGAAACCGCTGGTAT	6897
Db	5837	AGCGCAGGGTCCGAACACAGAGAGCGCAAGAGGGAGCTTCCAGGGGGGAAACCGCTGGTAT	5778
Qy	6898	CTTTATAGTCCTGTCCGGTTTTCCGCACCTCTGACTTTGAGGCTCGATTTTTTGTGATGCTCG	6957
Db	5777	CTTTATAGTCCTGTCCGGTTTTCCGCACCTCTGACTTTGAGGCTCGATTTTTTGTGATGCTCG	5718
Qy	6958	TCAGGGGGCGGAGCCCTATGGA AAAACGCCAGCAACCGCGCCCTTTTACGGTTCCTGGCC	7017
Db	5717	TCAGGGGGCGGAGCCCTATGGA AAAACGCCAGCAACCGCGCCCTTTTACGGTTCCTGGCC	5658
Qy	7018	TTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTTCGCGTTATCCCTGATTTCTGTGGATAAC	7077
Db	5657	TTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTTCGCGTTATCCCTGATTTCTGTGGATAAC	5598
Qy	7078	CGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCGCAGCGGACGACCGAGCGCAGC	7137
Db	5597	CGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCGCAGCGGACGACCGAGCGCAGC	5533
Qy	7138	GAGTCAGTGAGCAGGAAGCGGAAGCGCCCAATACGCAAAACCGCCTCTCCCGCGCGGT	7197
Db	5537	GAGTCAGTGAGCAGGAAGCGGAAGCGCCCAATACGCAAAACCGCCTCTCCCGCGCGGT	5478
Qy	7198	TGCGCGGATTCATTAATGACGCTGGCAGCAGAGGTTTCCGACTGGAAGCGGCGAGTGAG	7257
Db	5477	TGCGCGGATTCATTAATCAGCTGGCAGCAGAGGTTTCCGACTGGAAGCGGCGAGTGAG	5418
Qy	7258	CGCAACGCATTAATGTGAGTTACCTCACTCATATTAGGCACCCCGCTTTTACACTTATG	7317
Db	5417	CGCAACGCATTAATGTGAGTTACCTCACTCATATTAGGCACCCCGCTTTTACACTTATG	5358
Qy	7318	CTTCCGCGCTCCTATGTTGTGGAAATGTGAGCGGATAACAATTTCAACAGAAACAGC	7377
Db	5357	CTTCCGCGCTCGTATGTTGTGGAAATGTGAGCGGATAACAATTTCAACAGAAACAGC	5298
Qy	7378	TATGACCATGATTACGCCAAGCGCGCA	7404
Db	5297	TATGACCATGATTACGCCAAGCTTGCA	5271
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QY	2759	TTGACCCCAATGCGTCTCCCTTGTTCATCTAAACCCACACCGGGTGTCAATAATCAACCAATC	2818	TAAGCCTATTTTATAGGTTAAATGTCATGATAATAAATGGTTTCTTAGTATGATCAATAT	3897
Db	9846	GTAAAGCTTTCGGGGCTCTCTTGGCTT-----CCAAACCGAGTCAGAAATCGAGTTCCAAATC	9792	TAAGCCTATTTTATAGGTTAAATGTCATGATAATAAATGGTTTCTTAGTATGATCAATAT	8778
QY	2819	GTAAACCTTTCATCTCTTCCACCCATGCTCTCTTTGAGCAATAAAGCCGATAACAAAATCTTTT	2878	CAAAAGAAATGATAGCAATTGAAGATGAGACTTAATCCAAATGAGAGTGGCAGCATATAG	3957
Db	9791	CAAAAGTTTCACTGTCCAC-----CTGCTTCTGAATCAAAACGAAGGAATAAAGCAATG	9738	CAAAAGAAATGATAGCAATTGAAGATGAGACTTAATCCAAATGAGAGTGGCAGCATATAG	8718
QY	2879	GTCGCTCTTCGCAATGTCAACAGTACCTTAGTATATATCTCCAGTAGATAGGAGCCCTT	2938	AAACAGCTAAAGGGTGTCTGGAAGGAAGCATACGATACCCCGCATGGAAATGGGATAATAT	4017
Db	9737	AGGTTTCTGTGAAGCTGACAGTAGTAGTATGTGTGAGTCTTTTGGAAATACGAGTCTTTT	9678	AAACAGCTAAAGGGTGTCTGGAAGGAAGCATACGATACCCCGCATGGAAATGGGATAATAT	8658
QY	2939	GCATGACAAATCTGTCTAATCAATCAAAAGGCTCTAGTCTCTTTGTTACTCTTCTGCGC	2998	CACAGGAGGTACTAGACTACTCTTTCATCAATAAATAGACGCATATAAGTACGCATTT	4077
Db	9677	-----AATAACTGGGAAACCGAGGAACCTTGTGTTATCTTGTCCAGCACTCATCTCCA	9626	CACAGGAGGTACTAGACTACTCTTTCATCAATAAATAGACGCATATAAGTACGCATTT	8598
QY	2999	CTGCTTCAAAACCGCTAAACATACCTGGGCCACACACACCGGTGTGCAATTCGTAATGTCTGC	3058	AAGCATAAAACACGCACTATGCGGTTCTTCTCATGTATATATACAGGCAACACGCGAG	4137
Db	9625	TGCAGT-----TGCAGATATCAATGCGGTAACTATTGACGAGGCCAAACATCCTC	9573	AAGCATAAAACACGCACTATGCGGTTCTTCTCATGTATATATACAGGCAACACGCGAG	8538
QY	3059	CAATCTGCTGTTCTGATATACACCGCAGAGTACTGCAATTTGACTGTATTTACCAATGTC	3118	ATATAGGTGCGAGTGAACAGTGAAGTGTATGTGCGCAGCTCGCGTTGCAITTTTCGGAG	4197
Db	9572	CTTAGGTTGATTTACGAAACACGCGCAACCAAGTATTTTCGGAGTGCCTGAACTATTTTATA	9513	ATATAGGTGCGAGTGAACAGTGAAGTGTATGTGCGCAGCTCGCGTTGCAITTTTCGGAG	8478
QY	3119	AGCAAAATTTCTGCTCTCGAAGAGTAAAAAATTTGACTTGGCGGATATGCTTTTAGCGG	3178	CGCTCGGTTTTCGAAAACGCTTTTGAAGTTTCTTATTTCCGAAGTTTCTTATCTCTAGAAAATG	4257
Db	9512	TG-----CTTTTACAGACTTGAATTTTCTTGCATTAACCGGGTCAATGTT	9465	CGCTCGGTTTTCGAAAACGCTTTTGAAGTTTCTTATTTCCGAAGTTTCTTATCTCTAGAAAATG	8418
QY	3179	CTTAACTGTGCCCCCTCCATGGGAAATCAGTCAAGATATCCACATGTGTGTTTTAGTAAACA	3238	TAGGAACTTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAAGACGCACTTTTCAAAAAC	4317
Db	9464	TCTCTTTCTATTGGGCACACATATAATACCCAGCAAGTCAGCATCGGAATCTAG--AGCA	9407	TAGGAACTTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAAGACGCACTTTTCAAAAAC	8358
QY	3239	AATTTTGGGACCTAATGCTTCACTAATCCAGTAATTTCTTGTGTGTAC--GAACATCCA	3297	CAAAAACGCGACCGACTGTAAACGAGCTACTAAATAATTTGCGAATACCCGCTTCCACAAACA	4377
Db	9406	CAATCTGCGGCTCTGTGCTCTGCAAGCGCGAACTTTTCAACCAATGGACCAAGACTACCT	9347	CAAAAACGCGACCGACTGTAAACGAGCTACTAAATAATTTGCGAATACCCGCTTCCACAAACA	8298
QY	3298	ATGAAGCACACAAGTTTGTGCTTTTCTGTCATGATATAAATAGCTTGGCAGCAACAG	3357	TTGCTCAAAAGTATCTCTTGTCTATATATCTCTGTCTATATCCCTATATAACCTACCCA	4437
Db	9346	GTGAATTAATTAACAGACATCTCCAGCTGCTTTGTGCTGTATATCAAGTATACTAC	9287	TTGCTCAAAAGTATCTCTTGTCTATATATCTCTGTCTATATCCCTATATAACCTACCCA	8238
QY	3358	GACTAGGATGAGTAGCAGCGTTCCTTTATATGTAGTCTTTTCGACATGATTTATCTCGTT	3417	TCCACCTTTCGCTCGCTTGAACCTTGCATCTAACTCGACCTCTACATTTTATGTTTATC	4497
Db	9286	GTGCTCAATPAGTCACCAATGCCCTCCCTTTGGGCCCTCTCC-----TTTTCTTT	9238	TCCACCTTTCGCTCGCTTGAACCTTGCATCTAACTCGACCTCTACATTTTATGTTTATC	8178
QY	3418	TCCTGAGGTTTGTCTGTGCTGAGTGGTTTGAAGATCTGGGCAATTTCAATGTTCTT	3477	TCTAGTATTAATCTTTTAGACAAAATAATTTGAGTAAGAACTATTTCATAGAGTGAATCGAA	4557
Db	9237	TTTCGACCGAATTAATCTTAAATCGGCAAAAATAAAGCTCCGGA-----T	9190	TCTAGTATTAATCTTTTAGACAAAATAATTTGAGTAAGAACTATTTCATAGAGTGAATCGAA	8118
QY	3478	CAACACTACATATGATATATATACCAATCTAAGTCTGTGCTCTCTTCTGTTCTTCT	3537	AACAATACGAAAATGTAAACATTTTCTTATAGTAGTATATAGAGACAAAATAGAGAAGAC	4617
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QY	3538	TCTGTTCCGAGATTACCGAATCAAAAAATTTTCAAGAAACCGAAATCAAAAAAAGAAAT	3597	CGTTTCATAATTTTCTGACCAATGAAGAAATCATCAACGCTATCATTTCTGTTTCAAAAGT	4677
Db	9129	TCTGGCGTCAATAACTGCAAGTACACATATATTA-----CGATGCTGTCTATTAAAT	9078	CGTTTCATAATTTTCTGACCAATGAAGAAATCATCAACGCTATCATTTCTGTTTCAAAAGT	7998
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QY	3658	GCTCTGATGCGCATAGTTTAAGCCAGCCCGACACCCCGCAACCCCGCTCAGCGGCCT	3717	CCGCGAGTTCGCTAGTAAATCAGTAAACGCGGGAAGTGGAGTTCAGGCTTTTTTATGGAA	4797
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Db	7637	TTTGTTTGAATAATAGCGCTCTCGCGTTGCAATTTTGTGTTTACAAAAATGAAGCAAGA	7578
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Db 5477 TGGCGGATTCATTAAATGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 5418
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RESULT 15
LOCUS PRS426/c
DEFINITION Yeast episomal vector pRS426 with URA3 marker, complete sequence.
ACCESSION U03451
VERSION U03451.1 GI:416322
KEYWORDS Cloning vector pRS426
ORGANISM Cloning vector pRS426
REFERENCE 1 (bases 1 to 5726)
AUTHORS Sikorski, R.S. and Hieter, P.
TITLE A system of shuttle vectors and yeast host strains designed for
efficient manipulation of DNA in Saccharomyces cerevisiae
JOURNAL Genetics 122 (1), 19-27 (1989)
MEDLINE 89276910
PUBMED 2659436
REFERENCE 2 (bases 1 to 5726)
AUTHORS Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. and
Hieter, P.
TITLE Multifunctional yeast high-copy-number shuttle vectors
JOURNAL Gene 110 (1), 119-122 (1992)
MEDLINE 92184105
PUBMED 1544568
REFERENCE 3 (bases 1 to 5726)
AUTHORS Stillman, D.J.
TITLE Direct Submision
JOURNAL Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132 USA
FEATURES
source
1..5726
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:31845"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5726 GACGAAGGCGCTCGTGATACGCCCTATTTTATAGGTTAAATGTCATGATAATATGTTT 5667
QY 3880 CTTAGTATGATCCATATCAAGGAATCATAGCAATTCGAGGAGGAGGAGGAGGAGGAGGAG 3939
Db 5666 CTTAGTATGATCCATATCAAGGAATCATAGCAATTCGAGGAGGAGGAGGAGGAGGAGGAG 5607
QY 3940 AGGAGTGGCAGCATATAGCAACAGCTAAAGGGTAGTGCTGAAGGAGGAGGAGGAGGAGGAG 3999
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Search completed: May 16, 2004, 08:37:31
Job time : 19630.2 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2004, 22:27:02 ; Search time 1826.33 Seconds
(without alignments)
18208.601 Million cell updates/sec

Title: US-10-067-449-9
Perfect score: 7828
Sequence: 1 atgcgcgtcggtcccaaca.....tttttaatttaatacaaaaa 7828

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	7828	100.0	7828	6	AAL49310 Human Glu
2	6975.2	89.1	7777	6	AAL49312 Human Glu
3	5908	75.5	6360	6	AAL49316 Human HXT
C 4	4492.6	57.4	8749	4	AAC87129 Nucleotid
C 5	4492.6	57.4	8941	4	AAC87131 Nucleotid
C 6	4492.6	57.4	9700	4	AAC30958 Plasmid p
C 7	4492.6	57.4	9749	4	AAC30959 Plasmid p
C 8	4492.6	57.4	10288	2	AAT71322 Plasmid p
C 9	4492.6	57.4	13414	2	AAT71321 Plasmid p
C 10	4469.6	57.1	7210	3	AAX49989 Yeast two
11	3623	46.3	9952	7	ABV77349 Yeast exp
12	3610.2	46.1	7622	5	AAD21455 Human ROM
13	3364	43.0	6671	9	ADC75054 T-cell re
14	3057.4	39.1	5181	2	AAX85877 Nucleotid
15	3045.4	38.9	7063	2	AAX85878 Synthetic
C 16	2273	29.0	6831	8	ACF57106 p416 GPD-
C 17	2207.2	28.2	3003	6	AAD46219 pFLC-II v
C 18	2207.2	28.2	7432	2	AAV61459 Vector pp
C 19	2207.2	28.2	20623	3	AAC68294 Lama2/APP
C 20	2206.2	28.2	5534	2	AAT43137 pMIGIT s
21	2205.4	28.2	9072	2	AAX07558 Synthetic
22	2204.6	28.2	6287	6	AAK38923 Human pMS
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ALIGNMENTS

RESULT 1

AAL49310					
ID	AAL49310	standard; DNA; 7828 BP.			
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XX	XX				
DT	07-NOV-2002	(first entry)			
XX	XX				
DE	Human Glut4	containing vector YEp4H7-HsGLUT4.			
XX	XX				
KW	Human; yeast;	GLUT4; glut transporter; hexose; antidiabetic; anorectic;			
KW	vector; ds.				
XX	XX				
OS	Homo sapiens.				
XX	XX				
FN	WO200264784-A2.				
XX	XX				
PD	22-AUG-2002.				
XX	XX				
PF	09-FEB-2002;	2002WO-EP001373.			
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PR	14-FEB-2001;	2001DE-01006718.			
XX	XX				
PA	(AVET)	AVENTIS PHARMA DEUT GMBH.			
PI	Mueller G,	Koller K, Boles E, Wieczorke R, Dlugai S;			
XX	XX				
DR	WPI;	2002-636632/68.			
XX	XX				
PT	New strains of yeast,	useful in screening for modulators of hexose			
PT	transport,	potential antidiabetic and antiobesity agents, lack native			
PT	hexose-transport	function.			
XX	XX				
PS	Claim 10;	Page 34-36; 58pp; German.			
XX	XX				
CC	The present invention	relates to a strain of Saccharomyces cerevisiae			
CC	carbon but the	ability to grow on such substrates is restored when the			
CC	GLUT4 gene is	expressed. A strain transformed to express the GLUT1 or			
CC	GLUT4 genes can	be used to identify compounds that increase/reduce hexose			
CC	transport by	these proteins. These compounds, optionally after			
CC	development,	are potential drugs for treating diabetes and obesity. The			
CC	present sequence	is a vector containing the human Glut4 coding sequence			
CC	as used in the	invention			
XX	XX				
SQ	Sequence	7828 BP; 2009 A; 1928 C; 1771 G; 2120 T; 0 U; 0 Other;			

[illegible]

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QY 3181 TAACTGTGCCCTCGATGGAAAAATCAGTCAAGATATCCATGTGTTTTTTAGTAAACAAA 3240

Db 3181 TAACTGTGCCCTCGATGGAAAAATCAGTCAAGATATCCATGTGTTTTTTAGTAAACAAA 3240
QY 3241 TTTTGGGACCTAATGCTTCAACTCACTCAGTAATTTCTTTGGTGGTACGAACATCCAAATG 3300
Db 3241 TTTTGGGACCTAATGCTTCAACTCACTCAGTAATTTCTTTGGTGGTACGAACATCCAAATG 3300
QY 3301 AAGCACACAAGTTTGTGTTTCTGTCGATGATATTAATAGCTTGGGACGAACAGGAC 3360
Db 3301 AAGCACACAAGTTTGTGTTTCTGTCGATGATATTAATAGCTTGGGACGAACAGGAC 3360
QY 3361 TAGGATGAGTAGCAGCAGCTTCTTATATGATGCTTTTCGACATGATTTATCTTCGTTTCC 3420
Db 3361 TAGGATGAGTAGCAGCAGCTTCTTATATGATGCTTTTCGACATGATTTATCTTCGTTTCC 3420
QY 3421 TGCAGGTTTTTGTCTGTGTCAGTTGGGTTAAGAAATCTGCGCAATTTTCATGTTTCTTCAA 3480
Db 3421 TGCAGGTTTTTGTCTGTGTCAGTTGGGTTAAGAAATCTGCGCAATTTTCATGTTTCTTCAA 3480
QY 3481 CACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTTCTTCTGTTCTTCTTCT 3540
Db 3481 CACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTTCTTCTGTTCTTCTTCT 3540
QY 3541 GTTTCGAGATTACCGAATCAAAAATTTTCAAGAAACCGAAATCAAAAAGAAATAAA 3600
Db 3541 GTTTCGAGATTACCGAATCAAAAATTTTCAAGAAACCGAAATCAAAAAGAAATAAA 3600
QY 3601 AAAAAATGATGAATTTGAATTTGAAAAGCTGTGATGTTGTTGCTTCTTCTTCTTCT 3660
Db 3601 AAAAAATGATGAATTTGAATTTGAAAAGCTGTGATGTTGTTGCTTCTTCTTCTTCT 3660
QY 3661 CTGATCGCGATGTTAAGCCAGCCCGACACCCGCGCAACACCCGCTGACGCGCCCTGAC 3720
Db 3661 CTGATCGCGATGTTAAGCCAGCCCGACACCCGCGCAACACCCGCTGACGCGCCCTGAC 3720
QY 3721 GGGCTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACGCTCTCCGGAGCTGCA 3780
Db 3721 GGGCTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACGCTCTCCGGAGCTGCA 3780
QY 3781 TGTGTCAGAGGTTTTTCAACCGTCAATCCGAAACCGCGAGACGAAAGGGCTCTGATAC 3840
Db 3781 TGTGTCAGAGGTTTTTCAACCGTCAATCCGAAACCGCGAGACGAAAGGGCTCTGATAC 3840
QY 3841 GCCTATTTTATAGGTTAATGTCATGATATAATGTTTCTTAGTATGATCCAAATACAA 3900
Db 3841 GCCTATTTTATAGGTTAATGTCATGATATAATGTTTCTTAGTATGATCCAAATACAA 3900
QY 3901 AGGAATGATAGCAATTTGAAGGATGAGCAATCCAAATGAGGAGTGGCAGCATATAGAC 3960
Db 3901 AGGAATGATAGCAATTTGAAGGATGAGCAATCCAAATGAGGAGTGGCAGCATATAGAC 3960
QY 3961 AGCTAAAGGGTAGTGTGAAGGAAGCATACGATACCCCGCATGGAATGGGATATATCAC 4020
Db 3961 AGCTAAAGGGTAGTGTGAAGGAAGCATACGATACCCCGCATGGAATGGGATATATCAC 4020
QY 4021 AGGAGTACTAGACTACTTCTCATATAATAATAGACGATATAGTACGATTTTAAG 4080
Db 4021 AGGAGTACTAGACTACTTCTCATATAATAATAGACGATATAGTACGATTTTAAG 4080
QY 4081 CATAAACCGCATATGCGGTTCTTCTCATGATATATATATACAGCAACACGAGATA 4140
Db 4081 CATAAACCGCATATGCGGTTCTTCTCATGATATATATATACAGCAACACGAGATA 4140
QY 4141 TAGGTGCGAGCTGAACAGTAGCTGTATGTGCGCAGCTCGCGTTGCAATTTTCGGAAGCGC 4200
Db 4141 TAGGTGCGAGCTGAACAGTAGCTGTATGTGCGCAGCTCGCGTTGCAATTTTCGGAAGCGC 4200
QY 4201 TCGTTTTTCGAAACGCTTTTGAAGTTCTTATTCGAAGTTCTTATCTCTAGAAAGTATAG 4260
Db 4201 TCGTTTTTCGAAACGCTTTTGAAGTTCTTATTCGAAGTTCTTATCTCTAGAAAGTATAG 4260
QY 4261 GAACTTTCAGAGCGCTTTTGAAGAACCAAAAGCGCTCTGAAAGCGCCTTTTCAAAAACCAA 4320
Db 4261 GAACTTTCAGAGCGCTTTTGAAGAACCAAAAGCGCTCTGAAAGCGCCTTTTCAAAAACCAA 4320

Qy	4321	AAACGACCGGACTCTAAAGAGCTACTAAATATTTGCGAATACCGCTTTCACAAACATTTG	4380	5401	TTTGGCGCATTTTGGCTTCTCTGCTCACCAGAAACGCTGGTGAAGTAAAGAT	5460
Db	4321	AAACGACCGGACTCTAAAGAGCTACTAAATATTTGCGAATACCGCTTTCACAAACATTTG	4380	5401	TTTGGCGCATTTTGGCTTCTCTGCTCACCAGAAACGCTGGTGAAGTAAAGAT	5460
Qy	4381	CTCAAAAGTATCTCTTTGCTATATATCTCTGCTGCTATATCCCTATATAAACCTACCCATCC	4440	5461	GCTGAAGATCAGTTGGGTGCAACGAGTGGTTATATCGAACTGGATCTCAACAGCGGTAAAG	5520
Db	4381	CTCAAAAGTATCTCTTTGCTATATATCTCTGCTGCTATATCCCTATATAAACCTACCCATCC	4440	5461	GCTGAAGATCAGTTGGGTGCAACGAGTGGTTATATCGAACTGGATCTCAACAGCGGTAAAG	5520
Qy	4441	ACCTTTGCGTCTTGAACTTGCACTTAACTCGACCTCTCAATTTTATGTTTATCTCT	4500	5521	ATCCTTGAGAGTTTTCGCCCGAAGAGGTTTCCCAATGATGAGCACTTTTAAAGTCTTG	5580
Db	4441	ACCTTTGCGTCTTGAACTTGCACTTAACTCGACCTCTCAATTTTATGTTTATCTCT	4500	5521	ATCCTTGAGAGTTTTCGCCCGAAGAGGTTTCCCAATGATGAGCACTTTTAAAGTCTTG	5580
Qy	4501	AGTATTACTCTTTAGACAAATAAATTTAGTAAGAACTATTTCATAGAGTGAATCGAAAC	4560	5581	CTATGTCGCGGTATTATCCCGTATTGACGCGGCAAGAGCAACTCGTCCGCGCAT	5640
Db	4501	AGTATTACTCTTTAGACAAATAAATTTAGTAAGAACTATTTCATAGAGTGAATCGAAAC	4560	5581	CTATGTCGCGGTATTATCCCGTATTGACGCGGCAAGAGCAACTCGTCCGCGCAT	5640
Qy	4561	ATAAGCAAAATGTAACATTTTCTATAGCTAGTATATAGACAAATAATAGAAAGACCGT	4620	5641	CACATTCTCAGAAATGATCTTGTTGAGTACTCACAGTCAACAGAAAGCATCTTACGGAT	5700
Db	4561	ATAAGCAAAATGTAACATTTTCTATAGCTAGTATATAGACAAATAATAGAAAGACCGT	4620	5641	CACATTCTCAGAAATGATCTTGTTGAGTACTCACAGTCAACAGAAAGCATCTTACGGAT	5700
Qy	4621	TCATAATTTCTGACCAATGAAGAAATCAACGCTATCACTTCTGTTTCAAAAGTATG	4680	5701	GGCATGACGTAGAGAAATATGCACTGCTGCCATACCATGAGTGATAAACACTGGGCC	5760
Db	4621	TCATAATTTCTGACCAATGAAGAAATCAACGCTATCACTTCTGTTTCAAAAGTATG	4680	5701	GGCATGACGTAGAGAAATATGCACTGCTGCCATACCATGAGTGATAAACACTGGGCC	5760
Qy	4681	CGCAATCCACATCGGTATAGATATAATCGGGATGCGCTTATCTTGAATAAATGCACCC	4740	5761	AACTTACTCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCGACAAACATG	5820
Db	4681	CGCAATCCACATCGGTATAGATATAATCGGGATGCGCTTATCTTGAATAAATGCACCC	4740	5761	AACTTACTCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCGACAAACATG	5820
Qy	4741	GCAGCTTCGCTAGTAAATCAGTAACCGGGAAGTGGAGTCAGGCTTTTTTATGGAAGAG	4800	5821	GGGATCATGTAACTCGCTTGTGGAAACCGGAGCTGAAATGAAGCCCATACCAAC	5880
Db	4741	GCAGCTTCGCTAGTAAATCAGTAACCGGGAAGTGGAGTCAGGCTTTTTTATGGAAGAG	4800	5821	GGGATCATGTAACTCGCTTGTGGAAACCGGAGCTGAAATGAAGCCCATACCAAC	5880
Qy	4801	AAAAATAGACACAAAGTAGCTTCTTAACTTAAACGGAACCTACAGTGCAAAAGTTAT	4860	5881	GACGAGGTGACACACGATGCTGTAGCAATGCGCAACAACTGATGAGCGGATATAA	5940
Db	4801	AAAAATAGACACAAAGTAGCTTCTTAACTTAAACGGAACCTACAGTGCAAAAGTTAT	4860	5881	GACGAGGTGACACACGATGCTGTAGCAATGCGCAACAACTGATGAGCGGATATAA	5940
Qy	4861	CAAGAGCTGCATTTAGAGCGCAAAAGGAAAGAAAGTAATCTAAGATGCTTTGTTA	4920	5941	GGCGAACTTACTTACTCTAGCTTCCCGCAACAACTAATAGACTGATGAGCGGATATAA	6000
Db	4861	CAAGAGCTGCATTTAGAGCGCAAAAGGAAAGAAAGTAATCTAAGATGCTTTGTTA	4920	5941	GGCGAACTTACTTACTCTAGCTTCCCGCAACAACTAATAGACTGATGAGCGGATATAA	6000
Qy	4921	GAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAAACAAAGAAAGTATAGATCTTTGT	4980	6001	GTTGACGAGCACTTCTGCGCTCGGCCCTTCCCGCTGGCTGTTTATGCTGATATAATCT	6060
Db	4921	GAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAAACAAAGAAAGTATAGATCTTTGT	4980	6001	GTTGACGAGCACTTCTGCGCTCGGCCCTTCCCGCTGGCTGTTTATGCTGATATAATCT	6060
Qy	4981	TGGTAAATAGCGCTCTCGGGTGCATTTCTGTTGTAATAAATGACAGTCTTCTTT	5040	6061	GGAGCCGTGAGCGTGGGTCTCGCGGTATCAATGAGCACTGGGGCCAGATGGTAAAGCCC	6120
Db	4981	TGGTAAATAGCGCTCTCGGGTGCATTTCTGTTGTAATAAATGACAGTCTTCTTT	5040	6061	GGAGCCGTGAGCGTGGGTCTCGCGGTATCAATGAGCACTGGGGCCAGATGGTAAAGCCC	6120
Qy	5041	GTTTGAATAATAGCGCTCTCGGGTGCATTTTGTGTAATAAATGAAAGCAAGATTC	5100	6121	TCCCGTATCGTAGTATCTACACGCGGGAGTCAAGCAACTATGATGAAACGAAATAGA	6180
Db	5041	GTTTGAATAATAGCGCTCTCGGGTGCATTTTGTGTAATAAATGAAAGCAAGATTC	5100	6121	TCCCGTATCGTAGTATCTACACGCGGGAGTCAAGCAACTATGATGAAACGAAATAGA	6180
Qy	5101	TTCTGTTGTAATAATAGCGCTTTTCGGGTGCAATTTCTGTTGTAATAATGCAAGTCA	5160	6181	CAGATCGCTGAGATAGTGGCTCTCACTGATTAAGCAATTTGTTAACTGACCAAGTTTAC	6240
Db	5101	TTCTGTTGTAATAATAGCGCTTTTCGGGTGCAATTTCTGTTGTAATAATGCAAGTCA	5160	6181	CAGATCGCTGAGATAGTGGCTCTCACTGATTAAGCAATTTGTTAACTGACCAAGTTTAC	6240
Qy	5161	TCCTTTGTTGAAAAATAGCGCTCTCGGGTGCATTTTGTGTAATAAATGAAAGCAAG	5220	6241	TCATATATCTTTAGATTTTAAACTTCAATTTTAAAGGATCTAGGTGAAG	6300
Db	5161	TCCTTTGTTGAAAAATAGCGCTCTCGGGTGCATTTTGTGTAATAAATGAAAGCAAG	5220	6241	TCATATATCTTTAGATTTTAAACTTCAATTTTAAAGGATCTAGGTGAAG	6300
Qy	5221	ATGCTTCGTTAGGTGGCACTTTTCGGGGAATGTCGGGAAACCCCTATTGTTTATTT	5280	6301	ATCCTTTTGTATATCTCATGACCAAAATCCCTTAAACGAGTGTTCGTTCCACCTGAGCG	6360
Db	5221	ATGCTTCGTTAGGTGGCACTTTTCGGGGAATGTCGGGGAATGTCGGGAAACCCCTATTGTTTATTT	5280	6301	ATCCTTTTGTATATCTCATGACCAAAATCCCTTAAACGAGTGTTCGTTCCACCTGAGCG	6360
Qy	5281	TTCTAAATACATTCAAATATGATATCGCTCATGAGCAATAACCTGATAAATGCTTCAA	5340	6361	TCAGACCCGTGAGAAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAAATC	6420
Db	5281	TTCTAAATACATTCAAATATGATATCGCTCATGAGCAATAACCTGATAAATGCTTCAA	5340	6361	TCAGACCCGTGAGAAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAAATC	6420
Qy	5341	TAATATTGAAAGGAGTATGATGATTTCAACATTTCCGTTGCGCCCTTATTTCCCTTT	5400	6421	TGCTGCTTGCAAAACAAACCAACCCGCTACAGCGTGGTGTGTTGTCGCGGATCAAGAG	6480
Db	5341	TAATATTGAAAGGAGTATGATGATTTCAACATTTCCGTTGCGCCCTTATTTCCCTTT	5400	6421	TGCTGCTTGCAAAACAAACCAACCCGCTACAGCGTGGTGTGTTGTTCCGCGGATCAAGAG	6480
				6481	CTACCAACTCTTTTTCCGAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAAAATCTGTCTC	6540

Db	7561	AAAAATCCCCACCATCTTTTCGAGATCCCTGTGAACCTTATTATTTGGCAACTGGAAGAAATGAAAA	7621		
Qy	7621	GGAGGAAAAATACAAAATATATACTAGAACTGAAAAGAAAAAGTATATAATAGAGACGATATA	7680		
Db	7621	GGAGGAAAAATACAAAATATATACTAGAACTGAAAAGAAAAAGTATATAATAGAGACGATATA	7680		
Qy	7681	TGCCAATACCTTCAAAATGTTTGCAGATCTATTTCTTCATTTGTCAGCTATTTGTTAAATAATAATA	7740		
Db	7681	TGCCAATACCTTCAAAATGTTTGCAGATCTATTTCTTCATTTGTCAGCTATTTGTTAAATAATAATA	7740		
Qy	7741	ACATCAAGAACAAACACAGCTCAACTTGTCTTTTCTTAAGAACAAAGATATAACACAAAAAC	7800		
Db	7741	ACATCAAGAACAAACACAGCTCAACTTGTCTTTTCTTAAGAACAAAGATATAACACAAAAAC	7800		
Qy	7801	AAAAAGTTTTTTTTTAATTTAATCAAAAA	7828		
Db	7801	AAAAAGTTTTTTTTTAATTTAATCAAAAA	7828		
RESULT 2					
ID	AAAL49312				
ID	AAAL49312	standard; DNA; 7777 BP.			
AC	AAAL49312;				
XX	07-NOV-2002	(first entry)			
XX	Human Glut1	containing vector YEp4H7-HsGLUT1.			
DE	Human; yeast; GLUT4;	glut transporter; hexose; antidiabetic; anorectic;			
KW	vector; ds.				
KW	Homo sapiens.				
OS	WO200264784-A2.				
XX	22-AUG-2002.				
XX	09-FEB-2002;	2002WO-EP001373.			
XX	14-FEB-2001;	2001DE-01006718.			
PR	(AVET)	AVENTIS PHARMA DEUT GMBH.			
PA	Mueller G, Koller K, Boles E, Wieczorke R, Dlugai S;				
XX	WPI; 2002-636632/68.				
XX	New strains of yeast, useful in screening for modulators of hexose				
PT	transport, potential antidiabetic and antioesity agents, lack native				
PT	hexose-transport function.				
XX	Example; Page 37-40; 58pp; German.				
PS	The present invention relates to a strain of <i>Saccharomyces cerevisiae</i>				
XX	that cannot grow on a substrate containing hexose as the only source of				
CC	carbon but the ability to grow on such substrates is restored when the				
CC	GLUT4 gene is expressed. A strain transformed to express the GLUT1 or				
CC	GLUT4 genes can be used to identify compounds that increase/reduce hexose				
CC	transport by these proteins. These compounds, optionally after				
CC	development, are potential drugs for treating diabetes and obesity. The				
CC	present sequence is a vector containing the human Glut1 coding sequence				
CC	as used in the invention				
XX					
SQ	Sequence 7777 BP; 2013 A; 1915 C; 1742 G; 2107 T; 0 U; 0 Other;				
Query Match					
Best Local Similarity 89.1%; Score 6975.2; DB 6; Length 7777;					
Matches 7297; Conservative 0; Mismatches 478; Indels 15; Gaps 2;					
Qy	39	GGAAACCCCTCAGCAGCAGTGAATGGACCCCTGGTCTCTTGTGTGTCTCTCGGTGCT	98		
Db	3	GGAGCCCGCAGCAGCAAGAGCTGACGGGTCCGCTCATCTGGCTGTGGAGGAGCAGTGCT	62		

Qy	99	TGGCTCCCTGCAAGTTGGGTAAACAATTTGGGTCAATCAATGCCCCCTCAGAAAGGTGATTGA	158
Db	63	TGGCTCCCTGCAAGTTGGGTAAACAATTTGGGTCAATCAATGCCCCCTCAGAAAGGTGATTGA	122
Qy	159	ACAGAGCTCAATGATGAGCTGGCTGGGAGCAGGGGCGCTGAGGGACCCAGCTCCATCCC	218
Db	123	GGAGTTTCTAACACAGACATGGGTCCACCGTATATGGG-----GAGAGCATCCT	170
Qy	219	TCCAGGACCCCTCACACCCCTCTGGGCCCTCTCGTGGCCATCTTTTTCGTGGGGCGCAT	278
Db	171	GCCACACGCTCACAGGCTCTGGTCCCTCTCAGTGGCCATCTTTTCTGTGGGGCGCAT	230
Qy	279	GATTTCTCTCTCTCATTTGGTATCATCTCTCAGTGGCTTTGGAAGGAAAGAGGCCATGCT	338
Db	231	GATTTGGCTCTCTCTCTGTGGGCCCTTTTCGTAAACCGCTTTGGCGCGGGAATTCATATGCT	290
Qy	339	GGTCAACAATGCTCTGGGGGTGCTGGGGGGGAGGCTCATGCGGCTGGCCACACGCTCGTGC	398
Db	291	GATGATGAACCTGCTGGGCTTCTGTGCGCGCTGCTCATGGGCTTCTCGAAAACCTGGGCAA	350
Qy	399	CTCCATGAAAGCTCATCTCTGGAGCATCTCTCATTTGGGCGCTACTCAGGGCTGACATC	458
Db	351	GTCTTTTGAGATGCTGATCTCTGGGCGGCTTTCATCATCGGTGTGCTGCGGCTGACCAAC	410
Qy	459	AGGGCTGGTGGCCATGATCGTGGGGGAGATGCTCCCACTCACCTGCGGGGCGCCCTGGG	518
Db	411	AGGCTTCTGGCCCATGATGATGGGTGAAGTGTACACCCACAGCCCTTCTGTGGGGCCCTGGG	470
Qy	519	GAGCTCAACCAACTGGCCATTTGTTATCGGCATTTCTGATCGGCCAGGTGCTGGGCTTGA	578
Db	471	CACCTTGACACCACTGGGCGATCGTGGGCTGCTCTCATCGCCAGGTGTTGGGCTGGA	530
Qy	579	GTCCCTCTGGGCACTGGCCGCTGTGGCCACTGCTCTGGGCTCACAGTGTACTCTGC	638
Db	531	CTCCATCATGGGCAACAAGGACCTGTGGCCCTCTCTGAGCATCATCTTCACTCCGGC	590
Qy	639	CTCTCTGAGCTGGTCTCTGCTGCCCTCTGTGCCGAGAGCCCGCTCACTCTTCACTCAT	698
Db	591	CTGTCTGAGTGCATCTGTGCTGCCCTCTGTGCCGAGAGTCCCGCTTCTGTCTCATCAA	650
Qy	699	CCAGAACTCTGAGGGGCTGCGCAGAAAGAGTCTGAAGCGCTGACAGGCTGGGCGCATGT	758
Db	651	CCGCAACGAGGAGAACCGGGCCAGAGTGTCTTAAAGAACTGCGCGGAGCAGCTGACGT	710
Qy	759	TTCTGAGTGTCTGGCTGAGCTGAGAGTGAAGAGGGAAGCTGGAGCGTGGAGCGCACT	818
Db	711	GACCCATGACCTGACAGGAGATGAAGGAAGAGATCGGCAGATGATGCGGGAGAAGAGT	770
Qy	819	GTCCCTGTCTCAGCTCTCTGGGCGAGCGCTPACCCACCGCGAGCCCTGATCATTTCCGCTCT	878
Db	771	CACCATCTTGAGCTGTTCCGCTCCCGCGCTACCGCAGCCCATCTCATCTGCTGTGT	830
Qy	879	GCTGAGCTGAGCCAGCACTCTCTGGCATCAATGCTGTTTTCTATTATTCGACACGAT	938
Db	831	GCTGAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCTTCTATTCTTACCTCCACGAGCAT	890
Qy	939	CTTCGAGACAGCAGGGGTAGGCCAGCTGCTTATGCCACCATAGGAGCTGGTGTGTCAA	998
Db	891	CTTCGAGAAAGGGGGGGTGCAGCAGCTGTGTATGCCCACCATTTGGCTCCGGTATCTGTCAA	950
Qy	999	CACAGTCTTCATCTGTCTGGTGTCTGTGCTGGAGCGGGCGGGCGCGGAGCTGCTCA	1058
Db	951	CAGGGCTTCTACTGTCTGTCTGTGTGTGGTGGAGGAGAGCGCGCGGAGCCCTGCA	1010
Qy	1059	TCTCTGGGCTGGGGGCGATGTGTGGCTGTGSCCATCTCTGATGATGTGTGGCTCTGCTCT	1118
Db	1011	CCTCATAGGCTCTGCTGGCATGGGGTGTGGCCATCTACTCATGACCATGCGCTAGCACT	1070
Qy	1119	GCTGGAGCGAGTTCCAGCCATGAGCTCATGCTCTCATTTGTGGCCATCTTTGGCTCTGTGGC	1178
Db	1071	GCTGGAGCAGCTACCTCGATGTCTCTATCTGAGCATCTGTGGCCATCTTTGGCTCTTTGTGGC	1130

	Db	2208	CCCTGATAGACGGTTTTTCGCCCTTTTGACGTGGAGTGCACGTTCTTTAATAGTGAATC	2267
	Qy	2319	TGTGTTCAAACTCGAAACAACACTCAAACCTATCTCGGTCTATTCTTTTGATTTATAAGGG	2378
	Db	2268	TGTGTTCCNAACTGGNACAACTCATCTCGGTCTATTCTTTTGATTTATAAGGG	2327
	Qy	2379	AATTTGCGGATTTGGCGGTATGGTTAAAAAATGAGCTGATTTTAACAAAATTTAACGCG	2438
	Db	2328	AATTTGCGGATTTGGCGGTATGGTTAAAAAATGAGCTGATTTTAACAAAATTTAACGCG	2387
	Qy	2439	AATTTTAACAAAAATTAACGTTTACAAATTCCTGATGCGGTATTTTCTCCTTACGCATC	2498
	Db	2388	AATTTTAACAAAAATTAACGTTTACAAATTCCTGATGCGGTATTTTCTCCTTACGCATC	2447
	Qy	2499	TGTGCGGTATTTTCACACGCGATAGGTAATAACTGATATAATTAATTAAGAGCTCTAAT	2558
	Db	2448	TGTGCGGTATTTTCACACGCGATAGGTAATAACTGATATAATTAATTAAGAGCTCTAAT	2507
	Qy	2559	TGTGAGTTTAGTATACATGCANTTACTTAATAACAGTTTTTTTAGTTTTGCTGGCGCAT	2618
	Db	2508	TGTGAGTTTAGTATACATGCANTTACTTAATAACAGTTTTTTTAGTTTTGCTGGCGCAT	2567
	Qy	2619	CTTCTCAAAATGCTTCCCAGCGCTTTTCTGTAAAGTTTACCCTCTACCTTAGCATCC	2678
	Db	2568	CTTCTCAAAATGCTTCCCAGCGCTTTTCTGTAAAGTTTACCCTCTACCTTAGCATCC	2627
	Qy	2679	CTTCCCTTTGCAAAATAGTCTCTTCCAAACAATAATATGTGAGATCTGTAGAGACCACA	2738
	Db	2628	CTTCCCTTTGCAAAATAGTCTCTTCCAAACAATAATATGTGAGATCTGTAGAGACCACA	2687
	Qy	2739	TCATCCACGGTTCTATACGTGTGACCCAATGCGTCTCCCTTGTCATCTAAACCCACACCG	2798
	Db	2688	TCATCCACGGTTCTATACGTGTGACCCAATGCGTCTCCCTTGTCATCTAAACCCACACCG	2747
	Qy	2799	GGTGTCAATCAACCAATCGTAACCTTCATCTCTTCCACCGATGTCTCTTTGAGCAATA	2858
	Db	2748	GGTGTCAATCAACCAATCGTAACCTTCATCTCTTCCACCGATGTCTCTTTGAGCAATA	2807
	Qy	2859	AAGCCGATACAAAATCTTTGTGCCTCTTCGCAATGTCAACAGTACCCTTAGTATATCT	2918
	Db	2808	AAGCCGATACAAAATCTTTGTGCCTCTTCGCAATGTCAACAGTACCCTTAGTATATCT	2867
	Qy	2919	CCAGTAGATAGGAGCCCTTGATGACAAATTCGCTAACATCAAAAGCCCTCTAGGTTC	2978
	Db	2868	CCAGTAGATAGGAGCCCTTGATGACAAATTCGCTAACATCAAAAGCCCTCTAGGTTC	2927
	Qy	2979	TTTGTTACTTCTTCGCGCCTGTCAAACGGCTAAACAATCTGCGGCCACCAACCG	3038
	Db	2928	TTTGTTACTTCTTCGCGCCTGTCAAACGGCTAAACAATCTGCGGCCACCAACCG	2987
	Qy	3039	TGTGCATTCGTAATGTCTGCCATTCGTCTATTCTGTATACCCCGCAGAGTACTGCAAT	3098
	Db	2988	TGTGCATTCGTAATGTCTGCCATTCGTCTATTCTGTATACCCCGCAGAGTACTGCAAT	3047
	Qy	3099	TTGACTGTATTACCAATGTACGAAAATTTTCTGTCTTCGAAGAGTAAAAATTTGACTTG	3158
	Db	3048	TTGACTGTATTACCAATGTACGAAAATTTTCTGTCTTCGAAGAGTAAAAATTTGACTTG	3107
	Qy	3159	GCGGATTAATGCTTTAGGGCTTAACTGTGCGCCTTCATGGAAAATCAGTCAAGATATCC	3218
	Db	3108	GCGGATTAATGCTTTAGGGCTTAACTGTGCGCCTTCATGGAAAATCAGTCAAGATATCC	3167
	Qy	3219	ACATGCTTTTTTACTGAACAAAATTTTGGGACCTAATGCTTCACTACTCCAGTAATTC	3278
	Db	3168	ACATGCTTTTTTACTGAACAAAATTTTGGGACCTAATGCTTCACTACTCCAGTAATTC	3227
	Qy	3279	TTGGTGGTACGAAACATCCAAATGAAGCACACAAGTTTGTGTTTTCTGCTGTCATGATTA	3338
	Db	3228	TTGGTGGTACGAAACATCCAAATGAAGCACACAAGTTTGTGTTTTCTGCTGTCATGATTA	3287
	Qy	3339	AATAGCTTGGCAGCAACGAGCTAGGATGATAGCAGCAGTCTCTTATATGTAGCTTTC	3398

3288 AATAGCTTGGCAGCAACAGGACTAGBAGTAGCAGCGTTCCCTTATATATGTAGCTTC 3349

3399 GACATGATTATCTTTCTGCTTCGCAGGTTTTTGTTCTGTGCAGTTCGGGTTAAGAATACT 3458

3348 GACATGATTATCTTTCTGCTTCGCAGGTTTTTGTTCTGTGCAGTTCGGGTTAAGAATACT 3407

3459 GGGCAATTTCAATGTTTCTTCAAACAATAATATGCGGTATATATACCAATCTAAAGTCTGTGC 3518

3408 GGGCAATTTCAATGTTTCTTCAAACAATAATATGCGGTATATATACCAATCTAAAGTCTGTGC 3467

3519 TCCCTTCCTTCGTTCTCTTCCTTCGTTTCGGAGATTAACCGAATCAAAAAATTTCAAAGAAC 3578

3468 TCCCTTCCTTCGTTCTCTTCCTTCGTTTCGGAGATTAACCGAATCAAAAAATTTCAAAGAAC 3527

3579 CGAAATCAAAAAAAGAAATAAAAAAAATCATGAATTTGAATTTGAAATGCGGTATATATGCGGTATG 3638

3528 CGNAATCAAAAAAAGAAATAAAAAAAATCATGAATTTGAATTTGAAATGCGGTATATATGCGGTATG 3587

3639 TGCACTCTCAGTACAATCTGCTCTGTATGCCGATAGTTAAAGCCAGCCCCGACACCCGCCA 3698

3588 TGCACTCTCAGTACAATCTGCTCTGTATGCCGATAGTTAAAGCCAGCCCCGACACCCGCCA 3647

3699 ACACCCTGACGGCCCTGACGGCTTGCTGCTCCCGCATCCGCTTACAGCAACAGCT 3758

3648 ACAACCGCTGACGGCCCTGACGGCTTGCTGCTCCCGCATCCGCTTACAGCAACAGCT 3707

3759 GTGACCGTCTCCGGGAGCTGCATGTGTACAGAGTTTTCACCGTCATCACCGAAACGGCG 3818

3708 GTGACCGTCTCCGGGAGCTGCATGTGTACAGAGTTTTCACCGTCATCACCGAAACGGCG 3767

3819 AGACGAAGGGCTCTGTGATACGGCTATATTTTATAGGTTAATGATCATGATAATAATCGTT 3878

3768 AGACGAAGGGCTCTGTGATACGGCTATATTTTATAGGTTAATGATCATGATAATAATCGTT 3827

3879 TCCTTAGTATGATCCAATATCAAGGAATATGATAGCATTTGAAGGATGAGACTAATCCAAAT 3938

3828 TCCTTAGTATGATCCAATATCAAGGAATATGATAGCATTTGAAGGATGAGACTAATCCAAAT 3887

3939 GAGAGTGGCAGCATATAGAAACAGCTAAAGGTAGTCTGCAAGGAAGCATACGATACCCC 3998

3888 GAGAGTGGCAGCATATAGAAACAGCTAAAGGTAGTCTGCAAGGAAGCATACGATACCCC 3947

3999 GCATGGAATGGGATTAATATCACAGGAGGTACTAGACTACCTTTTCATCCTCATATAAATAGA 4058

3948 GCATGGAATGGGATTAATATCACAGGAGGTACTAGACTACCTTTTCATCCTCATATAAATAGA 4007

4059 CGCATATAAGTACCCATTTAAGCATATAACACGCNACTATGCGGTTCTTCTCATGTATATAT 4118

4008 CGCATATAAGTACCCATTTAAGCATATAACACGCNACTATGCGGTTCTTCTCATGTATATAT 4067

4119 ATATACAGGCAACACGAGATATAGGTGCGACGTGAACAGTGAAGTCTGTATGTGCGCAGCT 4178

4068 ATATACAGGCAACACGAGATATAGGTGCGACGTGAACAGTGAAGTCTGTATGTGCGCAGCT 4127

4179 CGCGTTGCATTTTCGGAAGCGCTCGTTTTCGGAACCGCTTTTGAAGTTTCCATATCCGAAGT 4238

4128 CGCGTTGCATTTTCGGAAGCGCTCGTTTTCGGAACCGCTTTTGAAGTTTCCATATCCGAAGT 4187

4239 TCCTATTCTCTAGAAAGTATAGBACTTACAGAGCGCTTTTGAACACCAAAAGCGCTCTGA 4298

4188 TCCTATTCTCTAGAAAGTATAGBACTTACAGAGCGCTTTTGAACACCAAAAGCGCTCTGA 4247

4299 AGACGCACTTTCAAAAAACCAAAACGACCGGAGCTGTAACGAGCTACTATAAATATTGCG 4358

4248 AGACGCACTTTCAAAAAACCAAAACGACCGGAGCTGTAACGAGCTACTATAAATATTGCG 4307

4359 AATAACCGCTTCCAAAAACATTTGCTCAAAAGTATCTCTTGCATATATATCTCTGTGCTATA 4418

4308 AATAACCGCTTCCAAAAACATTTGCTCAAAAGTATCTCTTGCATATATATCTCTGTGCTATA 4367

4419 TCCCTATATAACCTTACCCATCCACTTTTCGCTCCCTTGAATTTGCACTTAACTCGACCTC 4478

4368 TCCCTATATAACCTTACCCATCCACTTTTCGCTCCCTTGAATTTGCACTTAACTCGACCTC 4427

QY	4479	TACATTTTATGTTTATCTCTAGTATTAATCTTTAGACAAAAAATGTAGTAAGAACT	4538	QY	5559	GATGAGCACTTTTAAAGTTCTGCTATCTGCGCGGTATTTATCCCGTATTTGACGCGCGCA	5618
DB	4428	TACATTTTATGTTTATCTCTAGTATTAATCTTTAGACAAAAAATGTAGTAAGAACT	4487	DB	5508	GATGAGCACTTTTAAAGTTCTGCTATCTGCGCGGTATTTATCCCGTATTTGACGCGCGCA	5567
QY	4539	ATTCTATAGAGTGAATCGAAAAACAATACGAAATGTAAACATTTCTCTATACGTAGTATATA	4598	QY	5619	AGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACCACT	5678
DB	4488	ATTCTATAGAGTGAATCGAAAAACAATACGAAATGTAAACATTTCTCTATACGTAGTATATA	4547	DB	5568	AGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACCACT	5627
QY	4599	GAGACAAATAGAGAACCGGTTCATTAATTTCTGACCAATGAAAGATCATCAACGCTAT	4658	QY	5679	CACAGAAAAGCATCTTACGGATGCGATGACAGTAGAAGAGATTAATGTCAGTGTCTGCCATTAAC	5738
DB	4548	GAGACAAATAGAGAACCGGTTCATTAATTTCTGACCAATGAAAGATCATCAACGCTAT	4607	DB	5628	CACAGAAAAGCATCTTACGGATGCGATGACAGTAGAAGAGATTAATGTCAGTGTCTGCCATTAAC	5687
QY	4659	CACTTTCTGTTTACAAAGTATGCGCAATCCACATCGGTATAGAAATTAATTCGGGGATGCC	4718	QY	5739	CATGAGTGAATAACAATCGCGGCAACTTTCTGACAAAGATCGAGAGACCGAAGAGCT	5798
DB	4608	CACTTTCTGTTTACAAAGTATGCGCAATCCACATCGGTATAGAAATTAATTCGGGGATGCC	4667	DB	5688	CATGAGTGAATAACAATCGCGGCAACTTTCTGACAAAGATCGAGAGACCGAAGAGCT	5747
QY	4719	TTTATCTTGAAAAATGACCGCGAGCTTCGCTAGTAAATCAGTAAACGCGGGAAGTGGAG	4778	QY	5799	AACCGCTTTTGTGCAAAATGCGGGATCATGTAATCTGCGCTTGTATCGTTGGGAACCGGA	5858
DB	4668	TTTATCTTGAAAAATGACCGCGAGCTTCGCTAGTAAATCAGTAAACGCGGGAAGTGGAG	4727	DB	5748	AACCGCTTTTGTGCAAAATGCGGGATCATGTAATCTGCGCTTGTATCGTTGGGAACCGGA	5807
QY	4779	TCAGGCTTTTATGGAAGAGAAATAGACACCAAGTAGCCTTCTTAAACCTTAACG	4838	QY	5859	GCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGATGCTGTAGCAATGGCAAC	5918
DB	4728	TCAGGCTTTTATGGAAGAGAAATAGACACCAAGTAGCCTTCTTAAACCTTAACG	4787	DB	5808	GCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGATGCTGTAGCAATGGCAAC	5867
QY	4839	GACCTACAGTGCAAAAAGTTATCAAGAGACTGCATTATAGAGCGCACAAAGGAGAAAAA	4898	QY	5919	AACGTTGCGCAAACTATTAACTGCGGAACTACTTACTCTAGCTTCCCGGCAACAAATTAAT	5978
DB	4788	GACCTACAGTGCAAAAAGTTATCAAGAGACTGCATTATAGAGCGCACAAAGGAGAAAAA	4847	DB	5868	AACGTTGCGCAAACTATTAACTGCGGAACTACTTACTCTAGCTTCCCGGCAACAAATTAAT	5927
QY	4899	AGTAATCTAAGATGCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAA	4958	QY	5979	AGACTGATGAGGCGGATAAAGTTGAGAGACCACTTCTGCGCTGCGGCTTCCCGCTGG	6038
DB	4848	AGTAATCTAAGATGCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAA	4907	DB	5928	AGACTGATGAGGCGGATAAAGTTGAGAGACCACTTCTGCGCTGCGGCTTCCCGCTGG	5987
QY	4959	AAAAGATGATAGATCTTTGTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTCTGT	5018	QY	6039	CTGCTTTATTTGCTGATAAATCTGAGCGCGGTGAGCGTGGTCTCGCGGTATCATTTGCAGC	6098
DB	4908	AAAAGATGATAGATCTTTGTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTCTGT	4967	DB	5988	CTGCTTTATTTGCTGATAAATCTGAGCGCGGTGAGCGTGGTCTCGCGGTATCATTTGCAGC	6047
QY	5019	AAAAATGCAGCTCAGATCTTTGTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGT	5078	QY	6099	ACTGGGCGCAGATGTTAAGCCCTCCCGTATGCTAGTTATCTACACGAGGAGATGACAGC	6158
DB	4968	AAAAATGCAGCTCAGATCTTTGTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGT	5027	DB	6048	ACTGGGCGCAGATGTTAAGCCCTCCCGTATGCTAGTTATCTACACGAGGAGATGACAGC	6107
QY	5079	TACAAAAATGAAGCACAGATCTTCGTTGGTAAATAGCGCTTTTCGGGTGCAATTTCTGT	5138	QY	6159	AACATGATGATGAAGCAATAGACAGATCGCTGAGATGAGTGGCTCCTCAGTATTAAGCATTG	6218
DB	5028	TACAAAAATGAAGCACAGATCTTCGTTGGTAAATAGCGCTTTTCGGGTGCAATTTCTGT	5087	DB	6108	AACATGATGATGAAGCAATAGACAGATCGCTGAGATGAGTGGCTCCTCAGTATTAAGCATTG	6167
QY	5139	TCGTAAAAATGCAGCTCAGATCTTTGTTGTTGTAATAATAGCGCTCTCGGTTGCAATTT	5198	QY	6219	GTAATCTGACAGCAAGTTTACTCATATATATCTTATGATTTGATTTTAACTTCATTTTAA	6278
DB	5088	TCGTAAAAATGCAGCTCAGATCTTTGTTGTTGTAATAATAGCGCTCTCGGTTGCAATTT	5147	DB	6168	GTAATCTGACAGCAAGTTTACTCATATATATCTTATGATTTGATTTTAACTTCATTTTAA	6227
QY	5199	TGTTCTTACAAAAATGAAGCACAGATGCTTCGTTTCAAGTGGCACTTTTCGGGGAATGTGCG	5258	QY	6279	ATTTAAAGGATCTAGGTGAAGATCTCTTTTGTGATTAATCTCATGACCAAAATCCCTTAAAG	6338
DB	5148	TGTTCTTACAAAAATGAAGCACAGATGCTTCGTTTCAAGTGGCACTTTTCGGGGAATGTGCG	5207	DB	6228	ATTTAAAGGATCTAGGTGAAGATCTCTTTTGTGATTAATCTCATGACCAAAATCCCTTAAAG	6287
QY	5259	CGGAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATTCGGCTCATGAGACA	5318	QY	6339	TGAGTTTTTCTGTTCCACTGAGCGGTGAGACCCCGTGAAGATCAAGAGATCTTCTTGAGA	6398
DB	5208	CGGAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATTCGGCTCATGAGACA	5267	DB	6288	TGAGTTTTTCTGTTCCACTGAGCGGTGAGACCCCGTGAAGATCAAGAGATCTTCTTGAGA	6347
QY	5319	ATAACCTGATTAATGCTTCATATATATGAAAGGAGAGATGATGATTTCAACATTT	5378	QY	6399	TCCTTTTTTCTGCGGTGATCTGCTGCTTCAAAACAAAAAACCACCGCTACCAAGCGGT	6458
DB	5268	ATAACCTGATTAATGCTTCATATATATGAAAGGAGAGATGATGATTTCAACATTT	5327	DB	6348	TCCTTTTTTCTGCGGTGATCTGCTGCTTCAAAACAAAAAACCACCGCTACCAAGCGGT	6407
QY	5379	CGGTGTCGCGCTTATTTCCCTTTTTCGGGCAATTTTTCGCTTCTGTTTGTCTCAACCCAGA	5438	QY	6459	GGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCGGAAGGTAACCTGCGTTCAGCAG	6518
DB	5328	CGGTGTCGCGCTTATTTCCCTTTTTCGGGCAATTTTTCGCTTCTGTTTGTCTCAACCCAGA	5387	DB	6408	GGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCGGAAGGTAACCTGCGTTCAGCAG	6467
QY	5439	AACGCTGTTGAAAGTAAAGATGCTGAAGATCAGTGTGGGTGACAGAGTGGGTTCATCGA	5498	QY	6519	AGCGCAGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTTAGCCACCACTTCAAGAA	6578
DB	5388	AACGCTGTTGAAAGTAAAGATGCTGAAGATCAGTGTGGGTGACAGAGTGGGTTCATCGA	5447	DB	6468	AGCGCAGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTTAGCCACCACTTCAAGAA	6527
QY	5499	ACTGGATCTCAACAGCGGTGAGATCTCTTGGAGTGTTCGCCCCCGAAGACGTTTTCCAAAT	5558	QY	6579	CTCTGTAGCACCCTTACATACCTCGCTCTGCTTAATCTGTTTACAGTGGGTGCTGCCAG	6638
DB	5448	ACTGGATCTCAACAGCGGTGAGATCTCTTGGAGTGTTCGCCCCCGAAGACGTTTTCCAAAT	5507	DB	6528	CTCTGTAGCACCCTTACATACCTCGCTCTGCTTAATCTGTTTACAGTGGGTGCTGCCAG	6587
				QY	6639	TGGCGATAAGTGTGTCTTTACCCGGGTGGACTCAAGACGATAGTTTACCGGATAAGCGCA	6698

Db 6588 TGGCGATAAGTCGTGCTTACCGGGTTGGACTCAAGACGATAGTACCGGATAGGCGCA 6647
QY 6699 GCGGTGCGGCTGAACCGGGGGTTCGTGCACACAGAGCCAGCTTCGAGCGAACAGCTACAC 6758
Db 6648 GCGGTGCGGCTGAACCGGGGGTTCGTGCACACAGAGCCAGCTTCGAGCGAACAGCTACAC 6707
QY 6759 CGAATGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGAGAAA 6818
Db 6708 CGAATGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGAGAAA 6767
QY 6819 GCGGACAGGATACCGGTAGCGGCGAGGTCGAGACAGGAGCGCACGAGGAGCTTCC 6878
Db 6768 GCGGACAGGATACCGGTAGCGGCGAGGTCGAGACAGGAGCGCACGAGGAGCTTCC 6827
QY 6879 AGGGGAAACCGCTTGTATCTTATAGTCTCTGCGGTTTTCGCCACCTCTGACTTGAGCG 6938
Db 6828 AGGGGAAACCGCTTGTATCTTATAGTCTCTGCGGTTTTCGCCACCTCTGACTTGAGCG 6887
QY 6939 TCGAATTTTGTGATGCTCGTCAGGGGGCGAGGCTATGAGAAACGCCAGCAACCGGC 6998
Db 6888 TCGAATTTTGTGATGCTCGTCAGGGGGCGAGGCTATGAGAAACGCCAGCAACCGGC 6947
QY 6999 CTTTTACGGTTCTGCGCTTTTGTGCGCTTTTGTCTCATGTTCTTCTCTCGGTTATC 7058
Db 6948 CTTTTACGGTTCTGCGCTTTTGTGCGCTTTTGTCTCATGTTCTTCTCTCGGTTATC 7007
QY 7059 CCCTGATTTGTGATTAACCGTATTACCGCTTTTGTAGTGAGCTGATACCGCTCGCGCAG 7118
Db 7008 CCCTGATTTGTGATTAACCGTATTACCGCTTTTGTAGTGAGCTGATACCGCTCGCGCAG 7067
QY 7119 CCAGAACCGACGCGCAGCGAGTCAGTGACGAGGAGGAGCGGAGCGCCCAATACGCAA 7178
Db 7068 CCAGAACCGACGCGCAGCGAGTCAGTGACGAGGAGGAGCGGAGCGCCCAATACGCAA 7127
QY 7179 ACCGCTCTCCCGCGGTTGCGGATTCATTAATGCGAGTGGCAGCAGCAGAGGTTCCCGA 7238
Db 7128 ACCGCTCTCCCGCGGTTGCGGATTCATTAATGCGAGTGGCAGCAGCAGAGGTTCCCGA 7187
QY 7239 CTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTACTCTACTATTAGGCACC 7298
Db 7188 CTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTACTCTACTATTAGGCACC 7247
QY 7299 CCAGGCTTTACATTTATGCTTCGCGCTCTATGTTGTGGAATTTGTAGCGGATAACA 7358
Db 7248 CCAGGCTTTACATTTATGCTTCGCGCTCTATGTTGTGGAATTTGTAGCGGATAACA 7307
QY 7359 ATTTCACAGGAAACAGCTATGACCATGATTAAGCCAGCGGCAATTAACCTCACTA 7418
Db 7308 ATTTCACAGGAAACAGCTATGACCATGATTAAGCCAGCGGCAATTAACCTCACTA 7367
QY 7419 AAGGGAACAAAGCTGGAGCTCGTAGGAACAATTTGGGGCCCTGGTGTTCTTCTGAGG 7478
Db 7368 AAGGGAACAAAGCTGGAGCTCGTAGGAACAATTTGGGGCCCTGGTGTTCTTCTGAGG 7427
QY 7479 TTCACTCTTTTACATTTGCTTCTGCTGATTAATTTTCAGAGGCAACAGGAAAAATTAGAT 7538
Db 7428 TTCACTCTTTTACATTTGCTTCTGCTGATTAATTTTCAGAGGCAACAGGAAAAATTAGAT 7487
QY 7539 GGCAGAAAGTCGCTTTCAAGGAAAAATCCCGACCATCTTTTCAGATCCCTGTAACTTA 7598
Db 7488 GGCAGAAAGTCGCTTTCAAGGAAAAATCCCGACCATCTTTTCAGATCCCTGTAACTTA 7547
QY 7599 TTGCAACTGAAAGATGAAGAGGAGGAAAAATACAAATATATCTAGAACTGAAAAAATAA 7658
Db 7548 TTGCAACTGAAAGATGAAGAGGAGGAAAAATACAAATATATCTAGAACTGAAAAAATAA 7607
QY 7659 AAGTATAAATAGACGATATATGCCAATCTTTCACAAATGTTCCGAATCTTCTCAATTT 7718
Db 7608 AAGTATAAATAGACGATATATGCCAATCTTTCACAAATGTTCCGAATCTTCTCAATTT 7667
QY 7719 GCAGCTATTGTAATAATTAATAACATCAAGAACAAACAGCTCAACTGTCTTCTTAAG 7778

Db 7668 GCAGCTATTGTAATAATAATAAACATCAAGAACAAACAGCTCAACTGTCTTCTTAAG 7727
QY 7779 AACAAAGATAAACACAAAAACAAAAAGTTTTTTTAAATTAATCAAAAA 7828
Db 7728 AACAAAGATAAACACAAAAACAAAAAGTTTTTTTAAATTAATCAAAAA 7777

RESULT 3
AAL49316
ID AAL49316 standard; DNA; 6360 BP.
XX
AC AAL49316;
XX
DT 07-NOV-2002 (first entry)
XX Human HXT7 promoter containing plasmid YEp4H7.
XX Human; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
XX plasmid; ds.
XX Homo sapiens.
XX WO200264784-A2.
XX 22-AUG-2002.
XX 09-FEB-2002; 2002WO-EP001373.
XX 14-FEB-2001; 2001DE-01006718.
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX Mueller G, Koller K, Boles E, Wiczorke R, Dlugai S;
XX WPI; 2002-636632/68.
XX New strains of yeast, useful in screening for modulators of hexose
XX transport, potential antidiabetic and antiobesity agents, lack native
XX hexose-transport function.
XX Example; Page 43-45; 58pp; German.
XX The present invention relates to a strain of *Saccharomyces cerevisiae*
XX that cannot grow on a substrate containing hexose as the only source of
XX carbon but the ability to grow on such substrates is restored when the
XX GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
XX GLUT4 genes can be used to identify compounds that increase/reduce hexose
XX transport by these proteins. These compounds, optionally after
XX development, are potential drugs for treating diabetes and obesity. The
XX present sequence is a plasmid described in the invention

SQ Sequence 6360 BP; 1771 A; 1485 C; 1336 G; 1768 T; 0 U; 0 Other;
Query Match 75.5%; Score 5908; DB 6; Length 6360;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 AGCTTATCGATACCGTCGACCTCGAGTCATGTAATAGTTAGTGTACGCTTACATTCAC 1591
Db 453 AGCTTATCGATACCGTCGACCTCGAGTCATGTAATAGTTAGTGTACGCTTACATTCAC 512
QY 1592 GCCTTCCCCCACCATCCGCTCTAACCGAAAAAGGAGGTTAGACAACTTGAAGTCTAGG 1651
Db 513 GCCTTCCCCCACCATCCGCTCTAACCGAAAAAGGAGGTTAGACAACTTGAAGTCTAGG 572
QY 1652 TCCTTATTTATTTTATAGTTATGTTAGTATTAAGAGCTTATTTATTTCAATTT 1711
Db 573 TCCTTATTTATTTTATAGTTATGTTAGTATTAAGAGCTTATTTATTTCAATTT 632
QY 1712 TTCTTTTTTTTCTGTACAGACGCTGTACGATGTAACATTATCTGAAACCTTGTCTG 1771
Db 633 TTCTTTTTTTTCTGTACAGACGCTGTACGATGTAACATTATCTGAAACCTTGTCTG 692

QY	1772	AGAGGTTTGGGACGCTCGAAGGCTTTAAATTTGGCGCGGTACCCAAATTCGCCCTATAG	1831	Db	1773	AGCAATAAAGCCGATACAAATCTTTGTCGCTCTTCGCAATGTCAACAGTACCTTAGT	1832
Db	693	AGAGGTTTGGGACGCTCGAAGGCTTTAAATTTGGCGCGGTACCCAAATTCGCCCTATAG	752	QY	2912	ATATTTCCAGTAGATAGGAGGCCCTTGCATGACAAATTTCTGCTAACATCAAAAGGCCTCT	2971
QY	1832	TCAGTCGTATTAACGGCGCTCATCTGCCGCTCGTTTACAACTGTCGTGACCTGGGAAACCC	1891	Db	1833	ATATTTCCAGTAGATAGGAGGCCCTTGCATGACAAATTTCTGCTAACATCAAAAGGCCTCT	1892
Db	753	TCAGTCGTATTAACGGCGCTCATCTGCCGCTCGTTTACAACTGTCGTGACCTGGGAAACCC	812	QY	2972	AGGTTCCCTTTGTTACTTTCTTCGCGGCTGCTTCAAAACCGCTAACAAATACCTGGGCCAC	3031
QY	1892	TGGCGTTACCCAACTTAATCGCTTTGCGAGCAGATCCCCCTTTCGCCAGCTGGCGTAATAG	1951	Db	1893	AGGTTCCCTTTGTTACTTTCTTCGCGGCTGCTTCAAAACCGCTAACAAATACCTGGGCCAC	1952
Db	813	TGGCGTTACCCAACTTAATCGCTTTGCGAGCAGATCCCCCTTTCGCCAGCTGGCGTAATAG	872	QY	3032	CACACCGTGTGCATTCGTAAATGTCTGCCCATTTCTGCTATTCTGTATACACCGCAGAGTA	3091
QY	1952	CGAAGAGGCCCGACACCGATCGCCCTTCCCAACAGTTGGCGAGCTGGAATGGCGAATGGCG	2011	Db	1953	CACACCGTGTGCATTCGTAAATGTCTGCCCATTTCTGCTATTCTGTATACACCGCAGAGTA	2012
Db	873	CGAAGAGGCCCGACACCGATCGCCCTTCCCAACAGTTGGCGAGCTGGAATGGCGAATGGCG	932	QY	3092	CTGCAATTTGACCTGTATTAACCAATGTCTGCAAAATTTTCTGCTTCGCAAGAGTAAATAAT	3151
QY	2012	CGACGCGCCTGTAGCGCGCATTAAGCGCGCGGGTGTGTGTTACGCGACGCGTAC	2071	Db	2013	CTGCAATTTGACCTGTATTAACCAATGTCTGCAAAATTTTCTGCTTCGCAAGAGTAAATAAT	2072
Db	933	CGACGCGCCTGTAGCGCGCATTAAGCGCGCGGGTGTGTGTTACGCGACGCGTAC	992	QY	3152	GTACTTGGCGGATAATGCTTTAGTAAACAAATTTTGGGACCTAAATGCTTCAACTCTCAGTAA	3211
QY	2072	CGCTACATCTGCGAGCGCCTAGCGCGCGCTTCCCTTTCCTTCTCTTCTCTCTCTCTCGC	2131	Db	2073	GTACTTGGCGGATAATGCTTTAGTAAACAAATTTTGGGACCTAAATGCTTCAACTCTCAGTAA	2132
Db	993	CGCTACATCTGCGAGCGCCTAGCGCGCGCTTCCCTTTCCTTCTCTTCTCTCTCTCTCGC	1052	QY	3212	GATATCCACATGTGTTTTTGTAGTAAACAAATTTTGGGACCTAAATGCTTCAACTCTCAGTAA	3271
QY	2132	CACGTTTCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCCGATT	2191	Db	2133	GATATCCACATGTGTTTTTGTAGTAAACAAATTTTGGGACCTAAATGCTTCAACTCTCAGTAA	2192
Db	1053	CACGTTTCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCCGATT	1112	QY	3272	TAATTCCTTGGTGTAGCAACATCAATGAAGACACAAAGTTTGTTCGCTTTTCGTCAT	3331
QY	2192	TAGTCGTTTACGGCACCTCGACCCCAAAATTTGATTTAGGGTGTATGTTTCACTAGTGG	2251	Db	2193	TAATTCCTTGGTGTAGCAACATCAATGAAGACACAAAGTTTGTTCGCTTTTCGTCAT	2252
Db	1113	TAGTCGTTTACGGCACCTCGACCCCAAAATTTGATTTAGGGTGTATGTTTCACTAGTGG	1172	QY	3332	GATATTAATAGCTTTGGCAGCAACAGACTAGGATGAGTAGCAGCAGCTTCTCTATATGT	3391
QY	2252	GCCATCGCCTGATAGACGGTTTTTCGCCCTTTGACGTTGAGTCCAGCTCTTTTATAG	2311	Db	2253	GATATTAATAGCTTTGGCAGCAACAGACTAGGATGAGTAGCAGCAGCTTCTCTATATGT	2312
Db	1173	GCCATCGCCTGATAGACGGTTTTTCGCCCTTTGACGTTGAGTCCAGCTCTTTTATAG	1232	QY	3392	AGCTTTTCGACATGATTTTATCTTCTGTCAGGTTTTTCTGTCAGTGTGGTTAA	3451
QY	2312	TGACCTCTTGTTCAAAACCTGGAACAACTCAACCTATCTCGGTCATCTCTTTGATT	2371	Db	2313	AGCTTTTCGACATGATTTTATCTTCTGTCAGGTTTTTCTGTCAGTGTGGTTAA	2372
Db	1233	TGACCTCTTGTTCAAAACCTGGAACAACTCAACCTATCTCGGTCATCTCTTTGATT	1292	QY	3452	GAATATCGGGAAATTTTCATGTTTCTTCAACATCATATGCTGATATATATACAAATCTAAG	3511
QY	2372	ATAAGGATTTTGGCGATTTTGGCGCTATTTGTTTAAAAATGAGCTGATTTTAAACAAAAT	2431	Db	2373	GAATATCGGGAAATTTTCATGTTTCTTCAACATCATATGCTGATATATATACAAATCTAAG	2432
Db	1293	ATAAGGATTTTGGCGATTTTGGCGCTATTTGTTTAAAAATGAGCTGATTTTAAACAAAAT	1352	QY	3512	TCGTGCT	3571
QY	2432	TAAACGGAATTTTAAACAAAATTTAAACGTTTAAACGTTTAAACGTTTAAACGTTTAAAC	2491	Db	2433	TCGTGCT	2492
Db	1353	TAAACGGAATTTTAAACAAAATTTAAACGTTTAAACGTTTAAACGTTTAAACGTTTAAAC	1412	QY	3572	AAGAAACCGAAATCAAAACAAAATCAAAACAAAATCAAAACAAAATCAAAACAAAATCAAA	3631
QY	2492	ACGCATCTGTGGGTATTTTCAACCGCATAGGTAATTAATCTGATATAATTAATTAATTAAT	2551	Db	2493	AAGAAACCGAAATCAAAACAAAATCAAAACAAAATCAAAACAAAATCAAAACAAAATCAAA	2552
Db	1413	ACGCATCTGTGGGTATTTTCAACCGCATAGGTAATTAATCTGATATAATTAATTAATTAAT	1472	QY	3632	GGTATGTGCATCTCAGTACAAATCTGCTCTGATGCCGATAGTTAAGCCAGCCGAC	3691
QY	2552	TCTAATTTGTAGTTTGTATATACATGCAATTTACTTATAATACAGTTTTTATAGTTTGTG	2611	Db	2553	GGTATGTGCATCTCAGTACAAATCTGCTCTGATGCCGATAGTTAAGCCAGCCGAC	2612
Db	1473	TCTAATTTGTAGTTTGTATATACATGCAATTTACTTATAATACAGTTTTTATAGTTTGTG	1532	QY	3692	CCGCCAAACCCGCTGACGCGCTGACGCGCTTGTCTGCTCCGCGATCCGCTTACAG	3751
QY	2612	GGCGATCTTCTCAATATGCTTCCAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2671	Db	2613	CCGCCAAACCCGCTGACGCGCTTGTCTGCTCCGCGATCCGCTTACAG	2672
Db	1533	GGCGATCTTCTCAATATGCTTCCAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1592	QY	3752	ACAAGCTGTGACCGCTCTCCGGAGCTGATGTGTGAGAGGTTTTTCAACGTCATACCCGAA	3811
QY	2672	AGCATCCCTTCCCTTTGCAATATGCTTCCCAACATAATATGTCAGATCTCTGTAGA	2731	Db	2673	ACAAGCTGTGACCGCTCTCCGGAGCTGATGTGTGAGAGGTTTTTCAACGTCATACCCGAA	2732
Db	1593	AGCATCCCTTCCCTTTGCAATATGCTTCCCAACATAATATGTCAGATCTCTGTAGA	1652	QY	3812	ACGCGCAGAGAAAGGCCCTCGTATACCGCTATTTTATAGTTTATGTCATGATAT	3871
QY	2732	GACCAATCATCCAGGTTCTATGTTGACCCCAATGGCTCTCCCTTGTGTCATCTAAAC	2791	Db	2733	ACGCGCAGAGAAAGGCCCTCGTATACCGCTATTTTATAGTTTATGTCATGATAT	2792
Db	1653	GACCAATCATCCAGGTTCTATGTTGACCCCAATGGCTCTCCCTTGTGTCATCTAAAC	1712	QY	3872	AATGGTTTCTTAGTATGATCCAAATCAAAAGCAATGATAGCATTGAAGGATGAGACTAA	3931
QY	2792	CACACGGGTGTCAATCAACCAATCGTAACTTCTCTTCCACCCATGCTCTTTG	2851	Db	2793	AATGGTTTCTTAGTATGATCCAAATCAAAAGCAATGATAGCATTGAAGGATGAGACTAA	2852
Db	1713	CACACGGGTGTCAATCAACCAATCGTAACTTCTCTTCCACCCATGCTCTTTG	1772	QY	3932	TCCAAATGAGAGTGGCAGCATATAGAAACAGCTTAAAGGGTGTGCTGAAAGGAGCATAGC	3991
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Db 3453 AAGAACCTATTATAGAGTGAATCGAAACCAATACGAAATGTAAACATTTCTTATACGTA 3512
Qy 4592 GTATATAGACAAATATAGAAACCGTTTCATATTTTCTGACCAATGAAGATCATCA 4651
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Qy 4652 ACCCTATCACTTTCTGTTCAAAAGTATGCGCAATCCACATCGTATAGAAATATATCGG 4711
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DB 5433 TCAGCAGAGCGCAGATACCAATACTGCTCTTAGTGTAGCGGTAGTTAGGCCACCACT 5492
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DB 5493 TCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTCTTAATCTGTTACCAAGTGGCTG 5552
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DB 5613 AGCGCAGCGGTGCGGGCTGAACGGGGGTTGCTGCACACAGCCAGCTTGGAGCGAACGA 5672
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DB 5673 CTTACACCGAATGATGATACCTTACAGCTGAGCTATGAGAAAGCGCCACCGTTCCCGAAG 5732
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DB 6093 TACGCAAAACCGCTCTCCCGCGCTTCCCGGATTTCAATATGAGCTGCGACCAAGT 6152
QY 7232 TTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTACCTCACTCATT 7291

RESULT 4

AAC87129/c

ID AAC87129 standard; DNA; 8749 BP.

XX AAC87129;

AC AAC87129;

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of plasmid pGB1023.

XX PKD2 gene; Caenorhabditis elegans; CEPDK2; polycystin; ADPKD;
XX autosomal dominant polycystic kidney disease; epithelial structure;
XX kidney nephron; circular; cyclic; ss.

XX Synthetic.

OS Aequorea victoria.

OS Caenorhabditis elegans.

OS Unidentified.

XX Key Location/Qualifiers

FH CDS 1402..2259

FT /*tag= a

FT /note= "ampicillin resistance sequence"

FT 4243..4944

FT /*tag= b

FT /note= "trp gene"

FT 7153..7891

FT /*tag= d

FT /note= "PADH1 promoter"

FT 7891..8331

FT /*tag= c

FT /note= "GAL4 DNA binding domain"

FT 8401..87486

FT /*tag= e

FT /note= "PKD2 gene"

XX GB2351496-A.

XX 03-JAN-2001.

XX 01-JUN-2000; 2000GB-00013413.

XX 01-JUN-1999; 99GB-00012748.

XX (DEVG-) DEVGEN NV.

XX Kaletta T, Vangeel A, Bogaert T, Van De Craen M;

XX WPI; 2001-105117/12.

XX Novel nucleic acids isolated from the CEPDK2 gene of Caenorhabditis
XX elegans, used to produce transgenic organisms used to identify compounds
XX for use in the treatment of autosomal dominant polycystic kidney disease.

XX Disclosure; Fig 4; 105pp; English.

XX The present sequence represents a plasmid which was used to express the

CC PKD2 gene of Caenorhabditis elegans (designated CEPD2). The PKD2 protein
CC is part of the polycystin family. Defects in the PKD2 gene are
CC responsible for about 15% of autosomal dominant polycystic kidney disease
CC (ADPKD) cases. It is possible that PKD2 proteins perform a general task
CC in maintaining epithelial structure in kidney nephron tubules, especially
CC the maintenance of tubule width. Transgenic C. elegans comprising
CC plasmids expressing the PKD2 gene, or deletions thereof, are useful for
CC identifying compounds which may be used to treat ADPKD
XX
SQ Sequence 8749 BP; 2471 A; 1837 C; 1935 G; 2505 T; 0 U; 1 Other;

Query Match 57.4%; Score 4492.6; DB 4; Length 8749;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

QY 1559 TCATGTAATAGTATGTCAGCGCTACATTCAGCGCCCTCCGCCACATCCGCTCTAACCG 1618
DB |||||||
QY 1619 AAAAGGAAGGAGTGTAGACAACTGAAGTCTAGTCCCTATTTATTTTATAGTTATGT 1678
DB |||||||
QY 1679 TAGTATTAAGAAAGTATTTATTTATTTTCAATTTTCTTTTCTTTTCTGTACAGCGGTGT 1738
DB |||||||
QY 1739 ACCCATGTAACTATTAATCTGAAACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT 1798
DB |||||||
QY 1799 TAAATTCGCGCGGTACCCCAATTCGCCCTATAGTGTAGTCTGATTAATCGCGGCTCACTGGC 1858
DB |||||||
QY 1859 CGTGGTTTACACGTCGTGACCTGGGAAACCTTGGGTTTACCACTTAATCGCCTTGC 1918
DB |||||||
QY 1919 AGCACATCCCTTTTCGCGAGCTGGGCTAATAGCGAAGGCGCGACCGATCGCCCTTC 1978
DB |||||||
QY 1979 CCACAGTTGCGCAGCTGAATCGCGAATCGCGAAGGCGCGCGCTGTAGCGGCGCATTAAG 2038
DB |||||||
QY 2039 CGCGGCGGTGTGGTGTAGCGGCGAGCGGTGACCGCTACACTTGCAGCGCCCTAGCGCC 2098
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DB |||||||
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DB |||||||
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DB |||||||
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DB |||||||

DB |||||||
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QY |||||||
DB 2459 GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGCACTCTGCGGTATTTTACACCGC 2518
DB |||||||
DB 5060 GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGCACTCTGCGGTATTTTACACCGC 5001
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QY 2519 ATAGGTAATACTGATATATAATTAATTTGAAGCTCTAAATTTGTGAGTTTATGATATG 2578
DB |||||||
DB 5000 ATAGATCGGCAAGTGCACAACTACTTAAATAAATACTACTCAGTAATAAATCTATTTTC 4941
QY |||||||
QY 2579 ATTTACTATATATACAGTTTATTTAGTTTGTGCGCGCATCTTCTCAAAATATGTTCCCA 2638
DB |||||||
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QY |||||||
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DB |||||||
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QY |||||||
QY 2759 TTGACCCCAATGCGTCTCCCTTGTCTATCAACCCACACCGGGTGTATATCAACCAATC 2818
DB |||||||
DB 4792 GTAAGCTTTTGGGGGCTCTCTTGCCTT-----CCAACCCAGTCAAGAAATCGAGTTCCAA 4738
QY |||||||
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DB |||||||
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QY |||||||
QY 2879 GTGCTCTTTGCAATGTCAACAGTACCTTGTATATTTCTCCAGTATAGTAGGAGGCCCTT 2938
DB |||||||
DB 4683 AGTTTCTGTGAAGCTGCACTGAGTAGTATTTGTCAGTCTTTTGGAAATAACGAGTCTTTT 4624
QY |||||||
DB 2939 GCATGACAATTTGCTTAAATCAAAAGGCTCTAGGTTCTTTGTTACTTCTTCTGCGC 2998
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QY |||||||
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QY |||||||
DB 3358 GACTAGGATGAGTAGCAGCAGCTTCTTATATGTAGCTTTTCGACATGATTTATCTTCGTT 3417
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DB |||||||
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QY 4438 TCCACCTTTCCGCTCTTGAACCTTTGATCTTAACTCGACCTCTACATTTTTTTATGTTTTATC 4497
DB |||||
QY 3183 TCCACCTTTCCGCTCTTGAACCTTTGATCTTAACTCGACCTCTACATTTTTTTATGTTTTATC 3124
DB |||||
QY 4498 TCTAGTATTACTCTTTTAGCAAAAAATTTGTAGTAAGAACTATTTCATAGAGTGAATCGAA 4557
DB |||||
QY 3123 TCTAGTATTACTCTTTTAGCAAAAAATTTGTAGTAAGAACTATTTCATAGAGTGAATCGAA 3064
DB |||||
QY 4558 AACATACGAAATGTAACATTTTCTATACGTAGTATATAGAGNCAAAATAGAGAAAC 4617
DB |||||
QY 3063 AACATACGAAATGTAACATTTTCTTATACGTAGTATATAGAGNCAAAATAGAGAAAC 3004
DB |||||

QY 4618 CGTTCAATAATTTCTGACCAATGAAGAAATCATCAACGCTATCACTTTCTGTTCAAAAGT 4677
DB |||||
QY 3003 CGTTCAATAATTTCTGACCAATGAAGAAATCATCAACGCTATCACTTTCTGTTCAAAAGT 2944
DB |||||
QY 4678 ATGCGCAATCCACATCGGTATAGAATAATATATCGGGATGCTTTATCTTTGAAAAATGCA 4737
DB |||||
QY 2943 ATGCGCAATCCACATCGGTATAGAATAATATATCGGGATGCTTTATCTTTGAAAAATGCA 2884
DB |||||
QY 4738 CCGCAGCTTCGCTAGTAAATCAGTAAACCGGGAGTGAGCTCAGGCTTTTTTTATGGAA 4797
DB |||||
QY 2883 CCGCAGCTTCGCTAGTAAATCAGTAAACCGGGAGTGAGCTCAGGCTTTTTTTATGGAA 2824
DB |||||
QY 4798 GAGAAAAATAGACACAAAAGTAGCTTTCTTAACTTAAACGAGACCTACAGTGCAAAAAAGT 4857
DB |||||
QY 2823 GAGAAAAATAGACACAAAAGTAGCTTTCTTAACTTAAACGAGACCTACAGTGCAAAAAAGT 2764
DB |||||
QY 4858 TATCAAGAGACTGCTATATAGAGCGCAAAAAGGAGAAAAAAGTAATCTAAGATGCTTTG 4917
DB |||||
QY 2763 TATCAAGAGACTGCTATATAGAGCGCAAAAAGGAGAAAAAAGTAATCTAAGATGCTTTG 2704
DB |||||
QY 4918 TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAAAAAGAAAGATATAGATTTCT 4977
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DB |||||
QY 4978 TGTGTGTAATAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAAATAATGAGCTCAGATTC 5037
DB |||||
QY 2643 TGTGTGTAATAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAAATAATGAGCTCAGATTC 2584
DB |||||
QY 5038 TTTGTTTTGAAAAATAGCGCTCTCGCGTTGCAATTTTGTGTTTTTAACAAAAATGAGCACAGA 5097
DB |||||
QY 2583 TTTGTTTTGAAAAATAGCGCTCTCGCGTTGCAATTTTGTGTTTTTACAAAAATGAGCACAGA 2524
DB |||||
QY 5098 TTCTTTCGTTGTAATAATAGCGCTTTTCGCTGTCATTTCTGTTCTGTAAATAATGAGCTCA 5157
DB |||||
QY 2523 TTCTTTCGTTGTAATAATAGCGCTTTTCGCTGTCATTTCTGTTCTGTAAATAATGAGCTCA 2464
DB |||||
QY 5158 GATTCTTTGTTGAAAAATAGCGCTCTCGCGTTGCAATTTTGTGTTCTACAAAAATGAAAGCA 5217
DB |||||
QY 2463 GATTCTTTGTTGAAAAATAGCGCTCTCGCGTTGCAATTTTGTGTTCTACAAAAATGAAAGCA 2404
DB |||||
QY 5218 CAGATGCTTCGTTCAGTGCGCACTTTTCGCGGAAATGTGCGGAAACCCCTATTGTTTTA 5277
DB |||||
QY 2403 CAGATGCTTCGTTCAGTGCGCACTTTTCGCGGAAATGTGCGGAAACCCCTATTGTTTTA 2344
DB |||||
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QY 5338 CAATAATATTGAAAAAGGAGATGATGATATTCAACATTTCCGCTGCGCTTATTTCC 5397
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QY 2283 CAATAATATTGAAAAAGGAGATGATGATATTCAACATTTCCGCTGCGCTTATTTCC 2224
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QY 5398 TTTTTCGCGCATTTTCGCTTCTGTTTTCGCTACCCAGAAACGCTGTTGAAAGTAAAA 5457
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DB |||||
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DB |||||
QY 2163 GATGCTGAAGATCAGTTGGGTGACAGTGCTTACATCGAATCGATCTCAACAGCGCT 2104
DB |||||
QY 5518 AAGATCCTTGAGAGTTTTTCGCCCCGAAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTT 5577
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QY 2103 AAGATCCTTGAGAGTTTTTCGCCCCGAAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTT 2044
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DB |||||
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DB |||||
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DB |||||
QY 1983 ATACACTATTCTCAGAAATGACTTGTGTTGAGTACTCACCAGTCCACAGAAAGCATCTTACG 1924
DB |||||
QY 5698 GATGGCATGACAGTAAGAGAAATTATGACAGTGTGCTGCCATACCAATGAGTGAATAACTGCG 5757
DB |||||

Db	1923	GATGGCATGACAGTAAGAGAAATTATGACAGTGCCTGCCATAACCATGAGTGATACACTGGCG	1864
Qy	5758	GCCAACTTACTTCTTGACAAAGATCGGAGGACCGAAGGAGCTAAACCGCTGTTTTTTGGCAAC	5817
Db	1863	GCCAACTTACTTCTTGACAAAGATCGGAGGACCGAAGGAGCTAAACCGCTGTTTTTTGGCAAC	1804
Qy	5818	ATGGGGATCATGTAACTCSCCTTTGATCGTTGGGAAACCGAGCTGTAATGAAGCCATACCA	5877
Db	1803	ATGGGGATCATGTAACTCSCCTTTGATCGTTGGGAAACCGAGCTGTAATGAAGCCATACCA	1744
Qy	5878	AACGACGAGCGTGACACCAAGATGCCCTGTAGCAATGSCCAACAAGTTGCCGAACCTATT	5937
Db	1743	AACGACGAGCGTGACACCAAGATGCCCTGTAGCAATGSCCAACAAGTTGCCGAACCTATT	1684
Qy	5938	ACTGGCGAACTACTTACTCTAGCTTCCCGGCACAAATTAATAGACTGGAATGGAGGCGGAT	5997
Db	1683	ACTGGCGAACTACTTACTCTAGCTTCCCGGCACAAATTAATAGACTGGAATGGAGGCGGAT	1624
Qy	5998	AAAGTTGACGAGCAACTTCTGCGCTCGGCCCTCCCGCTCGCTGGTGTATTGCTGATAAA	6057
Db	1623	AAAGTTGACGAGCAACTTCTGCGCTCGGCCCTCCCGCTCGCTGGTGTATTGCTGATAAA	1564
Qy	6058	TCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCAATTGCACACTGSGGCCAGATGTTAAG	6117
Db	1563	TCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCAATTGCACACTGSGGGCCAGATGTTAAG	1504
Qy	6118	CCCTCCCGTATCGTAGTTATCTACACGACGGGAGTCAGGCAACTATGGAATGAACGAAT	6177
Db	1503	CCCTCCCGTATCGTAGTTATCTACACGACGGGAGTCAGGCAACTATGGAATGAACGAAT	1444
Qy	6178	AGACAGATCGCTGAGATAGGTGCCCTCACTGATTAAGCAATTGGTAACTGTGACAGCCAA	6237
Db	1443	AGACAGATCGCTGAGATAGGTGCCCTCACTGATTAAGCAATTGGTAACTGTGACAGCCAA	1384
Qy	6238	TACTCATATATACCTTTAGATTGATTAAACCTCACTATTTTAAATTTTAAAGGATCTAGGTG	6297
Db	1383	TACTCATATATACCTTTAGATTGATTAAACCTCACTATTTTAAATTTTAAAGGATCTAGGTG	1324
Qy	6298	AAGATCCCTTTTGATATCTCATGACCAAAATCCCTTAAACGTCAGTTTTCGTTCCCACTGA	6357
Db	1323	AAGATCCCTTTTGATATCTCATGACCAAAATCCCTTAAACGTCAGTTTTCGTTCCCACTGA	1364
Qy	6358	GCCTCAGACCCCGTAGAAAAAGATCAAAAGGATCTTTCTTGAGATCCTTTTTTCTGCGCGTA	6417
Db	1263	GCCTCAGACCCCGTAGAAAAAGATCAAAAGGATCTTTCTTGAGATCCTTTTTTCTGCGCGTA	1204
Qy	6418	ATCTGCTGCTTGCAAAACAAAAAACACCCGTCACAGCGGTGTTGTTTTCGCGGATCAA	6477
Db	1203	ATCTGCTGCTTGCAAAACAAAAAACACCCGTCACAGCGGTGTTGTTTTCGCGGATCAA	1144
Qy	6478	GAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGCGCAGATACCAATACT	6537
Db	1143	GAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGCGCAGATACCAATACT	1084
Qy	6538	GTCCCTTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCCGCTACA	6597
Db	1083	GTCCCTTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCCGCTACA	1024
Qy	6598	TACTCGCTCTGTAAATCTGTTTACAGTGGCTGTGCCAGTGGCGGATTAAGTCGTGCTTT	6657
Db	1023	TACTCGCTCTGTAAATCTGTTTACCAAGTGGCTGTGCCAGTGGCGGATTAAGTCGTGCTTT	964
Qy	6658	ACCGGTTGCACTCAAGACGATAGTTACCGGATAAGCGCAGCGGTCCGGCTGAACGGGG	6717
Db	963	ACCGGTTGCACTCAAGACGATAGTTACCGGATAAGCGCAGCGGTCCGGCTGAACGGGG	904
Qy	6718	GGTTCGTGCACACAGCCCGAGCTTGGAGCGGAACGACCTTACACCGAACTGAGATACCTACAG	6777
Db	903	GGTTCGTGCACACAGCCCGAGCTTGGAGCGGAACGACCTTACACCGAACTGAGATACCTACAG	844
Qy	6778	CGTGAGCTATGAGAAAGCGCAACGCTTCCGAAAGGGAGAAAGCGGACAGGTATCCGGTA	6837

Db	843	CGTGAGCTATGAGAAACGCCACGCTTCCCGAAGGGGAGAAAGCGGACACGCTATCCGGTA	784
Qy	6838	AGCGGAGGGTCCGAAACAGGAGAGCGCACAGAGGAGCTTCCAGGGGAAACGCTCGTAT	6897
Db	783	AGCGGAGGGTCCGAAACAGGAGAGCGCACAGAGGAGCTTCCAGGGGAAACGCTCGTAT	724
Qy	6998	CTTTATAGTCCTGTCCGGTTTCGCCACCTCTGACTTTGAGCGTCAATTTTTGTGATGCTCG	6957
Db	723	CTTTATAGTCCTGTCCGGTTTCGCCACCTCTGACTTTGAGCGTCAATTTTTGTGATGCTCG	664
Qy	6958	TCAGGGGGCGGAGCCTATGGAAAGCGCCAGCAACGCGGGCCTTTTACGGTTCCTGGCC	7017
Db	663	TCAGGGGGCGGAGCCTATGGAAAGCGCCAGCAACGCGGGCCTTTTACGGTTCCTGGCC	604
Qy	7018	TTTTGCTGGCCTTTTGTCTCACATGTTCTTTCCCTGCGTTATCCCTGATTCCTGTGGATAAC	7077
Db	603	TTTTGCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCTGATTCCTGTGGATAAC	544
Qy	7078	CGTATTAACCGCTTTTGTAGTGAGCTGATACCGCTCGCGCAGCCGAAACGACCGAGCGCAGC	7137
Db	543	CGTATTAACCGCTTTTGTAGTGAGCTGATACCGCTCGCGCAGCCGAAACGACCGAGCGCAGC	484
Qy	7138	GAGTCAGTGAGCGGAGCGGAGAGCGGCCCAATAGCGAAACCGCCTCTCCCGCGCGT	7197
Db	483	GAGTCAGTGAGCGGAGCGGAGAGCGGCCCAATAGCGAAACCGCCTCTCCCGCGCGT	424
Qy	7198	TGGCCGATTCATTAATGCAGCTGGCAGCAGAGTTTCCCGACTGGAAAGCGGCGAGTGAG	7257
Db	423	TGGCCGATTCATTAATGCAGCTGGCAGCAGAGTTTCCCGACTGGAAAGCGGCGAGTGAG	364
Qy	7258	CGCAACGCAATTAATGTGAGTTACCTCACTCATTTAGSCACCCAGGCTTTTACACTTTATG	7317
Db	363	CGCAACGCAATTAATGTGAGTTACCTCACTCATTTAGSCACCCAGGCTTTTACACTTTATG	304
Qy	7318	CTTCCGGCTCGTATGTTGTGTGAAATGTGAGCGGATTAACAATTTACACAGGAAACAGC	7377
Db	303	CTTCCGGCTCGTATGTTGTGTGAAATGTGAGCGGATTAACAATTTACACAGGAAACAGC	244
Qy	7378	TATGACCATGATTACGCCAAGCGCGCA	7404
Db	243	TATGACCATGATTACGCCAAGCTTGCA	217
RESULT 5			
AAC87131/c			
ID	AAC87131 standard; DNA; 8941 BP.		
XX	AAC87131;		
AC	AAC87131;		
DT	20-APR-2001 (first entry)		
DE	Nucleotide sequence of plasmid pGB1025.		
XX	PDK2 gene; Caenorhabditis elegans; CEPDK2; polycystin; ADPKD;		
KW	autosomal dominant polycystic kidney disease; epithelial structure;		
KW	kidney nephron; circular; cyclic; ss.		
XX	Synthetic.		
OS	Aequorea victoria.		
OS	Caenorhabditis elegans.		
OS	Unidentified.		
XX	Key		
FT	Location/Qualifiers		
FT	1402..2259		
FT	/*tag= a		
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FT	7153..7891		
FT	/*tag= c		
FT	promoter		
FT	/*note= "PADH1 promoter"		
FT	7891..8331		
FT	CDS		

Qy	3119	AGCAAAATTTTCTGCTTTCGAAAGAGTAAAAATTTGTACTTTCGGCGGATTAATGCCTTTAGCGG	3178
Db	4458	TG-----CTTTTACAGACATTGAAATTTTCTTTGCAATAACGGGGTCAATTTGT	4411
Qy	3179	CTTAACTGTGCCCCCTCCATCGGAAATCAGTCAAGATATCCACATGTGTTTTTATTAGTAAACA	3238
Db	4410	TCTCTTTCTATTTGGGCACACATATATATACCCAGCAGTCAAGTACCGGAATCTTAG--AGCA	4353
Qy	3239	AAATTTTGGGACCTTAATGCTTCAACTAACTCCAGTAAATTCCTTTGGTGGTAC-GAACATCCA	3297
Db	4352	CATTCTCGGGCCTCTGTGCTCTGCAAGCGCAAACTTTTCCAAATGGACAGAACTACCT	4293
Qy	3298	ATGAAGACACAGAATTTGTTGCTTTTCTGTCGTCATGATATTTAAATAGCTTTGGCAGCAACAG	3357
Db	4292	GTGAAATTAATAAACAGACATACTCCAAGCTGCCCTTTGTGTCTTTAATCACTATACTCAC	4233
Qy	3358	GACTAGGATGAGTAGCAGCAGTTCCTTATATGTAGCTTTTCGACATGATTTAICTTCGTT	3417
Db	4232	GTGCTCAATAGTCAACCAATGCCCTCCCTCTTTGGGCCCTCTCC-----TTTTCCTTT	4184
Qy	3418	TCCTGCAAGGTTTTTGTCTGTGCACTTGGGTGTAAGATACTTGGGCAATTTTCATGTTTCTTT	3477
Db	4183	TTTTCGACCGAATTAATTTCTTAATCGGCCAAAAAAGAAAGCTCCGGA-----T	4136
Qy	3478	CAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTCTCTCTTCTGTTCTTCCT	3537
Db	4135	CAAGATTGTACGTAAGGTGACACAGCTATTTTCAATAAAGAAATATCTTCCACTACTGCCA	4076
Qy	3538	TCTGTTCCGGAGATTACCGAATCAAAAAATTTTCAAGAAACCGGAATCAAAAAAAGAAT	3597
Db	4075	TCTGGCGTCATACTGCAAAATGACACATATATTA-----CGATGCTGTCTATTAAAT	4024
Qy	3598	AAAAAAAATGATGAATTGAATTTGAAAGAGCTGTGGTATGGTGCACTCTCAGTACAAATCT	3657
Db	4023	GCTTCCTATATATATATATATAGTAAATGTGTGTGATCTATGGTGCACTCTCAGTACAAATCT	3964
Qy	3658	GCTCTGATGCGCATAGTTTAAGCAGCCCCGACACCCCGCAACCCCGCTGACGCGCCCT	3717
Db	3963	GCTCTGATGCGCATAGTTTAAGCAGCCCCGACACCCCGCAACCCCGCTGACGCGCCCT	3904
Qy	3718	GACGGGCTTGTCTGCTCCGGCATCCCGTTACAGACAAAGCTGTGACCGCTCTCCGGGAGCT	3777
Db	3903	GACGGGCTTGTCTGCTCCGGCATCCCGTTACAGACAAAGCTGTGACCGCTCTCCGGGAGCT	3844
Qy	3778	GCATGTCTCAGAGGTTTTTCCCGTCAATCCCGAAACGCGGAGACGAAAGGGCTCTGTGA	3837
Db	3843	GCATGTCTCAGAGGTTTTTCCCGTCAATCCCGAAACGCGGAGACGAAAGGGCTCTGTGA	3784
Qy	3838	TACGCTATTTTTTATAGGTTAATGTCAATGAATAATTAATGGTTTTCTTAGTATGATCCAAATAT	3897
Db	3783	TACGCTATTTTTTATAGGTTAATGTCAATGAATAATTAATGGTTTTCTTAATATGATCCAAATAT	3724
Qy	3898	CAAAAGGAATGATAGATTGAAGGATGAGACTAAATCCAAATTTGAGGAGTGGCAGCATATAG	3957
Db	3723	CAAAAGGAATGATAGATTGAAGGATGAGACTAAATCCAAATTTGAGGAGTGGCAGCATATAG	3664
Qy	3958	AACAGCTAAAGGGTAGTGCTGAAGGAAGCATACCATATCCCGCATGGAATGGGATATAT	4017
Db	3663	AACAGCTAAAGGGTAGTGCTGAAGGAAGCATACCATATCCCGCATGGAATGGGATATAT	3604
Qy	4018	CACAGGAGTACTAGACTACCTTTTCATCCCTACATAAAATAGACGCATATAAGTACGCATTTT	4077
Db	3603	CACAGGAGTACTAGACTACCTTTTCATCCCTACATAAATAGACGCATATAAGTACGCATTTT	3544
Qy	4078	AAGCATAAACACGCATATGCGGTTCTTCTCATGTATATATATATATACAGGCAACACGCAG	4137
Db	3543	AAGCATAAACACGCATATGCGGTTCTTCTCATGTATATATATATATACAGGCAACACGCAG	3484
Qy	4138	ATATAGGTGCGACGTGAACAGTAGTGAGCTGTAATGTCGCAGCTCCGGTTGCAATTTTCGGAAG	4197
Db	3483	ATATAGGTGCGACGTGAACAGTAGTGAGCTGTAATGTCGCAGCTCCGGTTGCAATTTTCGGAAG	3424
Qy	4198	CGCTCGTTTTTCGGAACCGCTTTTGAAGTTTCCTATTTCCGAAGTTTCTATTTCTTAGAAAGTA	4257

Db	3423		CGCTCGTTTTCGGAAACGCTTTGAAGTTCCTATTTCGGAAGTTCCTATTCTCTAGAAAGTA	3364
Qy	4258	TAGGAACCTTCAGAGCGCTTTTGAAGACCAAAAGCGCTCTGAAGACGCACCTTTTCAAAAAC	4317	
Db	3363	TAGGAACCTTCAGAGCGCTTTTGAAGACCAAAAGCGCTCTGAAGACGCACCTTTTCAAAAAC	3304	
Qy	4318	CAAAAACGCCACCGGACTGTAAACGAGCTACTAAATATATGCGAATACCGCTTCCACAAACA	4377	
Db	3303	CAAAAACGCCACCGGACTGTAAACGAGCTACTAAATATATGCGAATACCGCTTCCACAAACA	3244	
Qy	4378	TTGCTCAAAAGTATCTCTTGGCTATATATCTCTGTGTCTATATCCCTATATAAACCCTACCCA	4437	
Db	3243	TTGCTCAAAAGTATCTCTTGGCTATATATCTCTGTGTCTATATCCCTATATAAACCCTACCCA	3184	
Qy	4438	TCCACCTTTTCGCTCCTTGAACCTTGCACTCTAAACCTCGACCTCTACATTTTTTATGTTTTATC	4497	
Db	3183	TCCACCTTTTCGCTCCTTGAACCTTGCACTCTAAACCTCGACCTCTACATTTTTTATGTTTTATC	3124	
Qy	4498	TCTAGTATTACTCTTTAGACAAAAAATTTCTAGTAAGAACTATTTCATAGAGTGAATCGAA	4557	
Db	3123	TCTAGTATTACTCTTTAGACAAAAAATTTCTAGTAAGAACTATTTCATAGAGTGAATCGAA	3064	
Qy	4558	AACAATACGAAATGTATAACATTTCTTATACGTAGTATATAGAGACAAAAATAGAAAGAAC	4617	
Db	3063	AACAATACGAAATGTATAACATTTCTTATACGTAGTATATAGAGACAAAAATAGAAAGAAC	3004	
Qy	4618	CGTTCATAATTTCTTGACCAATGAAGAACTCATCAACGCTATCACTTCTCTGTTCCACAAAGT	4677	
Db	3003	CGTTCATAATTTCTTGACCAATGAAGAACTCATCAACGCTATCACTTCTCTGTTCCACAAAGT	2944	
Qy	4678	ATGCGCAATCCACATCGGTATAGAATAATAATCGGGATGCGCTTTATCTTGAAAAAATGCA	4737	
Db	2943	ATGCGCAATCCACATCGGTATAGAATAATAATCGGGATGCGCTTTATCTTGAAAAAATGCA	2884	
Qy	4738	CCGCGAGCTTCGCTAGTAATCAGTAAACGCGGGAAGTGGAGTCAAGGCTTTTTTTATGCGAA	4797	
Db	2883	CCGCGAGCTTCGCTAGTAATCAGTAAACGCGGGAAGTGGAGTCAAGGCTTTTTTTATGCGAA	2824	
Qy	4798	GAGAAATAGNACCAAAAGTAGCTTCTCTAACCTTAAACGGACCTACAGTGCAGAAAAGT	4857	
Db	2823	GAGAAATAGNACCAAAAGTAGCTTCTCTAACCTTAAACGGACCTACAGTGCAGAAAAGT	2764	
Qy	4858	TATCAAGAGACTGCATTATAGAGCGCACAAAGGAGAAAAAAGTAATCTAAGATGCTTTG	4917	
Db	2763	TATCAAGAGACTGCATTATAGAGCGCACAAAGGAGAAAAAAGTAATCTAAGATGCTTTG	2704	
Qy	4918	TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCTT	4977	
Db	2703	TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCTT	2644	
Qy	4978	TGTTGTTAAATAGCGCTCTCGGGTGCATTTCTGTCTCTGTAATAATGCAGCTCAGATT	5037	
Db	2643	TGTTGTTAAATAGCGCTCTCGGGTGCATTTCTGTCTCTGTAATAATGCAGCTCAGATT	2584	
Qy	5038	TTTCTTTTAAAAATATAGCGCTCTCGCGTTGCATTTTGTGTTTTTACAAAAATGAAGACAGA	5097	
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Qy	5098	TTCTTCGTTGGTAAAAATAGCGCTTCGCGTTGCATTTCTGTTCTGTAATAATGCAGCTCA	5157	
Db	2523	TTCTTCGTTGGTAAAAATAGCGCTTCGCGTTGCATTTTGTGTTTTTCTCAAAAATGAAGCA	2464	
Qy	5158	GATTCTTTGTTTGAANAATTAGCGCTCTCGGGTGCATTTTGTGTTTTTCTCAAAAATGAAGCA	5217	
Db	2463	GATTCTTTGTTTGAANAATTAGCGCTCTCGGGTGCATTTTGTGTTTTTCTCAAAAATGAAGCA	2404	
Qy	5218	CAGATGCTTCGTTTCAGGTGGCACTTTTTCGGGGAATGTCGCGGAAACCCCTATTGTTTA	5277	
Db	2403	CAGATGCTTCGTTTCAGGTGGCACTTTTTCGGGGAATGTCGCGGGAACCCCTATTGTTTA	2344	
Qy	5278	TTTTTCTAAATACAAATATGATCCGCTCATAGACAATAAACCCCTGATAAATGCTTT	5337	

Db 2343 TTTTCTAAATCATTTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTT 2284
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Db 1923 GATGCGATGACAGTAAAGAGATTTATGAGTGTGCTGCATTAACCATGAGTAAACACTGCG 1864
Qy 5758 GCCAATCTTCTGACAAACGATCGGAGGACCGAAGAGAGCTAAACCGCTTTTTCGACAAAC 5817
Db 1863 GCCAATCTTCTGACAAACGATCGGAGGACCGAAGAGAGCTAAACCGCTTTTTCGACAAAC 1804
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Qy 6118 CCTCCCGTATCGTAGTTATCTACACGACGGGAGCTCAGGCAACTATGATGATCAACGAAT 6177
Db 1503 CCTCCCGTATCGTAGTTATCTACACGACGGGAGCTCAGGCAACTATGATGATCAACGAAT 1444
Qy 6178 AGACAGATCGCTGAGATAGTGCCTCACTGATTAAGCAATGGTAACTCTGACAGCAAGTT 6237
Db 1443 AGACAGATCGCTGAGATAGTGCCTCACTGATTAAGCAATGGTAACTCTGACAGCAAGTT 1384
Qy 6238 TACTCATATATCTTATGATTTTAAACCTTCAATTTTAAAGGATCTAGTG 6297
Db 1383 TACTCATATATCTTATGATTTTAAACCTTCAATTTTAAAGGATCTAGTG 1324
Qy 6298 AAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAACGCTGAGTTTTCGTTCCACTGA 6357
Db 1323 AAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAACGCTGAGTTTTCGTTCCACTGA 1264
Qy 6358 GGTGACAGCCCGTGAAGAAAGATCAAGATCTTCTGAGATCCTTTTTCGCGCGTA 6417
Db 1263 GGTGACAGCCCGTGAAGAAAGATCAAGATCTTCTGAGATCCTTTTTCGCGCGTA 1204

Qy 6418 ATCTGCTGCTTGAAAAAACAACCAACCGCTACACGCGTGGTTTGTTCGCGGATCAA 6477
Db 1203 ATCTGCTGCTTGAAAAAACAACCAACCGCTACACGCGTGGTTTGTTCGCGGATCAA 1144
Qy 6478 GAGTACCAACTCTTTTCCGAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAAACT 6537
Db 1143 GAGTACCAACTCTTTTCCGAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAAACT 1084
Qy 6538 GTCCCTTCTAGTACCGGTAGTGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACA 6597
Db 1083 GTCCCTTCTAGTACCGGTAGTGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACA 1024
Qy 6598 TACCTCGCTCTGCTAACTCTGTTTACCACTGCTGCTGCTGCTGCTGCTGCTGCT 6657
Db 1023 TACCTCGCTCTGCTAACTCTGTTTACCACTGCTGCTGCTGCTGCTGCTGCT 964
Qy 6658 ACCGGTGGATCAAGACGATGTTACCGGATTAAGCGCAGCGCTCGGGTGAACGGG 6717
Db 963 ACCGGTGGATCAAGACGATGTTACCGGATTAAGCGCAGCGCTCGGGTGAACGGG 904
Qy 6718 GGTTCGTGACACAGCCAGCTTGGAGGGAACGCTTACACCGAACTGAGATACCTACG 6777
Db 903 GGTTCGTGACACAGCCAGCTTGGAGGGAACGCTTACACCGAACTGAGATACCTACG 844
Qy 6778 CGTGAGCTATGAGAAAGCGCCTTCCGAAAGGAGGAGGAGGAGGATATCCGTA 6837
Db 843 CGTGAGCTATGAGAAAGCGCCTTCCGAAAGGAGGAGGAGGAGGATATCCGTA 784
Qy 6838 AGCGCAGGCTCGGAAACAGGAGCGCAAGGAGCTTCCAGGGGGAACCGCTGGTAT 6897
Db 783 AGCGCAGGCTCGGAAACAGGAGCGCAAGGAGCTTCCAGGGGGAACCGCTGGTAT 724
Qy 6898 CTTTATAGTCTGCTGCGGTTTCGCCACTCTGACTGAGCGCTGATTTTGTGATGCTCG 6957
Db 723 CTTTATAGTCTGCTGCGGTTTCGCCACTCTGACTGAGCGCTGATTTTGTGATGCTCG 664
Qy 6958 TCAGGGGGGCGGAGCTTATGGAAGAAACGCGCAACCGCGGCTTTTACGGTTCTCGGCC 7017
Db 663 TCAGGGGGGCGGAGCTTATGGAAGAAACGCGCAACCGCGGCTTTTACGGTTCTCGGCC 604
Qy 7018 TTTTGTGCGCTTTTGTCTACATGTTCTTCTCTGCTGCTTATCCCTGATTTCTGTGATAC 7077
Db 603 TTTTGTGCGCTTTTGTCTACATGTTCTTCTCTGCTGCTTATCCCTGATTTCTGTGATAC 544
Qy 7078 GGTATTAACCGCTTTGAGTGAAGTATACCGCTCGCGCAGCGCAACGAGCGGCGAGC 7137
Db 543 GGTATTAACCGCTTTGAGTGAAGTATACCGCTCGCGCAGCGCAACGAGCGGCGAGC 484
Qy 7138 GAGTCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7197
Db 483 GAGTCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 424
Qy 7198 TGGCCGATTCATTAATCAGCTGCAAGAGTTTCCGATCTGGAAGCGGGGAGTGAAG 7257
Db 423 TGGCCGATTCATTAATCAGCTGCAAGAGTTTCCGATCTGGAAGCGGGGAGTGAAG 364
Qy 7258 CGCAACGCAATTAATGAGTTACTCACTTATGAGCAGCGGCTTACCTTTATG 7317
Db 363 CGCAACGCAATTAATGAGTTACTCACTTATGAGCAGCGGCTTACCTTTATG 304
Qy 7318 CTTCCGCTCTCTATGTTGTGGAAATGTGAGCGGATTAACAAATTTTCAACAGGAAACAGC 7377
Db 303 CTTCCGCTCTCTATGTTGTGGAAATGTGAGCGGATTAACAAATTTTCAACAGGAAACAGC 244
Qy 7378 TATGACCATGATTAACGCAAGCGGCA 7404
Db 243 TATGACCATGATTAACGCAAGCGGCTTGA 217

RESULT 6
AAC90958/c
ID AAC90958 standard; cdna; 9700 BP.

XX AAC90958;
 XX 19-MAR-2001 (first entry)
 XX Plasmid pGC1037 nucleotide sequence SEQ ID NO:91.
 XX Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
 XX protein-protein interaction; identification; ss.
 XX Synthetic.
 XX WO200073328-A2.
 XX 07-DEC-2000.
 XX 02-JUN-2000; 2000WO-EP005108.
 XX 01-JUN-1999; 99GB-00012755.
 XX (DEVG-) DEVGEN NV.
 XX Van Criekeinge W, Roelens I, Bogaert T, Verwaerde P;
 XX WPI; 2001-016508/02.
 XX Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
 XX human unc-5Hs1 cDNA, useful in yeast two hybrid experiments for
 XX identifying unknown human cDNAs which encode proteins that interact with
 XX the human unc-5C protein.
 XX Example 4; Page 228-230; 246pp; English.
 XX The present invention describes 3 variants of human unc-5C cDNAs (unc-
 XX 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
 XX 5C transcripts, and a human unc-5Hs1 cDNA which shares homology with the
 XX Rattus norvegicus unc-5Hs1 cDNA. Also described are assays based on
 XX protein-protein-interactions between the unc-5 protein and a variety of
 XX different interacting proteins. The unc-5C variant cDNAs and unc-5Hs1
 XX cDNA are useful in methods for identifying compounds which reduce or
 XX inhibit the lethal phenotype associated with the expression of the unc-5
 XX death domain in yeast. They are also useful in yeast two hybrid
 XX experiments for identifying unknown human cDNAs which encode proteins
 XX that interact with the human unc-5C protein. AAC90914 to AAC90971 and
 XX AAB50646 to AAB50693 represent sequences used in the exemplification of
 XX the present invention
 XX Sequence 9700 BP; 2604 A; 2193 C; 2236 G; 2666 T; 0 U; 1 Other;
 XX
 XX Query Match 57.4%; Score 4492.6; DB 4; Length 9700;
 XX Best Local Similarity 87.3%; Pred. No. 0;
 XX Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
 XX
 XX 1559 TCATGTAATTAGTATGTACGGTTACATTCACGGCTCCGCCACATCGGCTCTAACCG 1618
 XX 7263 TCATGTAATTAGTATGTACGGTTACATTCACGGCTCCGCCACATCGGCTCTAACCG 7204
 XX 1619 AAAAGGAAGGAGTTAGACACACCTGAAGTCTAGCTCCCTATTTATTTTATAGTTATGT 1678
 XX 7203 AAAAGGAAGGAGTTAGACACACCTGAAGTCTAGCTCCCTATTTATTTTATAGTTATGT 7144
 XX 1679 TAGTATTAAAGACGTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGGGTGT 1738
 XX 7143 TAGTATTAAAGACGTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGGGTGT 7084
 XX 1739 ACCATGTATACATATATCTGAAACCTTGTCTGAGAGGTTTGGGACCGCTCGAAGCTT 1798
 XX 7083 ACGCATGTATACATATATCTGAAACCTTGTCTGAGAGGTTTGGGACCGCTCGAAGCTT 7024
 XX 1799 TAATTTGGCGCGGTACCCCAATTCGCCCTATAGTATAGTATGATCGGCGCTCACTGGC 1858
 XX 7023 TAATTTG-----CAAAGCTCGGGATCTCGAGCTCGCGAAAGCTTGGACGACTGGC 6974
 XX
 QY 1859 CGTCGTTTTCACACGTCGTGACCTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCCTTGC 1918
 DB 6973 CGTCGTTTTCACACGTCGTGACCTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCCTTGC 6914
 QY 1919 AGCACATCCCTTTTCGCGAGCTGGCGTAATAGCGAGAGGCGCGACCGATCGCCCTTC 1978
 DB 6913 AGCACATCCCTTTTCGCGAGCTGGCGTAATAGCGAGAGGCGCGACCGATCGCCCTTC 6854
 QY 1979 CCAACAGTTTGGCAGCCTGAATGGCGAATGGCGCGACCGCTGTAGCGCGCATTAAG 2038
 DB 6853 CCAACAGTTTGGCAGCCTGAATGGCGAATGGCGCGACCGCTGTAGCGCGCATTAAG 6794
 QY 2039 CGCGCGGGTGTGGTGTACGCGAGCGTACCGCTACACTTTGCGAGCGCCCTAGCGCC 2098
 DB 6793 CGCGCGGGTGTGGTGTACGCGAGCGTACCGCTACACTTTGCGAGCGCCCTAGCGCC 6734
 QY 2099 CGCTCCTTTTCGCTTCTTCCCTTCTCCCTTCTCGCACGTTGCGCGGCTTTCCCGCTCAAGC 2158
 DB 6733 CGCTCCTTTTCGCTTCTTCCCTTCTCCCTTCTCGCACGTTGCGCGGCTTTCCCGCTCAAGC 6674
 QY 2159 TCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAA 2218
 DB 6673 TCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAA 6614
 QY 2219 AAAAATTGATAGGTGATGGTTACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCG 2278
 DB 6613 AAAAATTGATAGGTGATGGTTACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCG 6554
 QY 2279 CCCTTTGAGTTGGAGTCCACGTTCTTTTAAATAGTGAACCTTGTTCGAACTCGAACAC 2338
 DB 6553 CCCTTTGAGTTGGAGTCCACGTTCTTTTAAATAGTGAACCTTGTTCGAACTCGAACAC 6494
 QY 2339 ACTCAACCTATCTCGGTCTATTCTTTTGAATTTAAGGATTTTGCCTGATTTGGGCTA 2398
 DB 6493 ACTCAACCTATCTCGGTCTATTCTTTTGAATTTAAGGATTTTGCCTGATTTGGGCTA 6434
 QY 2399 TTGGTTAAAAAATAGCTGATTTAAACAAAAATTTAAACGGAAATTTTAAACAAAAATTTAAC 2458
 DB 6433 TTGGTTAAAAAATAGCTGATTTAAACAAAAATTTAAACGGAAATTTTAAACAAAAATTTAAC 6374
 QY 2459 GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGATCTGCGGTATTTTACACCGC 2518
 DB 6373 GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGATCTGCGGTATTTTACACCGC 6314
 QY 2519 ATAGGTAATAACTGATATAATTTAAATTTGAAGTCTTAAATTTGTGAGTTAGTATACATGC 2578
 DB 6313 ATAGATCGGCAAGTGACAAACAATACTTAAATAATACTACTCAGTAATAACTATTTC 6254
 QY 2579 ATTTACTTATAATACAGTTTTTTTGTGTTGTTGCGCGCATCTTCTCAAAATATGCTTCCCA 2638
 DB 6253 TTAGCATTTTTCACGAAATTTTGTCTATTTTGTAGAGTCTTTTACACCAATTTGTCTCCACA 6194
 QY 2639 GCCTGCTTTTCTGTAACGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTTGCATATAGTCC 2698
 DB 6193 CCTCCGCTTACATCAAC-----ACCAATAACGC 6166
 QY 2699 TCTTCCAAACAATAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2758
 DB 6166 CATTTAATCTAAGCGCATCACCAACATTTTCTGGGCTGATGATGATGATGATGATGATGATG 6106
 QY 2759 TTGACCCAAATGCTCTCCCTTGTCTATTAACCCACACCGGGGTGTCTATTAACCAATC 2818
 DB 6105 GTAAGCTTTTCGGGGCTCTCTTGGCTT-----CCAAACCCAGTCAAGAAATCGAGTTCCAATC 6051
 QY 2819 GTAAACCTTCTCTCTTCCACCCATGTCTTTTGGAGCAATAAAGCCGATTAACAAATCTTT 2878
 DB 6050 CAAAAGTTTCACTGTCTCCAC-----CTGCTTCTGAAATCAAAACAGGGAATTAACGAATG 5997
 QY 2879 GTGCTCTTTTCGCAATGTCAACAGTACCTTGTATATTTCTTCTAGTATAGTATAGGAGCCCTT 2938
 DB 5996 AGGTTTCTGTGAAGCTGCTGAGTATGTTGAGTCTTTTGGAAATACGAGTCTTTT 5937
 QY 2939 GCATGAATACTGTCTAACATCAAAAGGCTCTAGGTTCTTCTTGTCTTCTTCTTCTCCGC 2998


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Db      1616  CTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATTAACAATTTCCACAGGAACAGC 1557
QY      7378  TATGACCATGATTACGCCAAGCGCCA 7404
Db      1556  TATGACCATGATTACGCCAAGCTTGCA 1530

RESULT 7
AAC90959/c
ID      AAC90959 standard; cDNA; 9749 BP.
AC      AAC90959;
XX
XX
DT      19-MAR-2001 (first entry)
XX
XX      Plasmid pGC1003 nucleotide sequence SEQ ID NO:92.
DE
XX      Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
KW      protein-protein interaction; identification; ss.
XX
XX      Synthetic.
XX
XX      WO200073328-A2.
PN
XX      07-DEC-2000.
PD
XX
XX      02-JUN-2000; 2000WO-EP005108.
PF
XX
XX      01-JUN-1999; 99GB-00012755.
PR
XX
XX      (DEVG-) DEVGEN NV.
PA
XX
XX      Van Criekeinge W, Roelens I, Bogaert T, Verwaerde P;
PI      WPI; 2001-016508/02.
DR
XX
XX      Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
PT      human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
PT      identifying unknown human cDNAs which encode proteins that interact with
PT      the human unc-5C protein.
XX
XX      Example 4; Page 231-233; 246pp; English.
PS
XX
XX      The present invention describes 3 variants of human unc-5C cDNAs (unc-
CC      5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
CC      5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
CC      Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
CC      protein-protein-interactions between the unc-5 protein and a variety of
CC      different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
CC      cDNA are useful in methods for identifying compounds which reduce or
CC      inhibit the lethal phenotype associated with the expression of the unc-5
CC      death domain in yeast. They are also useful in yeast two hybrid
CC      experiments for identifying unknown human cDNAs which encode proteins
CC      that interact with the human unc-5C protein. AAC90914 to AAC90971 and
CC      AAB50646 to AAB50693 represent sequences used in the exemplification of
CC      the present invention
XX
SQ      Sequence 9749 BP; 2764 A; 2006 C; 2176 G; 2802 T; 0 U; 1 Other;

Query Match      57.4%; Score 4492.6; DB 4; Length 9749;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

QY      1559  TCATGTAATTAGTTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 1618
Db      8560  TCATGTAATTAGTTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 8501
QY      1619  AAAAGGAGGAGCTTAGACAACTGAAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 1678
Db      8500  AAAAGGAGGAGCTTAGACAACTGAAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 8441
QY      1679  TAGTATTAGAACGTTATTATATATTTCAAATTTTCTTTTCTTTCTGTGACAGCGCGTGT 1738

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Db      8440  TAGTATTAGAACGTTATTATATATTTCAAATTTTCTTTTCTGTGACAGCGGTGT 8381
QY      1739  ACGCATGTAACTATATATCTGAACCTTGTGTGAGAGGTTTGGGAGCTCGAAGGCTT 1798
Db      8380  ACGCATGTAACTATATATCTGAACCTTGTGTGAGAGGTTTGGGAGCTCGAAGGCTT 8321
QY      1799  TAATTTGCGGCGGTACCCCAATTCGCCCTATAGTGAGTCGTATTACGGCGCTCACTGGC 1858
Db      8320  TAATTTG-----CAAAGCTCGGGAATCTGAGCTCGGGAAGCTTGGACGACTGGC 8271
QY      1859  CGTCGTTTTTAAACGCTGCTGATCGGGAACCTCTGGCGTTTACCCAACTTAATTCGCTTGC 1918
Db      8270  CGTCGTTTTTAAACGCTGCTGATCGGGAACCTCTGGCGTTTACCCAACTTAATTCGCTTGC 8211
QY      1919  AGCACATCCCGCTTTTCGCCAGCTGGCGTAATAGCGAAGAGCGCCGACGATCGCCCTTC 1978
Db      8210  AGCACATCCCGCTTTTCGCCAGCTGGCGTAATAGCGAAGAGCGCCGACGATCGCCCTTC 8151
QY      1979  CCAACAGTTGCGCAGCTGTAATGCGGAATGCGCGAGCGCCCTGTAGCGGCGCAATTAAG 2038
Db      8150  CCAACAGTTGCGCAGCTGTAATGCGGAATGCGCGAGCGCCCTGTAGCGGCGCAATTAAG 8091
QY      2039  CGCGCGGGTGTGTGTTTACGCGCAGCGTGACCGCTACACTTGCACGCGCCCTAGCGCC 2098
Db      8090  CGCGCGGGTGTGTGTTTACGCGCAGCGTGACCGCTACACTTGCACGCGCCCTAGCGCC 8031
QY      2099  CGCTCCTTTTCGCTTTCTTCCCTTCTTCGCCACAGTTTCGCCGCTTTCCCGCTCAAGC 2158
Db      8030  CGCTCCTTTTCGCTTTCTTCCCTTCTTCGCCACAGTTTCGCCGCTTTCCCGCTCAAGC 7971
QY      2159  TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTTACGGCACCTCGACCCCAA 2218
Db      7970  TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTTACGGCACCTCGACCCCAA 7911
QY      2219  AAAACTTTGATTAGGGTGTGATGTTTACGCTAGTGGGCCATTCGCCCTGTATAGACGGTTCG 2278
Db      7910  AAAACTTTGATTAGGGTGTGATGTTTACGCTAGTGGGCCATTCGCCCTGTATAGACGGTTCG 7851
QY      2279  CCCTTTGACGTTGGAGTCCAGCTTCTTTAATAGTGGACTCTTGTTCGAACCTGGGAACAC 2338
Db      7850  CCCTTTGACGTTGGAGTCCAGCTTCTTTAATAGTGGACTCTTGTTCGAACCTGGGAACAC 7791
QY      2339  ACTCAACCCCTATCTCGGTCTATTCTTTTATTAAGGGATTTTTCGCGATTTTCGCGCTTA 2398
Db      7790  ACTCAACCCCTATCTCGGTCTATTCTTTTATTAAGGGATTTTTCGCGATTTTCGCGCTTA 7731
QY      2399  TTGTTTAAAAAATGAGCTGATTTTAAACAAAAATTTAAACGCGAATTTTAAACAAATATTAC 2458
Db      7730  TTGTTTAAAAAATGAGCTGATTTTAAACAAAAATTTAAACGCGAATTTTAAACAAATATTAC 7671
QY      2459  GTTTTACAAATTTCCGATCGCGTATTCTCTTACGCACTGTGCGGTATTTTCACACCGC 2518
Db      7670  GTTTTACAAATTTCCGATCGCGTATTCTCTTACGCACTGTGCGGTATTTTCACACCGC 7611
QY      2519  ATAGGTAATAACCTGATATATAATTAATTAAGAGCTCTAATTTGTGAGTTTAGTATACATGC 2578
Db      7610  ATAGATCGGCAAGTGCAACAACATACTTAATAATACTACTCAGTAATAACCTATTTC 7551
QY      2579  ATTTACTTATAATACAGTTTATTTAGTTTGTGCGCGCATCTTCTCAAAATATGCTTCCCA 2638
Db      7550  TTAGCATTTTGTAGCAAAATTTGCTATTATTGTTAGAGTCTTTTACACCATTTTGTCTCCCA 7491
QY      2639  GCCTGCTTTTCTGTAAAGTTTACCCCTCTACCTTAGCATCCCTTCCCTTTGGAAATAGTCC 2698
Db      7490  CCTCCGCTTACATCAAC-----ACCAATAACGC 7463
QY      2699  TCTTCCAAACATAATAATGTGAGATCTGTAGAGACCAATCATCATCGGTTCTATACATG 2758
Db      7462  CATTTAATCTAAGCGCATCAACAATTTCTGGCGTCAGTCCACAGCTAACATAAAT 7403
QY      2759  TTGACCAATGCGGTCTCCCTTGTGTCATCTAAACCCACACCGGGTGTCAATTAATCAACAATC 2818

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Db 7402 GTAAAGCTTTGGGGCTCTCTTGGCTT-----CCAAACCCAGTCAGAAATCGAGTTCCAAATC 7348
Qy 2819 GTAAACCTTCATCTCTTCCACCCATGTCTCTTTGAGCAATAAAGCCGTAACAATAATCTTT 2878
Db 7347 CAAAAGTTTCACTGTGCCAC-----CTGCTTCTGAATCAAAACAAGGGAATAAAGCAATG 7294
Qy 2879 GTGGCTTTCCGAATGTCAACAGTACCCCTTAGTATATTTCCAGTAGATAGGAGGCCCTT 2938
Db 7293 AGGTTTCTGTGAAGCTGCACTGAGTAGATGTTGCAAGTCTTTTGGAAATACGAGTCTTTT 7234
Qy 2939 GCATGACAAATCTGTCTAAACATCAAAAGCCCTCTAGGTTCCTTTGTTACTTCTTCTGCGCG 2998
Db 7233 -----ATAACTGCAACCGAGGAATCTCTGGTATTTCTTGGCCAGACTCATCTCCA 7182
Qy 2999 CTGCTTCAAAACCGCTAAACAATCCTGGGCCCAACACACCGGTGCAATTCGTATGTCTGC 3058
Db 7181 TGCAGT-----TGGAGCATATCAATGCGGTAACTCATTGACAGAGCCAAACATCCTC 7129
Qy 3059 CCATCTGCTATCTGTATACACCGCGAGAGTACTGCAATTTGACTGTATATACCAATGTC 3118
Db 7128 CTTAGGTTGATTACGAACACGCGCAACCAAGTATTTTCGGAGTGCCTGAACTATTTTATA 7069
Qy 3119 AGCAAAATTTCTGTCTTTCGAAGAGTAAATAATTTGACTTTCGCGGATAATGCTTTAGCGG 3178
Db 7068 TG-----CTTTAAGACTTGAATTTTCTTGGCAATACCGGGTCAATGT 7021
Qy 3179 CTTAACTGTGCCCTCCATGGAAATCAGTCAAGATATCACATGTGTTTTTATAGTAAACA 3238
Db 7020 TCTCTTCTATTTGGGCACACATATAATACCAGCAAGTCAGCATCGGAATCTAG--AGCA 6963
Qy 3239 AATTTGGGACCTAAAGCTTCAACTAACTCCAGTAATCTCTGGTGGTAC-GAAACATCCA 3297
Db 6962 CATTTGCGGCCTCTGTGCTCTGCAAGCGCAAACTTTTCCAAATGGAACCAAGTACCT 6903
Qy 3298 ATGAAGCACACAAGTTTGTGCTTTTTCGTCATGATATTAATAGCTTTCGCGCAACAG 3357
Db 6903 GTGAAATTAATACAGACATCTCCAAAGCTGCTTTGTGCTTATACGATATCTAC 6843
Qy 3358 GACTAGGATGAGTACGACAGCTTCTTATATGTAGTCTTCGACATGATTTATCTCGTT 3417
Db 6842 GTGCTCAATAGTCACCAATGCCCTCCCTCTTGGCCCTCTCC-----TTTCTTTT 6794
Qy 3418 TCCTGCAAGTTTTTGTCTGTGAGTTGGGTTAAGAAATCTGGGCAATTTTCATGTTCTTT 3477
Db 6793 TTTTCGACCGAAATTAATTTCTTAATCGGCAGAAAAAGAAAGCTCCGGA-----T 6746
Qy 3478 CAACACTACATATGCGTATATATACCAATCTAAGTCTGTCTCTCTCTCTCTCTCTCT 3537
Db 6746 CAAGATTGTCGAAGTGCAAGCTATTTTCAATAAAGAAATCTTCCACTACTGCCA 6686
Qy 3538 TCTGTTCCGAGATTACCGAATCAAAAAATTTTCAAGAAACCGAAATCAAAAAAGAAAT 3597
Db 6685 TCTGGCGTCATACTGCAAGTACACATATTA-----CGATGCTGCTCTATTAAAT 6634
Qy 3598 AAAAAAATATGATTAATGAAATGAAAGCTGTGATGGTGACCTCTCAGTACAACTCT 3657
Db 6633 GCTTCTTATATATATATATAGTAATGTCGTTGATCTATGGTGCACTCTCAGTACAACTCT 6574
Qy 3658 GCTCTGATGCGCATAGTTAAGCCAGCCCGACACCGCCCAACACCGCTGACCGGCCCT 3717
Db 6573 GCTCTGATGCGCATAGTTAAGCCAGCCCGACACCGCCCAACACCGCTGACCGGCCCT 6514
Qy 3718 GAGGGCTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGCTCTCCGGGAGCT 3777
Db 6513 GACGGCTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGCTCTCCGGGAGCT 6454
Qy 3778 GCATGTGTACAGGTTTTCAACCGTATCAACCGAAACCGCGGAGACGAAAGGGCTCTGTGA 3837
Db 6453 GCATGTGTACAGGTTTTCAACCGTATCAACCGAAACCGCGGAGACGAAAGGGCTCTGTGA 6394
Qy 3838 TAGCCCTATTTTATAGTTAATGTCATGATATATGTTTCTTAGTATGATCCCAATAT 3897
Db 6393 TAGCCCTATTTTATAGTTAATGTCATGATATATGTTTCTTATATATGATCCCAATAT 6334

Qy 3898 CAAAGAAATGATAGCAATTGAAGATGAGACTAATCAAATTGAGGAGTGGCAGCATATAG 3957
Db 6333 CAAAGAAATGATAGCAATTGAAGATGAGACTAATCAAATTGAGGAGTGGCAGCATATAG 6274
Qy 3958 ACAGCTAAAGGGTAGTGTGAGGAAGCATACGATACCCCGCATCGGAATGGGATATAT 4017
Db 6273 ACAGCTAAAGGGTAGTGTGAGGAAGCATACGATACCCCGCATCGGAATGGGATATAT 6214
Qy 4018 CACAGAGGTACTAGACTACCTTTTCATCTCTACATAAATAGACCATATAGTAGTCGCAATT 4077
Db 6213 CACAGAGGTACTAGACTACCTTTTCATCTCTACATAAATAGACCATATAGTAGTCGCAATT 6154
Qy 4078 AGCATAAACACGCACTATGCGCTTCTCTCATGTATATATATACAGCAACACGCAAG 4137
Db 6153 AGCATAAACACGCACTATGCGCTTCTCTCATGTATATATATACAGCAACACGCAAG 6094
Qy 4138 ATATAGTGGAGGTGAACAGTGAGCTGTATGTGCGCAGCTCGCGTTGCAATTTTCGGAAG 4197
Db 6093 ATATAGTGGAGGTGAACAGTGAGCTGTATGTGCGCAGCTCGCGTTGCAATTTTCGGAAG 6034
Qy 4198 CGCTCGTTTTCGGAAACGCTTTTGAAGTTCCTATTTCGAAAGTTCCTATTCTCTAGAAAGTA 4257
Db 6033 CGCTCGTTTTCGGAAACGCTTTTGAAGTTCCTATTTCGAAAGTTCCTATTCTCTAGAAAGTA 5974
Qy 4258 TAGGAACTTCAGAGCGCTTTTGAACACCAAAAGCGCTCTGAAAGCAGCACTTTCAAAAAAC 4317
Db 5973 TAGGAACTTCAGAGCGCTTTTGAACACCAAAAGCGCTCTGAAAGCAGCACTTTCAAAAAAC 5914
Qy 4318 CAAAAACGCGGACGTGAACAGGCTACTAAATATTCGGAATTCGCGTTCCACAACA 4377
Db 5913 CAAAAACGCGGACGTGAACAGGCTACTAAATATTCGGAATTCGCGTTCCACAACA 5854
Qy 4378 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTATATCTCTGCTATATCCCTATATACTACCCA 4437
Db 5853 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTATATCTCTGCTATATCCCTATATACTACCCA 5794
Qy 4438 TCCACTTTTGGCTCTTGAACCTTGCATCTAAACTCGAACCTCTACATTTTATGTTTATC 4497
Db 5793 TCCACTTTTGGCTCTTGAACCTTGCATCTAAACTCGAACCTCTACATTTTATGTTTATC 5734
Qy 4498 TCTAGTATTACTCTTTTAGCAAAAAAATTTGTAGTAGAAGTATTCATAGTGAATCGAA 4557
Db 5733 TCTAGTATTACTCTTTTAGCAAAAAAATTTGTAGTAGAAGTATTCATAGTGAATCGAA 5674
Qy 4558 AACATACGAAATGTAACATTTCTTACGTAAGTATATAGAGACAAATATAGAGAAC 4617
Db 5673 AACATACGAAATGTAACATTTCTTACGTAAGTATATAGAGACAAATATAGAGAAC 5614
Qy 4618 CGTTCATAATTTTTCGACCAATGAAGAATCATCAACGCTATCATCTTCTGTTTCAAAAGT 4677
Db 5613 CGTTCATAATTTTTCGACCAATGAAGAATCATCAACGCTATCATCTTCTGTTTCAAAAGT 5554
Qy 4678 ATGCGCAATCCCATCGGTATAGATAATTAATCGGGATGCTTTTATCTTGAATAATGCA 4737
Db 5553 ATGCGCAATCCCATCGGTATAGATAATTAATCGGGATGCTTTTATCTTGAATAATGCA 5494
Qy 4738 CCGCAGCTTTGCTAGTAAATCAGTAAACGCGGAAGTGGAGTCAGGCTTTTTTATCGAA 4797
Db 5493 CCGCAGCTTTGCTAGTAAATCAGTAAACGCGGAAGTGGAGTCAGGCTTTTTTATCGAA 5434
Qy 4798 GAGAAATAGACACCAAGTAGCTTTCTTCTTAACTTAACTTAACTTAACTTAACTTAACTT 4857
Db 5433 GAGAAATAGACACCAAGTAGCTTTCTTCTTAACTTAACTTAACTTAACTTAACTTAACTT 5374
Qy 4858 TATCAAGAGCTCATTTATAGCGGCACAAAGAGAAAAAAGTAATCTAGATGCTTTG 4917
Db 5373 TATCAAGAGCTCATTTATAGCGGCACAAAGAGAAAAAAGTAATCTAGATGCTTTG 5314
Qy 4918 TTAGAAAAATAGCGCTCTCGGATGCAATTTTCTAGAAACAAAAAAGATATAGATCTTT 4977
Db 5313 TTAGAAAAATAGCGCTCTCGGATGCAATTTTCTAGAAACAAAAAAGATATAGATCTTT 5254

Db 3093 GAGTCAGTGACGAGGAGCGAAGAGCGCCCAATACGAAACCGCCTCTCCCGCGCGT 3034
 Qy 7198 TGGCCGATTCAATATCCAGCTGCGACGACAGAGTTTCCCGACTGGAAAGCGGCGAGTGAG 7257
 Db 3033 TGGCCGATTCAATATCCAGCTGCGACGACAGAGTTTCCCGACTGGAAAGCGGCGAGTGAG 2974
 Qy 7258 CGCAGCCCAATTAATGTAGTTACCTCACTCATTTAGGCACCCCGAGGCTTTACACTTTATG 7317
 Db 2973 CGCAACGCAATTAATGTAGTTACCTCACTCATTTAGGCACCCCGAGGCTTTACACTTTATG 2914
 Qy 7318 CTTCCGGCTCTATGTTGTGTGGAAATGTGAGCGGATAACAAATTTACACAGAAACAGC 7377
 Db 2913 CTTCCGGCTCTATGTTGTGTGGAAATGTGAGCGGATAACAAATTTACACAGAAACAGC 2854
 Qy 7378 TATGACCATGATTACGCCAAGCGCGCA 7404
 Db 2853 TATGACCATGATTACGCCAAGCTTGCA 2827

RESULT 8

AAT71322/c
 ID AAT71322 standard; DNA; 10288 BP.
 XX AC AAT71322;
 XX DT 11-SEP-1997 (first entry)
 XX DE Plasmid pCB51 encoding partial UNC-53 protein used as bait vector.
 XX KW UNC-53; neuronal regeneration; revascularisation; wound healing;
 KW neurodegenerative disease; Alzheimer's disease; Huntington's;
 KW peripheral neuropathies; metastasis inhibition; cancer; circular;
 KW Caenorhabditis elegans; ds.
 XX OS Synthetic.
 XX W09638555-A2.
 XX 05-DEC-1996. 96WO-EP002311.
 XX 31-MAY-1996; 95GB-00010944.
 XX 31-MAY-1995; 95GB-00010944.
 XX (BOGA/) BOGAERT T.
 XX (STRI/) STRINGHAM E.
 XX (VAND/) VANDEKERCKHOVE J.

Bogaert T, Stringham E, Vandekerckhove J;
 WPI; 1997-034369/03.

Caenorhabditis elegans UNC-53 protein 8A and 7A variants - useful to
 promote neuronal regeneration, revascularisation or wound healing.

Example 15; Page 139-145; 278pp; English.

AAT71321 and AAT71322 are plasmids pCB50 and pCB51, respectively. They
 are used as bait vectors in a yeast two hybrid system. pCB50 encodes the
 full length UNC-53 protein variant 7A of Caenorhabditis elegans and pCB51
 encodes a C-terminal portion of this protein. Both vectors were
 constructed by cloning the appropriate cDNA fragment into pAS1-CYH2
 (Clontech). The yeast two hybrid system was set up for identifying
 proteins that interact with UNC-53. UNC-53 protein 8A and 7A variants and
 nucleic acids encoding them are useful as medicaments to promote neuronal
 regeneration, revascularisation or wound healing, or for treatment of
 chronic neurodegenerative diseases (e.g. Alzheimer's or Huntington's
 disease) or acute traumatic injuries. Transgenic cells and organisms
 transfected with UNC-53 cDNA can be used to determine whether a substance
 is an inhibitor or enhancer of the regulation of cell shape or motility
 or the direction of cell migration by screening for a phenotypic change
 in the cell. Inhibitors can be used to alleviate the spread of disease
 inducing cells or metastasis. Probes derived from the cDNA sequences can

CC be used to identify homologues of the C. elegans unc-53 gene. The UNC-53
 CC protein can be used to identify proteins which are active in the signal
 CC transduction pathway that can be used as mentioned above
 XX
 SQ Sequence 10288 BP; 2909 A; 2218 C; 2242 G; 2918 T; 0 U; 1 Other;

Query Match 57.4%; Score 4492.6; DB 2; Length 10288;
 Best Local Similarity 87.3%; Pred. No. 0;
 Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

Qy 1559 TCATGTAAATTTAGTTATGTCAACGCTTACATTTACGCGCTCCCGCCACATCCGCTCTAACCG 1618
 Db 7878 TCATGTAAATTTAGTTATGTCAACGCTTACATTTACGCGCTCCCGCCACATCCGCTCTAACCG 7819
 Qy 1619 AAAAGGAAGGAGTTAGACAACTGAAGTCTAGTCCCTATTTATTTTATATAGTTATGT 1678
 Db 7818 AAAAGGAAGGAGTTAGACAACTGAAGTCTAGTCCCTATTTATTTTATATAGTTATGT 7759
 Qy 1679 TAGTATTAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTTTCTGTACAGACGCGTGT 1738
 Db 7758 TAGTATTAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTTTCTGTACAGACGCGTGT 7699
 Qy 1739 ACGCATGTAAACATTATCTGAAACCTTGTCTGAGAAGGTTTGGGACGCTCGAAGGCTT 1798
 Db 7698 ACGCATGTAAACATTATCTGAAACCTTGTCTGAGAAGGTTTGGGACGCTCGAAGGCTT 7639
 Qy 1799 TAATTTGGCGCGGTATCCCAATTTGCGCCTATATAGTGTGATTTATTCGCGCGCTCACTGGC 1858
 Db 7638 TAATTTG-----CAAAAGCTCGGATCTCGAAGCTTCGGAAGCTTCGACGACTGGC 7589
 Qy 1859 CGTCGTTTACAACGCTGTGACCTGGGAAACCCCTGGGTTTACCGAACTTAAATGCGCTTGC 1918
 Db 7588 CGTCGTTTACAACGCTGTGACCTGGGAAACCCCTGGGTTTACCGAACTTAAATGCGCTTGC 7529
 Qy 1919 AGCACATCCCGCTTTCGCCAGCTGGCGTAAATAGCGAGGCGCGACCGCATGCCCTTC 1978
 Db 7528 AGCACATCCCGCTTTCGCCAGCTGGCGTAAATAGCGAGGCGCGACCGCATGCCCTTC 7469
 Qy 1979 CCAACAGTTTGCAGCGCTGAATGCGGAAATGCGCGAGCGCCCTGTAGCGCGCGCATTAAG 2038
 Db 7468 CCAACAGTTTGCAGCGCTGAATGCGGAAATGCGCGAGCGCCCTGTAGCGCGCGCATTAAG 7409
 Qy 2039 CGCGCGCGGTGTGTGTACGCGGAGCGGTGACCGCTACACTTGCAGCGCGCTTAGCGCC 2098
 Db 7408 CGCGCGCGGTGTGTGTACGCGGAGCGGTGACCGCTACACTTGCAGCGCGCTTAGCGCC 7349
 Qy 2099 CGCTCCTTTTCCGCTTCTTCCCTTCTGCGCAGCTTCCGCGGCTTCCCGCTCAAGC 2158
 Db 7348 CGCTCCTTTTCCGCTTCTTCCCTTCTGCGCAGCTTCCGCGGCTTCCCGCTCAAGC 7289
 Qy 2159 TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAA 2218
 Db 7288 TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAA 7229
 Qy 2219 AAACTTGATTAGGGTGATGGTTTCACTAGTGGGCAATCGCCCTGATAGACGGTTTTTCG 2278
 Db 7228 AAACTTGATTAGGGTGATGGTTTCACTAGTGGGCAATCGCCCTGATAGACGGTTTTTCG 7169
 Qy 2279 CCCTTTGACGTTGAGTCCAGCTTCTTTAATAGTGTGACTCTTGTTCCAAACCTGGAACAAC 2338
 Db 7168 CCCTTTGACGTTGAGTCCAGCTTCTTTAATAGTGTGACTCTTGTTCCAAACCTGGAACAAC 7109
 Qy 2339 ACTCAACCCCTATCTCGGCTATTTCTTTTATATTAAGGGATTTGCGGATTTTCGGCTA 2398
 Db 7108 ACTCAACCCCTATCTCGGCTATTTCTTTTATTAAGGGATTTGCGGATTTTCGGCTA 7049
 Qy 2399 TTGGTTAAAAAATAGCTGATTTTAAACAAAATTTAAGCGCAATTTTAAACAAAATTTAAC 2458
 Db 7048 TTGGTTAAAAAATAGCTGATTTTAAACAAAATTTTAAACGCAATTTTAAACAAAATTTAAC 6989
 Qy 2459 GTTTACAAATTTCTCGATGGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGC 2518
 Db 6988 GTTTACAAATTTCTCGATGGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGC 6929

Qy	2219	AAAAC	TGATTAGGGTGA	TGGTTCA	CGTAGTGGGCCAT	CGCCCTG	ATAGACGGTTTTTCG	2278	
Db	10354	AAAAC	TTGATTAGGGGTGA	TGGTTAC	GTAGTGGGCCAT	CGCCCTG	ATAGACGGTTTTTCG	10295	
Qy	2279	CCCTTTG	ACGCTGGAGTCC	ACGTTCTTT	TAATAGTGAGCTCT	TGTGTTCC	AAACTGGAACAAC	2338	
Db	10294	CCCTTTG	ACGCTGGAGTCC	ACGTTCTTT	TAATAGTGAGCTCT	TGTGTTCC	AAACTGGAACAAC	10235	
Qy	2339	ACTCAAC	CCCTATCTCG	GTCTATTTCTTT	TGATTTATA	AGGGAATTTT	GC CGATTTTCGGCCTA	2398	
Db	10234	ACTCAAC	CCCTATCTCG	GTCTATTTCTTT	TGATTTATA	AGGGAATTTT	GC CGATTTTCGGCCTA	10175	
Qy	2399	TTGGTT	AAAAAATGAGCT	GTATTTAA	CAAAAAATTTT	TAACGCGAAATTTT	TACAAAAATATTAAC	2458	
Db	10174	TTGGTT	AAAAAATGAGCT	GTATTTAA	CAAAAAATTTT	TAACGCGAAATTTT	TACAAAAATATTAAC	10115	
Qy	2459	GTTTACAA	TTTCTGATG	CGGTATTTTCT	TCCCTAG	CGATCTCTG	CGGTATTTTACACACGC	2518	
Db	10114	GTTTACAA	TTTCTGATG	CGGTATTTTCT	TCCCTAG	CGATCTCTG	CGGTATTTTACACACGC	10055	
Qy	2519	ATAGGGT	TAATAACTG	ATATAATTA	ATTAATGA	AGCTCTAA	TTTGTGAGTTTTAGTATACATGC	2578	
Db	10054	ATAGATG	CGCAAGTC	GACAAACA	TACTTTAA	TAAATACT	CTCAGTAATAACCTATTTTC	9995	
Qy	2579	ATTTACT	TATAATACAG	TTTTTTTAG	TTTGTG	CGCGCATCTT	CTCAAAATATATGCTTCCCA	2638	
Db	9994	TTAGCAT	TTTTTTGAC	GAATTTTG	CTATTTTTT	TGTTAGAGTCTTTT	TACACCAATTTGTCTCTCCACA	9935	
Qy	2639	GCCTGCT	TTTTCTGT	TAAGTTT	CACCTCT	ACCTTAG	CATCCCTTCCCTTTGCAATATGTC	2698	
Db	9934	CCTCGCT	TTACATCAAC	-----	-----	-----	-----ACCAATTAACGC	9907	
Qy	2699	TCTTCCAA	CAATAAATATG	TCAGATCCT	GTAGAG	CCACATCAT	CAACGTTCTTATCTG	2758	
Db	9906	CATTAA	CTAAGGCAT	CACCAACAT	TTTCTG	GGCTCAGTCCA	CCAGCTAACATAAAAT	9847	
Qy	2759	TTGACCA	ATGCGTCTCC	CTTGTG	TCATTA	AAACCCAC	ACGGGTGCTAATCAACAATC	2818	
Db	9846	GTAAGCT	TTTCGGGCTCT	CTTGTG	CTT-----	CCACCC	AGTCAGAAATCGAGTTCCAAATC	9792	
Qy	2819	GTAACT	TTGATCTCTT	CCACC	ATGTCCT	TTTGAG	CGMATAAAGCCGATACAAATCTTT	2878	
Db	9791	CAAAAG	TTTACCTTGTCC	AC-----	CTGCTT	CTGAA	TCAAAACAGGGGAATAACGAAATG	9738	
Qy	2879	GTGCTCT	TCGCAATGT	CAACAG	TACCTTAG	TATATCT	CCAGTAGATAGGAGCCCTT	2938	
Db	9737	AGGTTCT	GTGAGCTGC	ATGAGT	AGTATGTTG	CAGTCTTTT	TGGAAATACGAGTCTTTT	9678	
Qy	2939	GCATG	CAATTTCTG	TAAACANT	AAAAAG	CGCTCTAG	GTTCCTTTGTACTTTCTTCTGCGCG	2998	
Db	9677	-----	AATAACT	TGCAAA	CCGAGAACTCT	TGGTATTTCT	TGCAACGACTCATCTCCA	9626	
Qy	2999	CTGCTT	CAACCGCTAAC	ATATCT	GGGCCAC	CAACCGTGT	GATTCGTTAATGTCTGC	3058	
Db	9625	TGCAGT	-----	TGAC	CGATATCA	ATGCGGTAAT	CATTGACGAGCGCAAAACATCTCT	9573	
Qy	3059	CCATTCT	GTCTATTTCT	GTATAC	CCCGCAG	AGTACTG	CAATTTTGA	CTGTATTACCAATGTC	3118
Db	9572	CTTAGG	TTGATTAG	AAACAC	CGCCAC	CAAGTATTTT	CGGAGTGCCTGAACTATTTTATA	9513	
Qy	3119	AGCAAA	TTTTTCTGTCT	TCG	AAAGAGT	AAAAATTTG	TACTTTGGCGGATAATGCTTTAGCGG	3178	
Db	9512	TG-----	-----	CTTTT	ACAAGACT	GTGAAATTTT	TCCCTTGCAATAACCGGCTCAATGT	9465	
Qy	3179	CTTAA	CTGTGCCCTCC	ATG	GAATAA	TCAGTCA	AGATATCCATGTGTTTTTTAGTAAACA	3238	
Db	9464	TCCTCT	TTTATTTGGG	CACACAT	ATAATAC	CCGAC	AGTCAGCATCGGAATCTAG--AGCA	9407	
Qy	3239	AATTTT	GGGACCTTAA	TGCTT	CAACT	TAACCT	CCAGTAATTCCTTGGTGGTAC--GAACATCCA	3297	
Db	9406	CATTCT	GGGCTCTGT	GTCTCT	CAAG	CGGCAAACTTTT	CACANTGGACGAGACTACTCT	9347	
Qy	3298	ATGAAG	CACACA	CAAG	TTTTTGTG	TTTTTTCG	TGATGATTAATAATAGCTTGGCAGCAACAG	3357	

9346 GTGAAATTAAATAACAGACATACCTCAAAGCTGCCTTTGTGTGCTTAATACAGTATACCTCAC 9287
TCTGAGGATGAGTAGACAGCAGCTTCCCTTATATATGATGAGCTTTCCGACATGATTTATCTTCGCTT 3417
9286 GTGCTCAATAGTCAACCAATGCCCTCCCTCTTGGCCCTCTCC-----TTTCTCTTT 9238
3418 TCTGTCAGGTTTTTTGTTCTGTGTCAGTTGGGTTAAGAAATACTGGGCAATTTTCATGTTTTCTT 3477
9237 TTTTCGACCGAATTAAATTTCTTAATCGGCCAAAAGAAAGCTCCGGA-----T 9190
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4018 CACAGGAGGTACTAGACTACCTTTTCATCTCCTACATAAATAGACGGCATATAGTACGCATTT 4077
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6977 GATGGCATGACAGTAAGAGAAATATGACGTCTGCCATAACCATGAGTGAATAAAGTCTGCG 6918
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Db 6077 TACCTCGCTCTGCTAATCCCTGTTACAGTGGCTGCTGCCAGTGGCGATAGTCTGTCTT 6018
QY 6658 ACCGGGTTGACCTCAAGACATAGTTACCGGATAAGCGCGAGCGCTCGGCTCAACGGGG 6717
Db 6017 ACCGGGTTGACCTCAAGACATAGTTACCGGATAAGCGCGAGCGCTCGGCTCAACGGGG 5958
QY 6718 GGTTCGTGCAACACAGCCAGCTTTGGAGCGAACGACCTTACACCGAACTGAGATACCTACAG 6777
Db 5957 GGTTCGTGCAACACAGCCAGCTTTGGAGCGAACGACCTTACACCGAACTGAGATACCTACAG 5898
QY 6778 CFTGAGCTATGAGAAAGCGCCACGCTTCCGAGAGGAGAAAGCGGACAGCTATCCGTA 6837
Db 5897 CFTGAGCTATGAGAAAGCGCCACGCTTCCGAGAGGAGAAAGCGGACAGCTATCCGTA 5838
QY 6838 AGCGGAGGCTCGGAACAGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGTAT 6897
Db 5837 AGCGGAGGCTCGGAACAGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGTAT 5778
QY 6898 CTTTATAGTCTGTGCGGTTTCGCCACCTCTGACTTGGAGCGTGCATTTTGTGATGCTCG 6957
Db 5777 CTTTATAGTCTGTGCGGTTTCGCCACCTCTGACTTGGAGCGTGCATTTTGTGATGCTCG 5718
QY 6958 TCAGGGGGGCGAGCTTATGAAAACCGCAGCAACCGCGCTTTTACGGTTCCTGGCC 7017
Db 5717 TCAGGGGGGCGAGCTTATGAAAACCGCAGCAACCGCGCTTTTACGGTTCCTGGCC 5658
QY 7018 TTTTGTGCGCTTTTGTCTACATGTTCTTCTGCGTTATCCCTGATTCCTGTGGATAAC 7077
Db 5657 TTTTGTGCGCTTTTGTCTACATGTTCTTCTGCGTTATCCCTGATTCCTGTGGATAAC 5598
QY 7078 CGTATTACCGCTTTGAGTGAGCTGATACCGCTCGCGCAGCGAAGCGACGCGGCGAGC 7137
Db 5597 CGTATTACCGCTTTGAGTGAGCTGATACCGCTCGCGCAGCGAAGCGACGCGGCGAGC 5538
QY 7138 GAGTCAGTGAGGAGGAGCGGAGAGCGGCGCAATACGGAACCGCTCTCCCGCGCT 7197
Db 5537 GAGTCAGTGAGGAGGAGCGGAGAGCGGCGCAATACGGAACCGCTCTCCCGCGCT 5478
QY 7198 TGGCGGATTCATTAATCGAGCTGCGACGACAGGTTTCCGACCTGGAAAGCGGCGAGTGAG 7257
Db 5477 TGGCGGATTCATTAATCGAGCTGCGACGACAGGTTTCCGACCTGGAAAGCGGCGAGTGAG 5418
QY 7258 CGCAACGCAATTAATGTAGTTACCTCACTCATTTAGGACCCCGAGGCTTTTACATTTATG 7317
Db 5417 CGCAACGCAATTAATGTAGTTACCTCACTCATTTAGGACCCCGAGGCTTTTACATTTATG 5358
QY 7318 CTTCCGCTCCTATGTTGTGTAATGTCGAGCGGATTAACAATTTTACAGGAAACAGC 7377
Db 5357 CTTCCGCTCCTATGTTGTGTAATGTCGAGCGGATTAACAATTTTACAGGAAACAGC 5298
QY 7378 TATGACCATGATTAACGCAAGCGGCA 7404
Db 5297 TATGACCATGATTAACGCAAGCGGCA 5271
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RESULT 10

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AAZ49989/C
ID AAZ49989 standard; DNA; 7210 BP.
XX
AC AAZ49989;
XX
DT 25-APR-2000 (first entry)
XX
DE Yeast two hybrid vector plasmid pAS2-cyh2-HA-both T7-final.
XX
KW Double stranded RNA inhibition; dsRNAi; transgenic organism; T7 promoter;
KW pest infestation; plasmid pAS2-cyh2-HA-both T7-final; T7 RNA polymerase;
KW T3 promoter; Sp6 promoter; ds.
XX
OS Synthetic.
OS Enterobacteria phage T7.
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XX WO200001846-A2.
PN 13-JAN-2000.
XX
XX 02-JUL-1999; 99WO-EP004718.
XX
XX 03-JUL-1998; 98GB-00014536.
PR 09-DEC-1998; 98GB-00027152.
XX
XX (DEVG-) DEVGEN NV.
XX
XX Plaetinck G, Platteeuw C, Mortier K, Bogaert T;
PI WPI; 2000-171025/15.
XX
XX Characterizing and assigning gene function, and providing a mechanism for
XX alleviating pest infestation of plants.
XX
XX Claim 51; Page 51-52; 97pp; English.
XX
XX The patent discloses a method for characterisation and assigning gene
XX function and identifying DNA responsible for inducing a specific
XX phenotype, using double stranded RNA inhibition (dsRNAi), which results
XX in potent and specific interference with expression of endogenous genes
XX in a cell. The method can be used for producing transgenic organisms and
XX provides a selective mechanism for alleviating pest infestation of
XX plants, such that the expressed ds RNA in the plant inhibits the
XX expression of the DNA within the pest which is critical for its growth,
XX survival, proliferation or reproduction. The present sequence is yeast
XX two hybrid vector plasmid pAS2-cyh2-HA-both T7-final, comprising forward
XX and reverse T7/T3/Sp6 promoters, part of cyh gene and DNA encoding GAL4DB
XX and HA epitope. This plasmid can be used to transform Caenorhabditis
XX elegans for validating the clones by phenotype analysis
XX
XX Sequence 7210 BP; 2028 A; 1547 C; 1637 G; 1998 T; 0 U; 0 Other;
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Query Match 57.1%; Score 4469.6; DB 3; Length 7210;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5103; Conservative 0; Mismatches 629; Indels 116; Gaps 14;
QY 1559 TCATGTAATAGTATGTCACGCTTACATTCAGCCCTCCGCCACATCCGCTCTAACCG 1618
Db 5982 TCATGTAATAGTATGTCACGCTTACATTCAGCCCTCCGCCACATCCGCTCTAACCG 5923
QY 1619 AAAAGCAAGGAGTTAGACAACTGAGTCTAGGTCCCTATTATTTTATAGTTATGT 1678
Db 5922 AAAAGCAAGGAGTTAGACAACTGAGTCTAGGTCCCTATTATTTTATAGTTATGT 5863
QY 1679 TAGTATTAAGAACTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGGTGT 1738
Db 5862 TAGTATTAAGAACTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGGTGT 5803
QY 1739 ACCATGTAACATTTACTGAAACCTTGTTCGAGAGGTTTGGGACGCTCGAGGCTT 1798
Db 5802 ACCATGTAACATTTACTGAAACCTTGTTCGAGAGGTTTGGGACGCTCGAGGCTT 5743
QY 1799 TAATTTGGCGCGGTACCCAAATTCGCCCTATAGTGTGATTTACGCGGCTCACATGGC 1858
Db 5742 TAATTTG-----CAAGCTCGGATCTCGAGCTCGGAAAGCTTGGACGACATGGC 5693
QY 1859 CGTCGTTTTACACGTCGTGACCTGGGAAAACCTTCGGCTTTACCCAACTTAATCGCTTGC 1918
Db 5692 CGTCGTTTTACACGTCGTGACCTGGG- AAACCTTCGGCTTTACCCAACTTAATCGCTTGC 5634
QY 1919 AGCAGATCCCCCTTTCCGACGCTGGGTAATACGAGAGGCGGACCCATCGCCCTTC 1978
Db 5633 AGCAGATCCCCCTTTCCGACGCTGGGTAATACGAGAGGCGGACCCATCGCCCTTC 5574
QY 1979 CCAACAGTTGCGCAGCTGAATGCGCAATGCGCGACGCGCCCTGTAGCGGCGCATTAAG 2038
Db 5573 CCAACAGTTGCGCAGCTGAATGCGCAATGCGCGACGCGCCCTGTAGCGGCGCATTAAG 5514
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QY 2039 CGCGGGGTGGTGGTTCGCGAGCGGTGACCGCTACACTTGCAGCGCCCTAGCGCC 2098
Db 5513 CGCGGGGTGGTGGTTCGCGAGCGGTGACCGCTACACTTGCAGCGCCCTAGCGCC 5454
QY 2099 CGCTCTTTTCGCTTCTTCCCTTCTTCCCTTCTCGCGAGCTTCCCGGTCAAGC 2158
Db 5453 CGCTCTTTTCGCTTCTTCCCTTCTTCCCTTCTCGCGAGCTTCCCGGTCAAGC 5394
QY 2159 TCTAAATCGGGGGTCCCTTTAGGGTTCGGATTTAGTCTTTCAGGCACTTCGACCCCA 2218
Db 5393 TCTAAATCGGGGGTCCCTTTAGGGTTCGGATTTAGTCTTTCAGGCACTTCGACCCCA 5334
QY 2219 AAACTTGATTTAGGGTGGTTCACGTAGTGGCCATCGCCCTGATAGAGCGTTTTTCG 2278
Db 5333 AAACTTGATTTAGGGTGGTTCACGTAGTGGCCATCGCCCTGATAGAGCGTTTTTCG 5274
QY 2279 CCCTTTGAGTTGGAGTCCAGCTTCTTTAAATAGTGGACTCTTGTTCMAACTGGAACAC 2338
Db 5273 CCCTTTGAGTTGGAGTCCAGCTTCTTTAAATAGTGGACTCTTGTTCMAACTGGAACAC 5214
QY 2339 ACTCAACCTACTCTCGGTCTATCTTTGATTTAAGGGATTTTCCGATTTTCGGCCTA 2398
Db 5213 ACTCAACCTACTCTCGGTCTATCTTTGATTTAAGGGATTTTCCGATTTTCGGCCTA 5154
QY 2399 TTGGTTAAAAATGAGCTGATTTAAACAAAAATTTAAACCGCAATTTTAAACAAATATTTAA - 2457
Db 5153 TTGGTTAAAAATGAGCTGATTTAAACAAAAATTTAAACCGCAATTTTAAACAAATATTTAA 5094
QY 2458 CGTTTACAAATTTCTGATGCGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCG 2517
Db 5093 CGTTTACAAATTTCTGATGCGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCG 5034
QY 2518 CATAGGGTAATCAATGATTAATTAATTAAGTCTTAATTTGAGTTTGTAGTTAGTACATG 2577
Db 5033 CATAGTGGCAAGTGCAACAACTTAATAAATACTACTCAGTAATACTATTT 4974
QY 2578 CATTTACTTATAATACAGTTTTTTTATTTTGTGGCGCATCTTCTCAAATATGCTTCCC 2637
Db 4973 CTTAGCAATTTTGACGAATTTTGCTATTTTGTAGAGTCTTTACACCAATTTGTCTCCAC 4914
QY 2638 AGCTGCTTTTCTGTAAGTTCACCTCTACCTTACGATATCCCTTCCCTTCCGCAATAGTC 2697
Db 4913 ACCTCGCTTACATCAAC-----ACCAATAACG 4886
QY 2698 CTCTTCCCAACATAATATGTCAGATCTGTAGAGCACCATCATCCGTTCTATACT 2757
Db 4885 CCATTTAATCTAAGCGCATCAACAACTTTCTGCGGTGTCAGTCACACGCTAAATATAA 4826
QY 2758 GTTGACCCCAATCGCTCTCCCTTGTCTATCTAAACCCACACCGGGTGTCAATAACCAAT 2817
Db 4825 TGTAGCTTTTCGGGGTCTCTTGGCTT-----CCAAACCCAGTCAGAAATCGAGTTCCAAT 4771
QY 2818 CGTAACTTCTATCTCTTCCACCCATGTCTCTTTGAGCAATTAAGCCGATTAACAAATCTT 2877
Db 4770 CCAAAAGTTTCACTCTGCCAC-----CTGCTTCTGAAATCAACCAAGGGAAATAACGAA 4717
QY 2878 TGTGCTCTTCCCAATGTCACAGTACCTTGTAGTATATTTCTCCAGTAGATAGGAGCCCT 2937
Db 4716 GAGGTTTCTGTGAAGCTGCACTGAGTAGTATGTTGCACTCTTTTGGAAATACGAGTCTTT 4657
QY 2938 TGCATGACAAATTTCTGTAAACATCAAAAGCCCTTAGGTTCCCTTTGTTACTTCTTCTGCCG 2997
Db 4656 T-----ATAACTGGCAACCGAGGAATCTTGTGTATTTCTTGGCAGCATCATCTCC 4605
QY 2998 CTTGCTTCAACCGGTAAACAATCTTGGGCCCAACACACCGGTGTGCAATTCGTATGTCTG 3057
Db 4604 ATGCACT-----TGGACGATATCAATGCGGTATCAATGACACGAGCCAAACATCCT 4552
QY 3058 CCCATTTCTGCTATTTCTGTATACCCCGAGAGTCTGCAATTTTGCATCTATTTACCAATGT 3117
Db 4551 CTTTAGTTGATTAACAAACCGCAACCAAGTATTTTCGGAGTGCCTGACATTTTTAT 4492
QY 3118 CAGCAAAATTTTCTGTTCTGTAAGAGTAAAAAATTTGACTTGGCGGATAATGCCTTTAGCG 3177

Db 4491 ATG-----CTTTTACAAGACTTGAAATTTTCTTGCATAAACCGGGTCAATTTG 4444
QY 3178 GCTTAACTGTGCTCCATGGAATAATCAGTCAAGATATCACATGTGTTTTTAGTAAAC 3237
Db 4443 TTTCTTTCTATTGGGCACACATATAATACCAGCAAGTCAGCATCGGAATCTAG--AGC 4386
QY 3238 AAAATTTGGGACCTAAATGCTTCAACTAACTCAGTAATCTCTTGGTGGTAC--GAACATCC 3296
Db 4385 ACATTTCTGGGCTCTGTCTCTCAAGCCGCAACTTTCACCAATGACACGAACTACC 4326
QY 3297 AATGAAGCACACAAGTTGTTTGTGTCATGATATTAATAATGCTTGGCAGCAACA 3356
Db 4325 TGTGAAATTAATAACAGACATCTCCAAGCTGCTTTGTGTGCTTAATCACGTATATCA 4266
QY 3357 GACTAGATGAGTAGCAGCAGCTTCTTATATGATGCTTTGACATGATTTATCTTCT 3416
Db 4265 CGTGCTCAATAGTACCAGTCCCTCTCTTGGCCCTCTCC-----TTTTCTT 4217
QY 3417 TTCCTGAGGTTTTTGTGTCAGTGGTGAAGATACTGGGCAATTTTCATGTTTTCT 3476
Db 4216 TTTTCGACCGAATTAATTTCTTAATCGGCAAAAAGAAAGCTCCGA----- 4169
QY 3477 TCAACACTACATATGCTATATATACCAATCTAAGTCTGTGCTCTTCTCTGTTCTTCC 3536
Db 4168 TCAAGATTGTACGTAAGGTGACAAGCTATTTTCAATAAAGAAATATCTTCCACTACTGCC 4109
QY 3537 TTTCTGTCGGAGTATCCGATCAAAAATTTTCAAGAAACCGAAATCAAAAAAGAA 3596
Db 4108 ATCTGGCGTCATAACTCAAGAGTACATATATTA-----CGATGCTGTCTATTAAA 4057
QY 3597 TAAAAAAAATGATGAATTTGAATTTGAAAGCTGTGTTATGTTGTCATCTCAGTACAATC 3656
Db 4056 TGCTTCTATATATATATATAGTAAATGTCGTTGATCTATGTTGCACTCTCAGTACAATC 3997
QY 3657 TGCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCAACACCCGCTGACGCGCC 3716
Db 3996 TGCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCAACACCCGCTGACGCGCC 3937
QY 3717 TGAGGCTGTTCTGCTCCGGCATCCGTTTACAGCAAGCTGTGACCGTCTCCGGGAGC 3776
Db 3936 TGAGGCTGTTCTGCTCCGGCATCCGTTTACAGCAAGCTGTGACCGTCTCCGGGAGC 3877
QY 3777 TGCAATGTCAGAGGTTTTTCAACGTCATCACGAAACCGCGAGACGAAAGGCTCTGTCG 3836
Db 3876 TGCAATGTCAGAGGTTTTTCAACGTCATCACGAAACCGCGAGACGAAAGGCTCTGTCG 3817
QY 3837 ATAGCCTATTTTTATAGGTTAATGTCATGATAATAATGTTTCTTAGTATGATCAATA 3896
Db 3816 ATAGCCTATTTTTATAGGTTAATGTCATGATAATAATGTTTCTTAGTATGATCAATA 3757
QY 3897 TCAAGGAAATGATAGCATTTGAAGGATCAGACTAATCCAATTTAGGAGTGGCAGCATATA 3956
Db 3756 TCAAGGAAATGATAGCATTTGAAGGATCAGACTAATCCAATTTAGGAGTGGCAGCATATA 3697
QY 3957 GAAACAGCTAAAGGGTAGTGTGAAAGGAGCATACGATACCCGCAATGGAATGGGATAATA 4016
Db 3696 GAACAGCTAAAGGGTAGTGTGAAAGGAGCATACGATACCCGCAATGGAATGGGATAATA 3637
QY 4017 TCACAGAGGTACTAGACTACTCTTTTCATCTTACATAAATAAGACGATATAAGTACGCA 4076
Db 3636 TCACAGAGGTACTAGACTACTCTTTTCATCTTACATAAATAAGACGATATAAGTACGCA 3577
QY 4077 TTAGCATTAACACGCACTATGCGCTTCTTCTCATGTATATATATACAGGCAACACGCA 4136
Db 3576 TTAGCATTAACACGCACTATGCGCTGTATGTGCGCAGCTCGGTTGCAATTTTCGGAA 3517
QY 4137 GATATAGTGCAGCTGAAACAGTCAAGTGTATGTGCGCAGCTCGGTTGCAATTTTCGGAA 4196
Db 3516 GATATAGTGCAGCTGAAACAGTCAAGTGTATGTGCGCAGCTCGGTTGCAATTTTCGGAA 3457
QY 4197 GCGCTCGTTTCGGAACGCTTTTGAAGTTCTTATTTCCGAAGTTCTTATTTCTAGAAAT 4256

Db 3456 GCCTCGTTTCGAAACGCTTTGAAGTTCCTATTTCGGAAGTTCCTATTCTCTAGAAAGT 3397
Qy 4257 ATAGGAACCTTCAGAGCGCTTTGAAACCAAAAGCGCTCTGGAAGAGCGCACTTTCAAAAAA 4316
Db 3396 ATAGGAACCTTCAGAGCGCTTTGAAACCAAAAGCGCTCTGGAAGAGCGCACTTTCAAAAAA 3337
Qy 4317 CCAAAACGACCGGACTGTAAAGAGCTACTAAATAATTGCGGAATACCGCTTCCACAAAC 4376
Db 3336 CCAAAACGACCGGACTGTAAAGAGCTACTAAATAATTGCGGAATACCGCTTCCACAAAC 3377
Qy 4377 ATTGCTCAAAAGTATCTCTTGGCTATATATCTCTGCTATATATCCCTATATAACCTACCC 4436
Db 3276 ATTGCTCAAAAGTATCTCTTGGCTATATATCTCTGCTATATATCCCTATATAACCTACCC 3217
Qy 4437 ATCCACCTTCGCTCCTTGAACCTTGCACTTAAACTCGACCTTACACTTTTATGTTTAT 4496
Db 3216 ATCCACCTTCGCTCCTTGAACCTTGCACTTAAACTCGACCTTACACTTTTATGTTTAT 3157
Qy 4497 CTCTAGTATTACTCTTTAGACAAAATAATTGTAAGAACTATTATAGAGTGAATCGA 4556
Db 3156 CTCTAGTATTACTCTTTAGACAAAATAATTGTAAGAACTATTATAGAGTGAATCGA 3097
Qy 4557 AAAACAATACGAAATGTAAACATTTCTCTATACGCTAGTATATAGACAAAATAAGAA 4616
Db 3096 AAAACAATACGAAATGTAAACATTTCTCTATACGCTAGTATATAGACAAAATAAGAA 3037
Qy 4617 CCGTTTCAATAATTTCTGACCAATGAAGAATCATCAACGCTATCACTTTCTGTTTCAAAAG 4676
Db 3036 CCGTTTCAATAATTTCTGACCAATGAAGAATCATCAACGCTATCACTTTCTGTTTCAAAAG 2977
Qy 4677 TATGCGCAATCCACATCGGTATAGAAATATATCGGGATGCCCTTATCTTGAAATAATGC 4736
Db 2976 TATGCGCAATCCACATCGGTATAGAAATATATCGGGATGCCCTTATCTTGAAATAATGC 2917
Qy 4737 ACCCGCAGCTTCGCTAGTAAATAGTAAACGCGGAAGTGAGTCAAGCTTTTATGGA 4796
Db 2916 ACCCGCAGCTTCGCTAGTAAATAGTAAACGCGGAAGTGAGTCAAGCTTTTATGGA 2857
Qy 4797 AGAGAAAATAGACACCAAAAGTAGCTTTCTTCTAACCTTAAACGACCTACAGTCAAAAAG 4856
Db 2856 AGAGAAAATAGACACCAAAAGTAGCTTTCTTCTAACCTTAAACGACCTACAGTCAAAAAG 2797
Qy 4857 TTATCAAGAGACTGCATTATAGAGCGCAAAAGAGAAAAAGTAACTTATAGATCGCTT 4916
Db 2796 TTATCAAGAGACTGCATTATAGAGCGCAAAAGAGAAAAAGTAACTTATAGATCGCTT 2737
Qy 4917 GTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCT 4976
Db 2736 GTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCT 2677
Qy 4977 TTGTTGGTAAAAATAGCGCTCTCGGATGCAATTTCTGTTCTGTAAAAATGCACTCAGATT 5036
Db 2676 TTGTTGGTAAAAATAGCGCTCTCGGATGCAATTTCTGTTCTGTAAAAATGCACTCAGATT 2617
Qy 5037 CTTTGTGTTGAAAAATAGCGCTCTCGGATGCAATTTTGTGTTTACAAAAATGAGCACAG 5096
Db 2616 CTTTGTGTTGAAAAATAGCGCTCTCGGATGCAATTTTGTGTTTACAAAAATGAGCACAG 2557
Qy 5097 ATTCCTGTTGTTGAAAAATAGCGCTCTCGGATGCAATTTCTGTTCTGTAAAAATGCACTC 5156
Db 2556 ATTCCTGTTGTTGAAAAATAGCGCTCTCGGATGCAATTTCTGTTCTGTAAAAATGCACTC 2497
Qy 5157 AGATTCCTTGTGTTGAAAAATAGCGCTCTCGGATGCAATTTTGTGTTTCTACAAAATGAAGC 5216
Db 2496 AGATTCCTTGTGTTGAAAAATAGCGCTCTCGGATGCAATTTTGTGTTTCTACAAAATGAAGC 2437
Qy 5217 ACAGATGCTTCGTTTCAAGTGGCACTTTTGGGGAATATGTCGGGAAACCCCTATTATGTTT 5276
Db 2436 ACAGATGCTTCGTTTCAAGTGGCACTTTTGGGGAATATGTCGGGAAACCCCTATTATGTTT 2377
Qy 5277 ATTTTCTTAAATACATTCAAATATGATCGCTCATGAGACATACCCCTGATAAATGCT 5336
Db 2376 ATTTTCTTAAATACATTCAAATATGATCGCTCATGAGACATACCCCTGATAAATGCT 2317

Qy 5337 TCAATAATATTGAAAAAGGAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTC 5396
Db 2316 TCAATAATATTGAAAAAGGAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTC 2257
Qy 5397 CTTTTTGGCGCAATTTTGGCTTCTGCTTTTGTCTGACCCAGAAACCGTGTGGAAGTAAA 5456
Db 2256 CTTTTTGGCGCAATTTTGGCTTCTGCTTTTGTCTGACCCAGAAACCGTGTGGAAGTAAA 2197
Qy 5457 AGATGCTGAAGATCAGTTGGGTGCAAGAGTGGGTATACATCGAACTGGATCTCAACAGCG 5516
Db 2196 AGATGCTGAAGATCAGTTGGGTGCAAGAGTGGGTATACATCGAACTGGATCTCAACAGCG 2137
Qy 5517 TAAGATCTTGAAGAGTTTTCGCCCCGAAAGACGTTTTTCCAATGATGAGCACTTTTAAAGT 5576
Db 2136 TAAGATCTTGAAGAGTTTTCGCCCCGAAAGACGTTTTTCCAATGATGAGCACTTTTAAAGT 2077
Qy 5577 TCTGCTATGTCGGCGGTATATCCCGTATTGACGCGCGGCAAGACCACTCGGTGCGCG 5636
Db 2076 TCTGCTATGTCGGCGGTATATATCCCGTATTGACGCGCGGCAAGACCACTCGGTGCGCG 2017
Qy 5637 CATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACAGTCAAGAAAAGCATCTTAC 5696
Db 2016 CATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACAGTCAAGAAAAGCATCTTAC 1957
Qy 5697 GGATGCTATGACAGTAAAGAAATTTATGCAAGTGTCTGCCATAACCATGAGTGAACACTGC 5756
Db 1956 GGATGCTATGACAGTAAAGAAATTTATGCAAGTGTCTGCCATAACCATGAGTGAACACTGC 1897
Qy 5757 GGCCAACTTACTCTGCAACAGTCCGAGGACCGAAGAGTAAACCGCTTTTTCGCAAA 5816
Db 1896 GGCCAACTTACTCTGCAACAGTCCGAGGACCGAAGAGTAAACCGCTTTTTCGCAAA 1837
Qy 5817 CATGGGGATCATGTAATCTGCTCGCTTGCATCGTTGGGAACCGAGCTGAATGAAGCATAC 5876
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Qy 5937 AACTGGGAACTACTTACTCTAGCTTCCGCGCAACAAATTAATAGACTGGATGAGCGGA 5996
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Qy 5997 TAAAGTTGACGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGTTTATTCGTGATAA 6056
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Qy 6057 ATCTGAGCGGTGAGCGGTGCTCGCGTATCATTTGACGACTCGGGCCAGATGGTAA 6116
Db 1596 ATCTGAGCGGTGAGCGGTGCTCGCGTATCATTTGACGACTCGGGCCAGATGGTAA 1537
Qy 6117 GCGCTCCGCTATGCTAGTATTCTACACGAGCGGAGTCAAGCAACTATGATGAACGAAA 6176
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Db 1476 TAGACAGATCGCTGAGATAGTGCCTCACTGATTAGCAATTTGTTAACTGTGAGCAAGT 1417
Qy 6237 TTACTCATATATATCTTTAGATTGATTTAAACCTTCAATTTTAAAGGATCTAGGT 6296
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Qy 6297 GAAGATCTTTTGTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTCGTTCCACTG 6356
Db 1356 GAAGATCTTTTGTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTCGTTCCACTG 1297
Qy 6357 AGCGTCAGACCCCGTAGAAAAAGATCAAGAGTCTCTCTGAGATCCTTTTTTCTGCGCGT 6416
Db 1296 AGCGTCAGACCCCGTAGAAAAAGATCAAGAGTCTCTCTGAGATCCTTTTTTCTGCGCGT 1237

6417 AATCTGCTGCTGCAAAACAAAAACACCCAGCGTGTGTTGTTGTCGGATCA 6476
1236 AATCTGCTGCTGCAAAACAAAAACACCCAGCGTGTGTTGTTGTCGGATCA 1177
6477 AGAGTACCAACTCTTTTTCGAAGGTAACTGGCTTACGAGAGCGGAGATACCAATAC 6536
1176 AGAGTACCAACTCTTTTTCGAAGGTAACTGGCTTACGAGAGCGGAGATACCAATAC 1117
6537 TGTCTCTTCTAGTGTAGCGGTAGTTAGGCGCACCACTTCAAGAACTCTGTAGCAGCGCTAC 6596
1116 TGTCTCTTCTAGTGTAGCGGTAGTTAGGCGCACCACTTCAAGAACTCTGTAGCAGCGCTAC 1057
6597 ATACCTCGCTCTGCTTAATCTCTTTACCAAGTGGCTGCTGCCAGTGGCGATAGTGTCT 6656
1056 ATACCTCGCTCTGCTTAATCTCTTTACCAAGTGGCTGCTGCCAGTGGCGATAGTGTCT 997
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996 ATACCGGTTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGCGGTGGCTGAAAGGG 937
6717 GGGTTGCTGCACACAGCGCGCTTGGAGCGAAGCACTTACACCGAATGAGATACCTACA 6776
936 GGGTTGCTGCACACAGCGCGCTTGGAGCGAAGCACTTACACCGAATGAGATACCTACA 877
6777 GGGTTGCTGCATGAGAAAGCGCGCTTCCGAGAGGAGAAAGCGGAGCTATCCGGT 6836
876 GGGTTGCTGCATGAGAAAGCGCGCTTCCGAGAGGAGAAAGCGGAGCTATCCGGT 817
6837 AAGCGGAGGTTGCGAAGAGAGCGGACGAGGAGCTTCCAGGGGAAACGGCTGGTA 6896
816 AAGCGGAGGTTGCGAAGAGAGCGGACGAGGAGCTTCCAGGGGAAACGGCTGGTA 757
6897 TCTTTATAGTCTGCTGCGGTTTCCGACCTCTGACTGAGCGTGCATTTTGTGATGCTC 6956
756 TCTTTATAGTCTGCTGCGGTTTCCGACCTCTGACTGAGCGTGCATTTTGTGATGCTC 697
6957 GTACGGGGGGGAGGCTATGAAAAAGCCAGCAACCGCGCTTTTTCAGGTTCTCGG 7016
696 GTACGGGGGGGAGGCTATGAAAAAGCCAGCAACCGCGCTTTTTCAGGTTCTCGG 637
7017 CTTTGTGCTGCTTTGCTCAGATGTTCTTCTCGGTTATCCCTGATTTCTGTGATAA 7076
636 CTTTGTGCTGCTTTGCTCAGATGTTCTTCTCGGTTATCCCTGATTTCTGTGATAA 577
7077 CGGTATTACCGCTTTGAGTGAGTGATACGCTCGCGAGCGGAGCGGAGCGGAG 7136
576 CGGTATTACCGCTTTGAGTGAGTGATACGCTCGCGAGCGGAGCGGAGCGGAG 517
7137 CGAGTCAAGTCAAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 7196
516 CGAGTCAAGTCAAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 457
7197 TTGGCGGATTCATTAATGAGCTGGCAGCAGAGTTTCCGAGCTGGAAGCGGAGTGA 7256
456 TTGGCGGATTCATTAATGAGCTGGCAGCAGAGTTTCCGAGCTGGAAGCGGAGTGA 397
7257 GCGCAACGAATTAATGAGTGAATCTCACTATGAGCAGCGGAGCTTTACATTTAT 7316
396 GCGCAACGAATTAATGAGTGAATCTCACTATGAGCAGCGGAGCTTTACATTTAT 337
7317 GCTTCGGGCTCTATGTTGTTGGAATTTGTGAGCGGATAACAAATTTACAGGAGAAACAG 7376
336 GCTTCGGGCTCTATGTTGTTGGAATTTGTGAGCGGATAACAAATTTACAGGAGAAACAG 277
7377 CTATGACCAATGATTACGCCAAGCGGCA 7404
276 CTATGACCAATGATTACGCCAAGCGGCA 249

RESULT 11
ABV77349
ID ABV77349 standard; DNA; 9952 BP.
XX

AC ABV77349;
XX 24-FEB-2003 (first entry)
XX Yeast expression vector for the E. coli glucuronidase gene.
XX Gender-sorting; ligand dependent transactivation; sex separation;
XX poultry industry; glucuronidase gene; ds.
XX Saccharomyces cerevisiae.
XX Escherichia coli.
XX Homo sapiens.
XX Synthetic.
XX WO200286446-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US012590.
XX 23-APR-2001; 2001US-0286010P.
XX (LIFE-) LIFESENSORS INC.
XX Butt T, Tran HT;
XX WPI; 2003-075636/07.
XX New ligand dependent transactivation system, useful for accurate and
XX efficient gender sorting in mammalian and avian species, and for
XX assessing patient populations for their susceptibility to drugs and
XX predisposition to disease.
XX Disclosure; Fig 12; 79pp; English.
XX The invention relates to a new ligand dependent transactivation system
XX for gender-sorting in a test animal. The ligand dependent transactivation
XX system is useful for accurate and efficient gender sorting in mammalian
XX and avian species. The method may also be used to advantage to gender
XX sort other animal species, and to assess patient populations for their
XX susceptibility to drugs and predisposition to disease. The method of the
XX invention may be useful in the poultry industry. Unlike previous methods
XX (e.g. radioimmunoassays), which are cumbersome, expensive and not readily
XX adaptable to high throughput formats, the new method provides robustness,
XX cost-effectiveness, and is 100% accurate. The yeast transactivation is
XX 100-fold more sensitive to 17-beta estradiol when compared to mammalian
XX cell assays and no transactivation was observed with the indicated
XX concentration of oestrogen glucuronides. The current sequence represents
XX the yeast expression vector for the E. coli glucuronidase gene - pRS425-
XX GPD-Ub-GUS
XX Sequence 9952 BP; 2823 A; 2246 C; 2243 G; 2640 T; 0 U; 0 Other;
XX Query Match 46.3%; Score 3623; DB 7; Length 9952;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3820 GACGAAAGGGCCTCGTATAGCGCTATTTTATAGTTAATGTCATGATAATAGTTT 3879
Db 1 GACGAAAGGGCCTCGTATAGCGCTATTTTATAGTTAATGTCATGATAATAGTTT 60
Qy 3880 CTTAGTATGATCCCAATATCAAGGAAATGATAGCATTCGAAGGATGAGACTAATCCAATG 3939
Db 61 CTTAGTATGATCCCAATATCAAGGAAATGATAGCATTCGAAGGATGAGACTAATCCAATG 120
Qy 3940 AGGAGTGGCAGCATATAGAACAGCTAAAGGTTAGTGTGAGGAAGCATACATACCCCG 3999
Db 121 AGGAGTGGCAGCATATAGAACAGCTAAAGGTTAGTGTGAGGAAGCATACATACCCCG 180
Qy 4000 CATGGAATGGGATAATATCAAGGAGGTACTAGACTACCTTTTCATCCCTACATAATAGAC 4059
Db 181 CATGGAATGGGATAATATCAAGGAGGTACTAGACTACCTTTTCATCCCTACATAATAGAC 240

QY	4060	GCATATAAGTACGCAATTAAGCATATAACACGCACTATGCCGTTCTTCTCATGTATATATA	4119
Db	241	GCATATAAGTACGCAATTAAGCATATAACACGCACTATGCCGTTCTTCTCATGTATATATA	300
QY	4120	TATACAGGCAACACGCAATATAGTTCGAGCTGCAACAGTGAAGTGTATGTCGCGAGCTC	4179
Db	301	TATACAGGCAACACGCAATATAGTTCGAGCTGCAACAGTGAAGTGTATGTCGCGAGCTC	360
QY	4180	GCCTGTGCAATTTCCGAAAGCGCTCGTTTTCGAAACGCTTTGAAAGTTCCTATTCGGAAGTT	4239
Db	361	GCCTGTGCAATTTCCGAAAGCGCTCGTTTTCGAAACGCTTTGAAAGTTCCTATTCGGAAGTT	420
QY	4240	CCTATTTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAGCGCTCGAA	4299
Db	421	CCTATTTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAGCGCTCGAA	480
QY	4300	GACGCACTTTCAAAAAACCAAAACGCAACGCACTGTAACGAGCTACTTAAATATTGCGA	4359
Db	481	GACGCACTTTCAAAAAACCAAAACGCAACGCACTGTAACGAGCTACTTAAATATTGCGA	540
QY	4360	ATACCGCTTCCCAAAACCAATTTGCTCAAAAGTATCTCTTTGCTATATATCTCTGTGCTATAT	4419
Db	541	ATACCGCTTCCCAAAACCAATTTGCTCAAAAGTATCTCTTTGCTATATATCTCTGTGCTATAT	600
QY	4420	CCCTATATAACCTTACCACCTCCACTTTTCGCTCCTTGAACCTTGATCTAAACTCGACCTCT	4479
Db	601	CCCTATATAACCTTACCACCTCCACTTTTCGCTCCTTGAACCTTGATCTAAACTCGACCTCT	660
QY	4480	ACATTTTTTATGTTTATCTCTAGTATTACTCTTTAGACAAAAAATTTGTAAGAACTA	4539
Db	661	ACATTTTTTATGTTTATCTCTAGTATTACTCTTTAGACAAAAAATTTGTAAGAACTA	720
QY	4540	TTCTATAGAGTGAATTCGAAAAACAATFACGAAATGTAAACATTTCTCTATACGTAGTATATAG	4599
Db	721	TTCTATAGAGTGAATTCGAAAAACAATFACGAAATGTAAACATTTCTCTATACGTAGTATATAG	780
QY	4600	AGACAAATAGAGAAACCGTTTCAATATTTTCTGACCAATGAAGAAATCATCAACGCTATC	4659
Db	781	AGACAAATAGAGAAACCGTTTCAATATTTTCTGACCAATGAAGAAATCATCAACGCTATC	840
QY	4660	ACTTTCTGTTTCAAAAAGTATGCGCAATCCACATCGGTATAGAAATATAATCGGGAGTGCCT	4719
Db	841	ACTTTCTGTTTCAAAAAGTATGCGCAATCCACATCGGTATAGAAATATAATCGGGAGTGCCT	900
QY	4720	TTATCTTGAAAAAATGACCCGAGCTTCGCTAGTATCAGTAAACCGCGGAAAGTGAGT	4779
Db	901	TTATCTTGAAAAAATGACCCGAGCTTCGCTAGTATCAGTAAACCGCGGAAAGTGAGT	960
QY	4780	CAGCTTTTTTTATGGAAGAGAAATAGACACCAAGTAGCCTTCTTCTAACCTTAAACGG	4839
Db	961	CAGCTTTTTTTATGGAAGAGAAATAGACACCAAGTAGCCTTCTTCTAACCTTAAACGG	1020
QY	4840	ACCTACAGTCGAAAAAGTATCAGAGACTGCACTTATAGAGCGCACCAAGGAGAAAAA	4899
Db	1021	ACCTACAGTCGAAAAAGTATCAGAGACTGCACTTATAGAGCGCACCAAGGAGAAAAA	1080
QY	4900	GTAATCTAAGAGTCTTTGTTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAA	4959
Db	1081	GTAATCTAAGAGTCTTTGTTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAA	1140
QY	4960	AAAGAGTATAGATCTTTGTTGTAATAATAGCGCTCTCGGGTGCATTTCTGTTCGTA	5019
Db	1141	AAAGAGTATAGATCTTTGTTGTAATAATAGCGCTCTCGGGTGCATTTCTGTTCGTA	1200
QY	5020	AAATGAGCTCAGATCTTTGTTGAAAAATAGCGCTCTCGGTGCAATTTTGTGTTTT	5079
Db	1201	AAATGAGCTCAGATCTTTGTTGAAAAATAGCGCTCTCGGTGCAATTTTGTGTTTT	1260
QY	5080	ACAAAAATGAAGCAGATCTTCTGTTGTAATAATAGCGCTCTCGCGTTCGATTTCTGTT	5139
Db	1261	ACAAAAATGAAGCAGATCTTCTGTTGTAATAATAGCGCTCTCGCGTTCGATTTCTGTT	1320
QY	5140	CTGTAAAAATGCACTCAGATCTTTGTTGAAAAATAGCGCTCTCGCGTTCGATTTTAA	5199

Db	1321	CTGTAAAAATGCACTCAGATCTTTGTTGAAAAATAGCGCTCTCGCGTTCGATTTT	1380
QY	5200	GTTCTACAAAAATGAAGCAGATCTTCTGTTGAGTGGCACTTTTCCGGGAAAAATGTCGCG	5259
Db	1381	GTTCTACAAAAATGAAGCAGATCTTCTGTTGAGTGGCACTTTTCCGGGAAAAATGTCGCG	1440
QY	5260	GGAAACCCCTATTTGTTTCTTAAATACATTTCAAAATATGATCGCTCATGAGACAA	5319
Db	1441	GGAAACCCCTATTTGTTTCTTAAATACATTTCAAAATATGATCGCTCATGAGACAA	1500
QY	5320	TAAACCCCTGATTAATGCTTCAATTAATTTGAAAAAGGAGAGTATGAGTATTTCAACATTT	5379
Db	1501	TAAACCCCTGATTAATGCTTCAATTAATTTGAAAAAGGAGAGTATGAGTATTTCAACATTT	1560
QY	5380	CGTGTGCGCCCTTATTTCCCTTTTGGCGCAATTTTGCCTCTCTGTTTGTCTCACCCAGAA	5439
Db	1561	CGTGTGCGCCCTTATTTCCCTTTTGGCGCAATTTTGCCTCTCTGTTTGTCTCACCCAGAA	1620
QY	5440	ACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAGAGTGGTATACATCGAA	5499
Db	1621	ACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAGAGTGGTATACATCGAA	1680
QY	5500	CTGGATCTCAACAGCGGTAAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGT	5559
Db	1681	CTGGATCTCAACAGCGGTAAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGT	1740
QY	5560	ATGAGCACATTTTAAAGTCTTGTCTATGTGGCGCGTATTTCCCGTATTTGACGCGCGGCAA	5619
Db	1741	ATGAGCACATTTTAAAGTCTTGTCTATGTGGCGCGTATTTCCCGTATTTGACGCGCGGCAA	1800
QY	5620	GAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCACAGTC	5679
Db	1801	GAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCACAGTC	1860
QY	5680	ACAGAAAGCATCTTACGGATGCGATGACAGTAAAGAAATTTAGCAGTCTGCCATAACC	5739
Db	1861	ACAGAAAGCATCTTACGGATGCGATGACAGTAAAGAAATTTAGCAGTCTGCCATAACC	1920
QY	5740	ATGAGTGATAAACCTCGCGCAACTTACTTCTGCAACCAAGATCGAGGAGCAGGAGAGCTA	5799
Db	1921	ATGAGTGATAAACCTCGCGCAACTTACTTCTGCAACCAAGATCGAGGAGCAGGAGAGCTA	1980
QY	5800	ACCGCTTTTTTGCACAACTGCGGGATCATGTAACTCGCTTGCCTTGCCTGCGGAAACCGGAG	5859
Db	1981	ACCGCTTTTTTGCACAACTGCGGGATCATGTAACTCGCTTGCCTTGCCTGCGGAAACCGGAG	2040
QY	5860	CTGAATGAAGCCATACCAACAGAGCGGTGACACCAAGTCTGTAGCAATGGGCAACA	5919
Db	2041	CTGAATGAAGCCATACCAACAGAGCGGTGACACCAAGTCTGTAGCAATGGGCAACA	2100
QY	5920	ACGTTGCGCAACTTATTAACCTGCGCAACTTACTTCTAGCTTCCCGGCAACAATTAATA	5979
Db	2101	ACGTTGCGCAACTTATTAACCTGCGCAACTTACTTCTAGCTTCCCGGCAACAATTAATA	2160
QY	5980	GACTGAGGAGCGGATAAAGTTGAGGACCACTTCTGCGCTCGGCTTCCCGCTGCG	6039
Db	2161	GACTGAGGAGCGGATAAAGTTGAGGACCACTTCTGCGCTCGGCTTCCCGCTGCG	2220
QY	6040	TGGTTTATGCTGATTAATCTGAGCGGTGAGCGTGGTCTCGCGTATCATTTGACGA	6099
Db	2221	TGGTTTATGCTGATTAATCTGAGCGGTGAGCGTGGTCTCGCGTATCATTTGACGA	2280
QY	6100	CTGGGCGCAGATGCTTAAGCCTTCCCGTATCTAGTATCTTACACGAGCGGAGTCAAGCA	6159
Db	2281	CTGGGCGCAGATGCTTAAGCCTTCCCGTATCTAGTATCTTACACGAGCGGAGTCAAGCA	2340
QY	6160	ACTATGAGTGAACCAATAGACAGATGCTGAGATAGTGCCTCCTCATGATTAAGCATTTGG	6219
Db	2341	ACTATGAGTGAACCAATAGACAGATGCTGAGATAGTGCCTCCTCATGATTAAGCATTTGG	2400
QY	6220	TAACTGTACAGCAACGATTTACTCATATATATTTAGATTGATTTAAACTTTTAA	6279

Db 2401 TAACTGTGACAGCAAGTTTACTCATATATATCTTAGATTCATTTAAATTTTAA 2460
Qy 6280 TTAAAGAGTCTAGTCAAGATCTTTTTCATATCTCATGACCAAAATCCCTTACGT 6339
Db 2461 TTAAAGAGTCTAGTCAAGATCTTTTTCATATCTCATGACCAAAATCCCTTACGT 2520
Qy 6340 GAGTTTTCCTGCTCAGAGCGTCAAGCCCGTAGAAAAGATCAAGAGATCTTCTTGAGAT 6399
Db 2521 GAGTTTTCCTGCTCAGAGCGTCAAGCCCGTAGAAAAGATCAAGAGATCTTCTTGAGAT 2580
Qy 6400 CTTTTTTTCTGCGGTAATCTGCTGTGCAAAACAAAACCAACCGCTACAGCGGTG 6459
Db 2581 CTTTTTTTCTGCGGTAATCTGCTGTGCAAAACAAAACCAACCGCTACAGCGGTG 2640
Qy 6460 GTTTTGTTCGCGGATCAAGAGTCAACACTCTTTTCCGAGGTAACTGGCTTCAGCAGA 6519
Db 2641 GTTTTGTTCGCGGATCAAGAGTCAACACTCTTTTCCGAGGTAACTGGCTTCAGCAGA 2700
Qy 6520 GCGAGATACCAAAATCTGCTCTTAGTGTAGCGGTAGTTAGGCCACCACTTCAAGAAC 6579
Db 2701 GCGAGATACCAAAATCTGCTCTTAGTGTAGCGGTAGTTAGGCCACCACTTCAAGAAC 2760
Qy 6580 TCTGTAGCACCGCTACATACCTCGCTCTGTATATCTGTTTACAGTGGCTGTGCCAGT 6639
Db 2761 TCTGTAGCACCGCTACATACCTCGCTCTGTATATCTGTTTACAGTGGCTGTGCCAGT 2820
Qy 6640 GCGATAGTCTGCTTACCGGTTGGACTCAAGAGATAGTTACCGGATAGCGGCAG 6699
Db 2821 GCGATAGTCTGCTTACCGGTTGGACTCAAGAGATAGTTACCGGATAGCGGCAG 2880
Qy 6700 CGCTCGGCTGAACCGGGGTTCTGTGACACACAGCCAGCTTGGAGCGAACGACCTACACC 6759
Db 2881 CGCTCGGCTGAACCGGGGTTCTGTGACACACAGCCAGCTTGGAGCGAACGACCTACACC 2940
Qy 6760 GAACTGAGATACCTACAGCGTGAATATGAGAAAGCGCCACGCTTCCGAGGAGAAAG 6819
Db 2941 GAACTGAGATACCTACAGCGTGAATATGAGAAAGCGCCACGCTTCCGAGGAGAAAG 3000
Qy 6820 GCGACAGATATCCGTTAAGCGGAGGTTCGACACAGAGAGCGCACGAGGAGCTTCCA 6879
Db 3001 GCGACAGATATCCGTTAAGCGGAGGTTCGACACAGAGAGCGCACGAGGAGCTTCCA 3060
Qy 6880 GGGGAAACCGCTGTATCTTATAGTCTCTGCGGTTTCGCCACCTCTGACTTGAGCGT 6939
Db 3061 GGGGAAACCGCTGTATCTTATAGTCTCTGCGGTTTCGCCACCTCTGACTTGAGCGT 3120
Qy 6940 CGATTTTGTGATCTCTGAGGGGGCGGAGCCCTATGAAAAACGCCAGCAACCGCGCC 6999
Db 3121 CGATTTTGTGATCTCTGAGGGGGCGGAGCCCTATGAAAAACGCCAGCAACCGCGCC 3180
Qy 7000 TTTTACGGTTCCTGGCTTTTGTGCGCTTTTGTCTCATGTTCTTCTGCGGTATCC 7059
Db 3181 TTTTACGGTTCCTGGCTTTTGTGCGCTTTTGTCTCATGTTCTTCTGCGGTATCC 3240
Qy 7060 CTGATTTCTGTGATAACCGTATTACCGCTTTGAGTGAGTGTATACCGCTCGCGGAGC 7119
Db 3241 CTGATTTCTGTGATAACCGTATTACCGCTTTGAGTGAGTGTATACCGCTCGCGGAGC 3300
Qy 7120 CGAACGACCGAGCGAGCGAGTCACTGAGCGAGGAGCGGAGCGCCCAATACGAAA 7179
Db 3301 CGAACGACCGAGCGAGCGAGTCACTGAGCGAGGAGCGGAGCGCCCAATACGAAA 3360
Qy 7180 CGGCTCTCCCGCGGTTGGCGGATTCATTAATGCGAGTGGCAGCAGCGTTCCGAC 7239
Db 3361 CGGCTCTCCCGCGGTTGGCGGATTCATTAATGCGAGTGGCAGCAGCGTTCCGAC 3420
Qy 7240 TGGAAAGCGGCGAGTGGAGCGAAACCAATTAATGTGAGTTACCTCACTTAGGCAACC 7299
Db 3421 TGGAAAGCGGCGAGTGGAGCGAAACCAATTAATGTGAGTTACCTCACTTAGGCAACC 3480
Qy 7300 CAGGCTTTACATTTATGCTTCCGCTCCTATGTTGTGGAATGTGAGCGGATAACAA 7359
Db 3481 CAGGCTTTACATTTATGCTTCCGCTCCTATGTTGTGGAATGTGAGCGGATAACAA 3540

Qy 7360 TTTCACACAGAAACAGCTATGACCATGATTACGCCAAGCGCAATTAACCTCACTAA 7419
Db 3541 TTTCACACAGAAACAGCTATGACCATGATTACGCCAAGCGCAATTAACCTCACTAA 3600
Qy 7420 AGGGAACAAAAGCTGGAGCTCGT 7442
Db 3601 AGGGAACAAAAGCTGGAGCTCGT 3623

RESULT 12
AAH21455

ID AAH21455 standard; DNA; 7622 BP.

XX AAH21455;

XX AC AAH21455;

XX 18-SEP-2001 (first entry)

XX Human ROMK2 DNA p423 GPD-hROMK2.

XX Inhibitor; eukaryotic; potassium channel; TRK1, TRK2; TOK1; activator;

XX ds.

XX Homo sapiens.

XX WO200151519-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-EP000055.

XX 11-JAN-2000; 2000DE-01000651.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX Leberer E, Leeuw T, Ritscher A;

XX WPI; 2001-442137/47.

XX Identifying inhibitors and activators of eukaryotic potassium channels,

XX for use as pharmaceuticals, comprises using yeast cells that express

XX heterologous, but no endogenous, potassium channels.

XX Example 3; Page 52-56; 78pp; German.

This sequence represents a novel method for identifying inhibitors or activators (A) of a eukaryotic potassium channel (KC) by applying a test compound to a mutant *Saccharomyces cerevisiae* cell in which: (i) the three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (ii) a eukaryotic KC is expressed heterologously, where the effect of the compound on the eukaryotic KC is then determined. The method is used to identify inhibitors or activators (A) of a eukaryotic potassium channel. (A) are potentially useful as pharmaceuticals. The method is easily automated for parallel processing of many samples, using either different concentrations of test compounds and/or different levels of heterologous gene expression. It allows identification of compounds that inhibit human KC selectively. This sequence represents the human ROMK2 encoding DNA described in the method of the invention

XX Sequence 7622 BP; 2125 A; 1738 C; 1656 G; 2103 T; 0 U; 0 Other;

XX Query Match 46.1%; Score 3610.2; DB 5; Length 7622;

XX Best Local Similarity 99.8%; Pred. No. 0;

XX Matches 3626; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 3820 GACGAAGGCGCTCGTGATACGCTATTTTATAGGTTAATGTCATGATAATATGTTT 3879

Db 1 GACGAAGGCGCTCGTGATACGCTATTTTATAGGTTAATGTCATGATAATATGTTT 60

Qy 3880 CTTAGTATGATCCCAATATCAAGGAATGATAGCATTGAAGGATGAGACTAATCCAATTG 3939

Db 61 CTTAG-ATGATCCCAATATCAAGGAATGATAGCATTGAAGGATGAGACTAATCCAATTG 119

QY 3940 AGGATGGCAGCATATATAGAACAGCTAAAGGGTAGTGTCTGAAGGAGCATACGATACCCCG 3999
DB 120 AGGATGGCAGCATATATAGAACAGCTAAAGGGTAGTGTCTGAAGGAGCATACGATACCCCG 179
QY 4000 CATGGAATGGATAATATACAGAGGAGTACTAGACTACCTTTTCATCTACATATAAGAC 4059
DB 180 CATGGAATGGATAATATACAGAGGAGTACTAGACTACCTTTTCATCTACATATAAGAC 239
QY 4060 GCATATAAGTACGATTTAAGCATATAACAGCGACTATGCGGTCTCTCATGTATATATA 4119
DB 240 GCATATAAGTACGATTTAAGCATATAACAGCGACTATGCGGTCTCTCATGTATATATA 299
QY 4120 TATACAGGCAACGAGCATATAGTGTGAGAGTGAACAGTGAAGTGTGCGAGCTC 4179
DB 300 TATACAGGCAACGAGCATATAGTGTGAGAGTGAACAGTGAAGTGTGCGAGCTC 359
QY 4180 GCGTGTGATTTTCGGAAGCGCTCGTTTTCGGAACGCTTTGAAAGTTCCTAATCCGAGTT 4239
DB 360 GCGTGTGATTTTCGGAAGCGCTCGTTTTCGGAACGCTTTGAAAGTTCCTAATCCGAGTT 419
QY 4240 CCTATTCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAAGCGCTCTGAA 4299
DB 420 CCTATTCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAAGCGCTCTGAA 479
QY 4300 GACGCACTTTCAAAAACCAAAAACGCAACGCACTGTAACGAGTACTAAAAATATTGCGA 4359
DB 480 GACGCACTTTCAAAAACCAAAAACGCAACGCACTGTAACGAGTACTAAAAATATTGCGA 539
QY 4360 ATACCGCTTCCACAAACATTTGCTCAAAAGTATCTTTGCTATATATCTCTGTGCTATAT 4419
DB 540 ATACCGCTTCCACAAACATTTGCTCAAAAGTATCTTTGCTATATATCTCTGTGCTATAT 599
QY 4420 CCCTATATAACCTACCCATCCACTTTTCGCTCTCTGAACTTGCAATTCGAACTCGACCTCT 4479
DB 600 CCCTATATAACCTACCCATCCACTTTTCGCTCTCTGAACTTGCAATTCGAACTCGACCTCT 659
QY 4480 ACATTTTATAGTTTATCTCTAGTATTAATCTTTTAGACAAAAAATGTAGTAGAAGACTA 4539
DB 660 ACATTTTATAGTTTATCTCTAGTATTAATCTTTTAGACAAAAAATGTAGTAGAAGACTA 719
QY 4540 TTCTATAGAGTGAATCGAAACAAATACGAAATGTAACATTTTCTATACGTAGTATATAG 4599
DB 720 TTCTATAGAGTGAATCGAAACAAATACGAAATGTAACATTTTCTATACGTAGTATATAG 779
QY 4600 AGCAAAAATAGAGAAACCGTTTCATTAATTTTCTGACCAATGAAGAATCATCAACGCTATC 4659
DB 780 AGCAAAAATAGAGAAACCGTTTCATTAATTTTCTGACCAATGAAGAATCATCAACGCTATC 839
QY 4660 ACTTCTGTTCACAAAGTATGCGCAATCCACATCGGTATAGAAATATAATCGGGGATGCCT 4719
DB 840 ACTTCTGTTCACAAAGTATGCGCAATCCACATCGGTATAGAAATATAATCGGGGATGCCT 899
QY 4720 TTATCTTGAATAATGCACCCGAGCTTCGCTAGTAAATCAGTAAACGCGGAGTGGAGT 4779
DB 900 TTATCTTGAATAATGCACCCGAGCTTCGCTAGTAAATCAGTAAACGCGGAGTGGAGT 959
QY 4780 CAGGCTTTTATGGAAGAGAAAAATAGACACCAAAAGTAGCTTCTTCTAAACCTTAAACGG 4839
DB 960 CAGGCTTTTATGGAAGAGAAAAATAGACACCAAAAGTAGCTTCTTCTAAACCTTAAACGG 1019
QY 4840 ACTACAGTCAAAAAGTTATCAAGAGACTGCAATATAGAGCGCAAAAAGGAGAAAAAA 4899
DB 1020 ACTACAGTCAAAAAGTTATCAAGAGACTGCAATATAGAGCGCAAAAAGGAGAAAAAA 1079
QY 4900 GTAATCTAGATGCTTTGTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGACAAA 4959
DB 1080 GTAATCTAGATGCTTTGTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGACAAA 1139
QY 4960 AAAGAAGTATAGATTTCTTTGCTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTA 5019
DB 1140 AAAGAAGTATAGATTTCTTTGCTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTA 1199
QY 5020 AAAATGCAGCTCAGATTTCTTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTGTGTTT 5079

DB 1200 AAAATGCAGCTCAGATTTCTTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTGTGTTT 1259
QY 5080 AAAAAATGAAGCACAGATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5139
DB 1260 AAAAAATGAAGCACAGATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1319
QY 5140 CTGTAAAAATGCAAGCTCAGATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5199
DB 1320 CTGTAAAAATGCAAGCTCAGATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1379
QY 5200 GTTCTACAAAATGCAAGCTCAGATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5259
DB 1380 GTTCTACAAAATGCAAGCTCAGATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1439
QY 5260 GGAACCCCTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5319
DB 1440 GGAACCCCTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1499
QY 5320 TAAACCTGATAAATGCTTCAATAATATTGAAAAAGGAGATGATGATTTTCAACATTTTC 5379
DB 1500 TAAACCTGATAAATGCTTCAATAATATTGAAAAAGGAGATGATGATTTTCAACATTTTC 1559
QY 5380 CGTGTGCGCCCTTATTCCTTTTGGGCAATTTTGGCTTCTCTGTTTGTCTCACCCAGAA 5439
DB 1560 CGTGTGCGCCCTTATTCCTTTTGGGCAATTTTGGCTTCTCTGTTTGTCTCACCCAGAA 1619
QY 5440 ACSCTGCTGAAGTAAAGATGCTGAAGATCAGTTCGGTGCACGAGTGGGTATCATCGAA 5499
DB 1620 ACSCTGCTGAAGTAAAGATGCTGAAGATCAGTTCGGTGCACGAGTGGGTATCATCGAA 1679
QY 5500 CTGGATCTCAACAGCGGTAAAGATCTTTGAGAGTTCCTGCGCCCGAAAGAACCTTTTCCAATG 5559
DB 1680 CTGGATCTCAACAGCGGTAAAGATCTTTGAGAGTTCCTGCGCCCGAAAGAACCTTTTCCAATG 1739
QY 5560 ATGAGCACTTTTAAAGTTCGTATGTTGGCGCGGTATTTATCCCGTATTTGACGCGGCGAA 5619
DB 1740 ATGAGCACTTTTAAAGTTCGTATGTTGGCGCGGTATTTATCCCGTATTTGACGCGGCGAA 1799
QY 5620 GAGCAACTCGGTGCGCGCATACACTATCTCAGAAATGACTTGTGTAGTACTCACCAAGTC 5679
DB 1800 GAGCAACTCGGTGCGCGCATACACTATCTCAGAAATGACTTGTGTAGTACTCACCAAGTC 1859
QY 5680 ACAGAAAAGCATCTTACGGATGCGATGACAGTAAAGAGAAATTTATGCACTGCTGCATAAACC 5739
DB 1860 ACAGAAAAGCATCTTACGGATGCGATGACAGTAAAGAGAAATTTATGCACTGCTGCATAAACC 1919
QY 5740 ATGAGTGAATAACCTGCGGCAACTTTATCTTGAACAAAGATCGGAGAACCGAGGACTA 5799
DB 1920 ATGAGTGAATAACCTGCGGCAACTTTATCTTGAACAAAGATCGGAGAACCGAGGACTA 1979
QY 5800 ACCGCTTTTTCACAAACATGCGGGATCATGTAACCTGCGCTTGCATCGTTGGGAACCGGAG 5859
DB 1980 ACCGCTTTTTCACAAACATGCGGGATCATGTAACCTGCGCTTGCATCGTTGGGAACCGGAG 2039
QY 5860 CTGAATGAAGCCATACCAAAACGAGCGGTGACACCAAGATGCTGTAGCAATGGCAACA 5919
DB 2040 CTGAATGAAGCCATACCAAAACGAGCGGTGACACCAAGATGCTGTAGCAATGGCAACA 2099
QY 5920 ACCTTGGCAAACTATTAATCTGCGAACTATCTTAATCTCTAGCTTCCCGGCAACAAATTAATA 5979
DB 2100 ACCTTGGCAAACTATTAATCTGCGAACTATCTTAATCTCTAGCTTCCCGGCAACAAATTAATA 2159
QY 5980 GACTGATGAGGCGGATAAAGTTGAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGC 6039
DB 2160 GACTGATGAGGCGGATAAAGTTGAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGC 2219
QY 6040 TGGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGGTGCTCGCGTATCATTTGACGCA 6099
DB 2220 TGGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGGTGCTCGCGTATCATTTGACGCA 2279
QY 6100 CTGGGCGCATAGTGAAGCCCTCCCGTATCGTATGTTATCTTACACGAGCGGGAGTCAGGCA 6159

Db 2280 CTGGGCGCAGATGGTAAGCCCTCCGGTATCTAGTATCTACAGCGGGAGTCAGGCA 2339
Qy 6160 ACTATGGATGAACGAATAGACAGATCGCTCAGATAGTGTGCTCCTCAGTATTAAGCATGG 6219
Db 2340 ACTATGGATGAACGAATAGACAGATCGCTCAGATAGTGTGCTCCTCAGTATTAAGCATGG 2399
Qy 6220 TAACTGTGAGACCAAGTTTACTCATATATCTTTAGATTTGATTTAAACCTTCATTTTAA 6279
Db 2400 TAACTGTGAGACCAAGTTTACTCATATATCTTTAGATTTGATTTAAACCTTCATTTTAA 2459
Qy 6280 TTTAAAGGATCTAGGTGAAGATCTTTTGTGATTAATCTCATGACCAAAATCCCTTAAAGT 6339
Db 2460 TTTAAAGGATCTAGGTGAAGATCTTTTGTGATTAATCTCATGACCAAAATCCCTTAAAGT 2519
Qy 6340 GAGTTTCTGTTCCACTGAGCGTCAAGCCCTGAGAAAGATCAAGGATCTTCTTGAGAT 6399
Db 2520 GAGTTTCTGTTCCACTGAGCGTCAAGCCCTGAGAAAGATCAAGGATCTTCTTGAGAT 2579
Qy 6400 CTTTTTTTTCTGCGGTAATCTGCTGTTCGAAACCAAAAAACCAACCGCTACCAAGCGGTG 6459
Db 2580 CTTTTTTTTCTGCGGTAATCTGCTGTTCGAAACCAAAAAACCAACCGCTACCAAGCGGTG 2639
Qy 6460 GTTGTGTTCCGGATCAAGAGTACCAACTCTTTTCCGAAGGTAAGTGGCTTCAGCAGA 6519
Db 2640 GTTGTGTTCCGGATCAAGAGTACCAACTCTTTTCCGAAGGTAAGTGGCTTCAGCAGA 2699
Qy 6520 GCGAGATACCAATCTGCTCTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAC 6579
Db 2700 GCGAGATACCAATCTGCTCTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAC 2759
Qy 6580 TCTGTAGCACCGCTTACATACCTCTGCTCTGCTTAATCTGTTTACAGTGGCTTCCGAGT 6639
Db 2760 TCTGTAGCACCGCTTACATACCTCTGCTCTGCTTAATCTGTTTACAGTGGCTTCCGAGT 2819
Qy 6640 GCGATAAGTGTGTTCTTACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCAG 6699
Db 2820 GCGATAAGTGTGTTCTTACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCAG 2879
Qy 6700 CGGTGGGCTGACCGGGGGTTCGTGCACACAGCCAGCTTGGAGCGNACGACCTACACC 6759
Db 2880 CGGTGGGCTGACCGGGGGTTCGTGCACACAGCCAGCTTGGAGCGNACGACCTACACC 2939
Qy 6760 GAACTGAGATACCTACAGGTGAGTATGAGAAAGCGCCAGCTTCCGAAAGGAGAAAG 6819
Db 2940 GAACTGAGATACCTACAGGTGAGTATGAGAAAGCGCCAGCTTCCGAAAGGAGAAAG 2999
Qy 6820 GCGGACAGATATCCGGTAAGCGGAGGTTCGAAACAGAGAGCGCACGAGGAGCTTCCA 6879
Db 3000 GCGGACAGATATCCGGTAAGCGGAGGTTCGAAACAGAGAGCGCACGAGGAGCTTCCA 3059
Qy 6880 GGGGAAAGCGCTGTATCTTTATAGTCTGTTCGGGTTTCGCCACCTCTGACTTGAGGCT 6939
Db 3060 GGGGAAAGCGCTGTATCTTTATAGTCTGTTCGGGTTTCGCCACCTCTGACTTGAGGCT 3119
Qy 6940 CGATTTTGTGATGCTCGTCAGGGGGGAGCGCTTATCGAAAAACGCCAGCAACCGCGCC 6999
Db 3120 CGATTTTGTGATGCTCGTCAGGGGGGAGCGCTTATCGAAAAACGCCAGCAACCGCGCC 3179
Qy 7000 TTTTACGGTCTCTGGCCCTTTGCTGGCTTTTGTCTCATATGTTCTTTCTGCGTTATCC 7059
Db 3180 TTTTACGGTCTCTGGCCCTTTGCTGGCTTTTGTCTCATATGTTCTTTCTGCGTTATCC 3239
Qy 7060 CTGATTTCTGGATAACCGTATTAACCGCTTTGAGTGTAGTGTATACCGCTCGCGGAGC 7119
Db 3240 CTGATTTCTGGATAACCGTATTAACCGCTTTGAGTGTAGTGTATACCGCTCGCGGAGC 3299
Qy 7120 CGAACCGAGCGCAGCGAGTCACTGTAGCGAGGAGCGGAGAGCGCCCAATACGCAAA 7179
Db 3300 CGAACCGAGCGCAGCGAGTCACTGTAGCGAGGAGCGGAGAGCGCCCAATACGCAAA 3359
Qy 7180 CCGCTCTCTCCCGCGGTGGCCGATTCATTAATGACGTGGCAGCAGAGGTTTCCGAC 7239
Db 3360 CCGCTCTCTCCCGCGGTGGCCGATTCATTAATGACGTGGCAGCAGAGGTTTCCGAC 3419

Qy 7240 TGGAAAGCGGCGAGTGAGCGCAACGCAATTAATGTGAGTTACCTCACTCATTAGGCACCC 7299
Db 3420 TGGAAAGCGGCGAGTGAGCGCAACGCAATTAATGTGAGTTACCTCACTCATTAGGCACCC 3479
Qy 7300 CAGGCTTTACATTTTATGCTTCGGCTCCTATGTTGTGGAATTGTGAGCGGATAACAA 7359
Db 3480 CAGGCTTTACATTTTATGCTTCGGCTCCTATGTTGTGGAATTGTGAGCGGATAACAA 3539
Qy 7360 TTTTACACAGAAACAGCTATGACCATGATTCGCCAAGCGGCAATTAACCTCACATAA 7419
Db 3540 TTTTACACAGAAACAGCTATGACCATGATTCGCCAAGCGGCAATTAACCTCACATAA 3599
Qy 7420 AGGGAACAAAGCTGGAGCTCGTAGGAACAATTTTC 7454
Db 3600 AGGGAACAAAGCTGGAGCTCAGTTTATCATATC 3634

RESULT 13

ADC75054
ID ADC75054 standard; DNA; 6671 BP.

XX AC ADC75054;

XX XX 01-JAN-2004 (first entry)

XX XX T-cell receptor-related pYX112 DNA.

XX KW soluble T cell receptor; sTCR; TCR alpha; TCR beta chain;
XX KW immunosuppressive; antidiabetic; major histocompatibility complex; MHC;
XX KW tumour; ds; pYX122.

XX OS Unidentified.

XX FN W02003020763-A2.

XX XX 13-MAR-2003.

XX XX 30-AUG-2002; 2002WO-GB003986.

XX PR 31-AUG-2001; 2001GB-00021187.

XX PR 16-AUG-2002; 2002GB-00019146.

XX PR 16-AUG-2002; 2002US-0404182P.

XX PA (AVID-) AVIDEX LTD.

XX PI Jakobsen BK, Glick M;

XX XX WPI; 2003-313073/30.

XX XX Novel soluble T cell receptor comprising all or part of T cell receptor
alpha or beta chain which comprise functional variable domain and part of
constant domain of receptor chain, and lack transmembrane domain.

XX XX Example 15; Fig 107; 164pp; English.

XX XX The invention relates to a novel soluble T cell receptor (sTCR) which
comprises all or part of a TCR alpha or TCR beta chain, except its
transmembrane domain, where each chain comprises a functional variable
domain and at least a part of the constant domain of the TCR chain and
are linked by a disulphide bond between constant domain residues which is
not present in the native TCR. The molecule of the invention demonstrates
immunosuppressive and antidiabetic activities and may be useful for
detecting major histocompatibility complex (MHC)-peptide complexes, for
tracking or targeting cells presenting particular antigens in vitro or in
vivo and as intermediates for the production of further multivalent TCR
complexes having such uses. Furthermore, the molecules may be useful for
delivering anti-tumour molecules specific for tumour antigens. The
current sequence is that of the sTCR-related DNA of the invention.

XX SQ Sequence 6671 BP; 1781 A; 1529 C; 1433 G; 1928 T; 0 U; 0 Other;

Query Match 43.0%; Score 3364; DB 9; Length 6671;

Best Local Similarity 80.0%; Pred. No. 0; Matches 4443; Conservative 0; Mismatches 285; Indels 828; Gaps 8;			
Qy	1851	TCACTGCGCGCTGTTTTACAAAGTGTGAGTGGGAAACCTGGCGTTTACCCAACTTAAT	1910
Db	231	TCACTGCGCGCTGTTTTACAAAGTGTGAGTGGGAAACCTGGCGTTTACCCAACTTAAT	290
Qy	1911	CGCTTTCAGACATCCCTTTTCGCGAGTGTGCGTGAATAGCGAAGAGCCGCGACCGAT	1970
Db	291	CGCTTTCAGACATCCCTTTTCGCGAGTGTGCGTGAATAGCGAAGAGCCGCGACCGAT	350
Qy	1971	CGCCCTTCCAAAGTTGCGCAGCTGAATGGGGAATGGCGGCGCGCCCTGTAGCGGC	2030
Db	351	CGCCCTTCCAAAGTTGCGCAGCTGAATGGGGAATGGCGGCGCGCCCTGTAGCGGC	410
Qy	2031	GCATTAAAGCGCGGCGGTGTGTTTACGCGAGCGTACCGCTACACTTTCGCGAGGCC	2090
Db	411	GCATTAAAGCGCGGCGGTGTGTTTACGCGAGCGTACCGCTACACTTTCGCGAGGCC	470
Qy	2091	CTAGCGCGCGCTCTTTTCGCTTTCTCCCTTCCCTTCTCGCCACGTTTCGCGGCTTTCC	2150
Db	471	CTAGCGCGCGCTCTTTTCGCTTTCTCCCTTCCCTTCTCGCCACGTTTCGCGGCTTTCC	530
Qy	2151	CGTCAGCTCTAATCGGGGGCTCCCTTTAGGGTTCGGATTTAGTGTTCACGCACTC	2210
Db	531	CGTCAGCTCTAATCGGGGGCTCCCTTTAGGGTTCGGATTTAGTGTTCACGCACTC	590
Qy	2211	GACCCCAAAACCTTGAATAGGGTGTGTTTACGTAGTGGGCGCATCGCCCTGATAGCG	2270
Db	591	GACCCCAAAACCTTGAATAGGGTGTGTTTACGTAGTGGGCGCATCGCCCTGATAGCG	650
Qy	2271	GTTTTTCGCGCTTTGAGCTTGGAGTCCACGTTCTTTAATAGTGGACTCTTTGTTCCAACT	2330
Db	651	GTTTTTCGCGCTTTGAGCTTGGAGTCCACGTTCTTTAATAGTGGACTCTTTGTTCCAACT	710
Qy	2331	GGAAACACCTCAACCCCTATCTCGGTCTATCTTTGATTTAAGGGATTTTCGCGATT	2390
Db	711	GGAAACACCTCAACCCCTATCTCGGTCTATCTTTGATTTAAGGGATTTTCGCGATT	770
Qy	2391	TCGGCTTATTTGGTTTAAATAATGAGCTGATTTTAAACAAATAATTTTAAACAA	2450
Db	771	TCGGCTTATTTGGTTTAAATAATGAGCTGATTTTAAACAAATAATTTTAAACAA	830
Qy	2451	ATATTAACTTTTAACTTCTGATCGGTAATTTCTCTTACGCACTCTGTCGGTATTT	2510
Db	831	ATATTAACTTTTAACTTCTGATCGGTAATTTCTCTTACGCACTCTGTCGGTATTT	890
Qy	2511	CACCGCATAGGTAATACTGATATAATAATTGAAGCTCTAATTTGTGATTTAGT	2570
Db	891	CACCGCATAGGTAATACTGATATAATAATTGAAGCTCTAATTTGTGATTTAGT	950
Qy	2571	ATACATGATTTACTTATAATACGTTTTTTTGTGTTTGTGCGGCACTCTTCTCAAATAT	2630
Db	951	ATACATGATTTACTTATAATACGTTTTTTTGTGTTTGTGCGGCACTCTTCTCAAATAT	1010
Qy	2631	GCTTCCAGCGCTGTTTTCTGTAACGTTTACCCCTCTACCTTAGCATCCCTTCCCTTTGCA	2690
Db	1011	GCTTCCAGCGCTGTTTTCTGTAACGTTTACCCCTCTACCCCTTAGCATCCCTTCCCTTTGCA	1070
Qy	2691	AATAGTCTCTTCCAAATAATAATGTAGATCTGTAGACACCATCATCCAGGTT	2750
Db	1071	AATAGTCTCTTCCAAATAATAATGTAGATCTGTAGACACCATCATCCAGGTT	1130
Qy	2751	CTATAGTGTGACCAATGGTCTCCCTGTCTATTAACCCACCGGGTGTCAATC	2810
Db	1131	CTATAGTGTGACCAATGGTCTCCCTGTCTATTAACCCACCGGGTGTCAATC	1190
Qy	2811	AACCAATCGTAACCTTCACTCTTCCACCATGTCTTTGAGCAATAAAGCCGATAACA	2870
Db	1191	AACCAATCGTAACCTTCACTCTTCCACCATGTCTTTGAGCAATAAAGCCGATAACA	1250
Qy	2871	AAATCTTTGCTCTTCGGAATGTCAAGTAGCCCTTAGTATATTTCTCAGTAGATAGG	2930

Db	1251	AAATCTTTGCTGCTTCGCAATGTCAACAGTAGTACCTTAGTATATTTCTCCAGTAGATAGG	1310
Qy	2931	GAGCCCTTGATCAACAATCTGCTAAACATCAAAAGGCTCTAGGTCTCTTTGTTACTTCT	2990
Db	1311	GAGCCCTTGATCAACAATCTGCTAAACATCAAAAGGCTCTAGGTCTCTTTGTTACTTCT	1370
Qy	2991	TCGCGCGCTGCTTCAAAACCGCTTAAACAATACCTGGGCCCCACACACCGTGTGATTCGTA	3050
Db	1371	TCGCGCGCTGCTTCAAAACCGCTTAAACAATACCTGGGCCCCACACACCGTGTGATTCGTA	1430
Qy	3051	ATGCTGCGCCATCTGCTATTCGTATACACCGCAGAGTACTGCAATTTGACTGTATTA	3110
Db	1431	ATGCTGCGCCATCTGCTATTCGTATACACCGCAGAGTACTGCAATTTGACTGTATTA	1490
Qy	3111	CCAAATGTCAAGCAATTTCTGCTTCGAAAGAGTAAATAATTTGACTTGGCGGATAATGCC	3170
Db	1491	CCAAATGTCAAGCAATTTCTGCTTCGAAAGAGTAAATAATTTGACTTGGCGGATAATGCC	1550
Qy	3171	TTTAGCGGCTTAACTGTGCGCTCCATGGGAAATAATCAAGTCAAGATATCCACATGTGTTTT	3230
Db	1551	TTTAGCGGCTTAACTGTGCGCTCCATGGGAAATAATCAAGTCAAGATATCCACATGTGTTTT	1610
Qy	3231	AGTAAACAAATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTTGGTGGTACGA	3290
Db	1611	AGTAAACAAATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTTGGTGGTACGA	1670
Qy	3291	ACATCAATGAAGCACACAAGTTTGTGCTTTCTGTCGATGATATTAATAAGCTTGGCA	3350
Db	1671	ACATCAATGAAGCACACAAGTTTGTGCTTTCTGTCGATGATATTAATAAGCTTGGCA	1730
Qy	3351	GCAACAGGACTAGGATGAGTAGCAGCACGTTTCTTATATATGATAGCTTTCGACATGTTAT	3410
Db	1731	GCAACAGGACTAGGATGAGTAGCAGCACGTTTCTTATATATGATAGCTTTCGACATGTTAT	1790
Qy	3411	CTTCTGTTCTCTGCGAGTTTGTGCTGCGAGTTGGTAAAGTAATACTGGGCAATTTAT	3470
Db	1791	CTTCTGTTCTCTGCGAGTTTGTGCTGCGAGTTGGTAAAGTAATACTGGGCAATTTAT	1850
Qy	3471	GTTCCTTCAACACTACATATGCTATATATCAATCTAAGTCTGTGCTCTCTTCTCTCGT	3530
Db	1851	GTTCCTTCAACACTACATATGCTATATATCAATCTAAGTCTGTGCTCTCTTCTCTCGT	1910
Qy	3531	TCCTCTCTCTGTTGCGAGATTAACGAAATCAAAATAATTTCAAAGAAACCGAAATCAAAA	3590
Db	1911	TCCTCTCTCTGTTGCGAGATTAACGAAATCAAAATAATTTCAAAGAAACCGAAATCAAAA	1970
Qy	3591	AAAGAAATAAATAAATAATGAAATTTGAATTTGAAGAGCTGTGATGGTGCACCTCAGT	3650
Db	1971	AAAGAAATAAATAAATAATGAAATTTGAATTTGAAGAGCTGTGATGGTGCACCTCAGT	2030
Qy	3651	ACAATCTGCTCTGATCGCGCATAGTTAAGCCAGCCCGACACCCGCGCAACACCCGCTGAC	3710
Db	2031	ACAATCTGCTCTGATCGCGCATAGTTAAGCCAGCCCGACACCCGCGCAACACCCGCTGAC	2090
Qy	3711	GGCCCTGACCGGCTTGTCTGCTCCCGCATTCGCTTTACAGCAAGCTGTGACCGTCTCC	3770
Db	2091	GGCCCTGACCGGCTTGTCTGCTCCCGCATTCGCTTTACAGCAAGCTGTGACCGTCTCC	2150
Qy	3771	GGGAGCTGCATGTGTCAGAGGTTTTCCCGCTCATCCGAAACCGCGAGACGAAAGGGC	3830
Db	2151	GGGAGCTGCATGTGTCAGAGGTTTTCCCGCTCATCCGAAACCGCGAGACGAAAGGGC	2210
Qy	3831	CTCGTATACGCTATTTTTTATAGGTTAATGTATGATTAATATGTTTCTTAGTATGAT	3890
Db	2211	CTCGTATACGCTATTTTTTATAGGTTAATGTATGATTAATATGTTTCTTAGTATGAT	2264
Qy	3891	CCAATATCAAGGAAATGATAGCAATTTGAAGGATGAGACTAATCCAATTTGAGGAGTGGCAG	3950
Db	2265	-----	2264
Qy	3951	CATATAGAACAGCTAAAGGGTAGTGTCTGAAGGAGCATACGATACCCCGCATGGAATGGG	4010
Db	2265	-----	2264

QY 4011 ATAATATCACAGGAGTACTAGACTACCTTTTCATCTACATATAAATAGACGCATATAAGTA 4070
Db 2265 ----- 2264
QY 4071 CGCATTTAAGCATAAACACGCACCTATGCGGTTCTTCATGTATATATATACAGGCAA 4130
Db 2265 ----- 2264
QY 4131 CAGCGGATATAGTGGCGAGCGTGAACAGTACGTGTATGTGGCGAGCTCGGTTGCATTTT 4190
Db 2265 -----GACGGATCGCTTGGCTGTAACTTACACGGCGCTCGTATCTTTT 2307
QY 4191 TCGGAAGCGCTGTTTTCGGAAACGCTTTGAAGTTCTTATCCGGAAGTCTCTATCTCTA 4250
Db 2308 AATGATGGATTAATTTGGGAATTTACTCTGTGTTT----- 2342
QY 4251 GAAAGTATAGGAACCTTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAAGACGCACCTTC 4310
Db 2343 ----- 2342
QY 4311 AAAAAACCAAAACCGACCGGACTGTAAAGACTACTAAAAATATTTGGGATACCGCTTCC 4370
Db 2343 ----- 2342
QY 4371 ACAACATTGCTCAAAAGTATCTCTTGTATATATCTCTGTCTATATATCCCTATATAAC 4430
Db 2343 ----- 2342
QY 4431 CTACCCATCCACCTTTTCGCTCCTTGAACCTGCATCTAAACTCGACCTCTACATTTTAT 4490
Db 2343 -----ATTATTTT 2351
QY 4491 GTTTATCTCTAGTATNTACTCTTTAGACAAAAAATTTAGTAAGAACTATTTTCATAGAGTG 4550
Db 2352 TATGTTTGTATTTGGATTTTAGAAAGTAAATAAAGAAAGGTAGAGAGTTACGGAATGAA 2411
QY 4551 AATCGAAAAAATACGAAAACTGAAACATTTCTTATAGTAGTATATAGACAAAAATAG 4610
Db 2412 GAAAAAATAAACAAGGTTTAAAAAATTTCAACA-----AAAGCG 2455
QY 4611 AAGAAACCGTTCATATTTTCTGCAATGAAGAAATCATCAACGCTATCATTTCTGTTTC 4670
Db 2456 TACTTTACATATATATTTATAGACAAGAAAAAGCAGATTAATAATAGATATACATTCGATTA 2515
QY 4671 ACNAGTAGCCGCAATCCACATCGGTATAGATATATAATCGGGGATGCCCTTTATCTGNA 4730
Db 2516 ACGA-----TAAAGTAAATGTAAATATCAAGGATTTTCGTGTGGTCTTCTACACA 2567
QY 4731 AAATGCACCCGACGCTTCGCTAGTAAATCAGTAAACGCGGGAAGTGGAGTCAGGCTTTTTT 4790
Db 2568 GACNAGATGAACAATTCGGCATTAATACCTGAGAGCAGGAAG----- 2610
QY 4791 TATGGAAGAGAAAAATAGACACAAAAGTAGCCTTCTTAACTTAAACGGACCTACAGTGC 4850
Db 2611 ----- 2610
QY 4851 AAAAGTTATCAAGAGACTGCATTTATAGAGCGCAAAAGGAGAAAAAAGTAATCTAAGA 4910
Db 2611 -----AGCAGATAAA 2622
QY 4911 TGCCTTTGTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAAGAGTATA 4970
Db 2623 GGTAGTATTTGTGGGATCCCTCTAGAGTCTTTTACATCTTCGGAACAAAAAATCTATT 2682
QY 4971 GAATCTTTGTGTAATAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAATAAATGCAGCT 5030
Db 2683 TTTTCTTTA----- 2691
QY 5031 CAGATCTTTGTTGAAAAATTTAGCGCTCTCGGTTGCAATTTTCTTTTACAAAAATGAA 5090
Db 2692 -----ATTCTCTTTTACTTCTTATTTTAAATTTATATATATTTATATAAATAATTTAA 2745

QY 5091 GCACAGATTCTTCGTTGGTAAAAATAGCGCTTTTCGCGTTGCATTTTCTGTCTGTAAAAATG 5150
Db 2746 ----- 2745
QY 5151 CAGCTCAGATTCTTTGTTTGAATAATTTAGCGCTCTCGGTTTGCATTTTGTGTTCTTACAAA 5210
Db 2746 -----ATTATAATTAATTTTATAGCAG 2768
QY 5211 TGAACACAGATGCTTCGTTTCAGGTGGCACTTTTCGGGGAATGTGCGGGAACCCCTAT 5270
Db 2769 TGATGAAAAGGAGC-----CAGGTGGCACTTTTCGGGGAATGTGCGGGAACCCCTAT 2822
QY 5271 TTGTTTATTTTCTAAATATACATTCAAATATGTATCCGCTCATGAGACAATAACCTGATA 5330
Db 2823 TTGTTTATTTTCTAAATATACATTCAAATATGTATCCGCTCATGAGACAATAACCTGATA 2882
QY 5331 AATGCTTCAATAATAATTTGAAAAAGGAAGATGATGAGTATTCAAACATTTTCGTTGCGCCT 5390
Db 2883 AATGCTTCAATAATAATTTGAAAAAGGAAGATGATGAGTATTCAAACATTTTCGTTGCGCCT 2942
QY 5391 TATTCCTCTTTTTCGCGCATTTTTCGCTTCTGTTTTCCTCACCCAGAAACGCTGCTGAA 5450
Db 2943 TATTCCTCTTTTTCGCGCATTTTTCGCTTCTGTTTTCCTCACCCAGAAACGCTGCTGAA 3002
QY 5451 AGTAAAAAGATGCTGAAGATCAGTTGGGTGCACAGTGGTTTACATCGAACTGGATCTCAA 5510
Db 3003 AGTAAAAAGATGCTGAAGATCAGTTGGGTGCACAGTGGTTTACATCGAACTGGATCTCAA 3062
QY 5511 CAGCGTAAAGATCCTTTCGAGAGTTTTCGCGGGAAGAACGTTTTCCAATGATGAGCACTTT 5570
Db 3063 CAGCGTAAAGATCCTTTCGAGAGTTTTCGCGGGAAGAACGTTTTCCAATGATGAGCACTTT 3122
QY 5571 TAAAGTTCTGCTATGTCGCGGTATTTATCCGTTATTCGCTTACCGCGGGAAGAGCAACTCG 5630
Db 3123 TAAAGTTCTGCTATGTCGCGGTATTTATCCGTTATTCGCTTACCGCGGGAAGAGCAACTCG 3182
QY 5631 TCGCGCATACACTATTTCTCAGATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCA 5690
Db 3183 TCGCGCATACACTATTTCTCAGATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCA 3242
QY 5691 TCTTACCGATGGCATGACAGTAAGAGAAATTTATGAGTGTCTGCCATAACCATGAGTGATA 5750
Db 3243 TCTTACCGATGGCATGACAGTAAGAGAAATTTATGAGTGTCTGCCATAACCATGAGTGATA 3302
QY 5751 CACTGCGGCAACTTCTCTGCAACGATCGAGGACCGAAGAGCTTAAACGCTTTTTT 5810
Db 3303 CACTGCGGCAACTTCTCTGCAACGATCGAGGACCGAAGAGCTTAAACGCTTTTTT 3362
QY 5811 GCACAAATGGGGATCATGTACTCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGC 5870
Db 3363 GGACAAATGGGGATCATGTACTCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGC 3422
QY 5871 CATACAAACGACGAGGTGACACCATGCTCTGTAGCAATGCGCAACAACTGTCGCA 5930
Db 3423 CATACAAACGACGAGGTGACACCATGCTCTGTAGCAATGCGCAACAACTGTCGCA 3482
QY 5931 ACTATTAACTGGCGAACTACTTACTTAGCTTCCGCGCAACAACTTAATAGACTGATGA 5990
Db 3483 ACTATTAACTGGCGAACTACTTACTTAGCTTCCGCGCAACAACTTAATAGACTGATGA 3542
QY 5991 GCGGATAAAGTTGACGAGCACTTTCTGCGCTCGGCTTCCGCTGCTGCTGTTTATGTC 6050
Db 3543 GCGGATAAAGTTGACGAGCACTTTCTGCGCTCGGCTTCCGCTGCTGCTGTTTATGTC 3602
QY 6051 TGATAAATCTGAGCCGCTGAGCGTGGTCTCGCGGTATCATTTGACGACACTGGGGCCAGA 6110
Db 3603 TGATAAATCTGAGCCGCTGAGCGTGGTCTCGCGGTATCATTTGACGACACTGGGGCCAGA 3662
QY 6111 TGGTAAACCTCTCCGCTATCGTAGTTATCTACACGACGGGAGTCAGGCAACTATGATGA 6170
Db 3663 TGGTAAACCTCTCCGCTATCGTAGTTATCTACACGACGGGAGTCAGGCAACTATGATGA 3722
QY 6171 ACGAAATAGACAGATCGCTGAGATAGGTGCTCTACTGATTAAGCAATGCTGTAAC 6230

Db	294	ACTGATATAAATAAAGCTCTAAATTTGGAGTTTAGTATACATGCAATTACTTATA	353	1369	ATGAATGAAAAAGCTCTTTGTACCCATCAATGAATTTTGAACATCCGAACCTGGAGTTT	1428	
Qy	2590	ATACAGTTTTTTAGTTTTGCTGGCGCATCTCTCAAAATATGCTTCCAGCGCTGTTTTT	2649	Qy	3658	GCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCCAACACCCGCTGACGCGCCT	3717
Db	354	ATACAGTTTTTTAGTTTTGCTGGCGCATCTCTCAAAATATGCTTCCAGCGCTGTTTTT	413	Db	1429	TCCCTGAAACAGATAGTATATTTGAACTGTATATAATATATATAGTCTAGCGCTTTACGG	1488
Qy	2650	TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGGCAATAGTCTCTTCCAAACA	2709	Qy	3718	GACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAAGCTGTGACCCGCTCTCCGGAGCT	3777
Db	414	TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGGCAATAGTCTCTTCCAAACA	473	Db	1489	AAGACAATGTATGTATTTTCGGTCTCGGAGAACTATTTGCAATATTTGATAGGTAAATCT	1548
Qy	2710	TAAATATGTACAGTCTCTGAGAGACCAATCATCCAGTCTTCTATCTATGTTGACCCCAATG	2769	Qy	3778	-----GATGTGTGAGAGTTTTTACCGTCTATCACC--GAAACGGCGGAGACGAAAG	3827
Db	474	TAAATATGTACAGTCTCTGAGAGACCAATCATCCAGTCTTCTATCTATGTTGACCCCAATG	533	Db	1549	TGCAGTCTGATCCCGGTTCAATTTCTGCGTTTCCATCTTGCACCTTCAATAGCATATCT	1608
Qy	2770	CGTCTCCCTTGTCTATTAACCCACACCGGTGTCTAATCAACCAATCGTAACCTTCAT	2829	Qy	3828	GGCTCGTGATACGCTATTTTATAGTTAATGTCTATGATTAATAATGCTTTCTTAGTAT	3887
Db	534	CGTCTCCCTTGTCTATTAACCCACACCGGTGTCTAATCAACCAATCGTAACCTTCAT	593	Db	1609	TTGTTAAGAGCATCTGTGCTTCATTTGTAGAACAAAATGCAACCGGAGCGCTAA	1668
Qy	2830	CTCTCCACCCATGCTCTTTGAGCAATAAAGCCGATAAACAAATCTTTGTGCTCTTCG	2889	Qy	3888	GATCCAAATCAAGGAAATGATAGCATTTGAAGGATGAGACTAATCCAAATTTGAGAGTGG	3947
Db	594	CTCTCCACCCATGCTCTTTGAGCAATAAAGCCGATAAACAAATCTTTGTGCTCTTCG	653	Db	1669	TTTTTCAACAAAGAACTCTGAGCTGCATTTTACAGAACAGAAATGCAACGGAAGCGC	1728
Qy	2890	CAATGTCAACAGTACCTTAGTATATCTCCAGTAGATAGGGAGCCCTTGCATGACAAAT	2949	Qy	3948	CAGCATATAGAACAGCTAAAGGGTAGTGTGAAGAGAGCATACGATACCCCGCATGGAAAT	4007
Db	654	CAATGTCAACAGTACCTTAGTATATCTCCAGTAGATAGGGAGCCCTTGCATGACAAAT	713	Db	1729	TATTTTACCAACGAAGAACTCTGTCTTCAATTTTGTAAACAAAAATGCAACGCGAGAGC	1788
Qy	2950	CTGCTAAACATCAAAAGGCTCTAGGTTCTTTGTTTACTTCTTCTGCGGCTGCTTCAAC	3009	Qy	4008	GGGATATATACAGGAGGTACTAGA-CTACCTTTTCATCTTACATATAATAGACGCATATA	4066
Db	714	CTGCTAAACATCAAAAGGCTCTAGGTTCTTTGTTTACTTCTTCTGCGGCTGCTTCAAC	773	Db	1789	GCTAATTTTCAACAAAGAACTCTGAGCTGCATTTTACAGAACAGAAATGCAACGCGAG	1848
Qy	3010	CGCTAACATACCTGGGCCACACACCGTGTGCAATCGTAATGTCTGCCCATCTGCTA	3069	Qy	4067	AGTACGCATTTAAGCATAAACACACACTATGCGCTTCTTCTCATGTATATATATATACAG	4126
Db	774	CGCTAACATACCTGGGCCACACACCGTGTGCAATCGTAATGTCTGCCCATCTGCTA	833	Db	1849	AGCGTATTTTCAACAAAGAACTCTGAGCTGCATTTTACAGAACAGAAATGCAACGCGAG	1908
Qy	3070	TTCTGTATACACCCGACAGTACTGCAATTTGACTGTATTAACCAATGTACGCAAAATTTT	3129	Qy	4127	GCAACAG-----CAGATATAGTGTGCGAAGTGAACAGTGTGTATGTGCGAGCTGC	4180
Db	834	TTCTGTATACACCCGACAGTACTGCAATTTGACTGTATTAACCAATGTACGCAAAATTTT	893	Db	1909	AGAGCGCTATTTTCTAAACAAAGCATCTTAGATTTACTTTTTTCTCTCTGTCGCTCTA	1968
Qy	3130	TGCTCTGAGAGTAAAAATTTGACTTTGGCGGATTAATGCTTTAGCGGCTTAACCTGTC	3189	Qy	4181	CGTTGCAATTTTCGAAGCGCTCGTT-----TTTCGGAACGCTTTTGAAGTTCCCTAT	4230
Db	894	TGCTCTGAGAGTAAAAATTTGACTTTGGCGGATTAATGCTTTAGCGGCTTAACCTGTC	953	Db	1969	TATGTGAGTCTCTTGATTAACCTTTTGTGCACTGAGTCCGTTTGAAGTTAGAGAGGCTAC	2028
Qy	3190	CTTCAATGAAATTCAGTCAAGATATCCATGTGTTTTTTAGTAAACAAATTTTGGAC	3249	Qy	4231	TCCGAAGTTCCTATTTCTCT-----AGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAAC	4284
Db	954	CTTCAATGAAATTCAGTCAAGATATCCATGTGTTTTTTAGTAAACAAATTTTGGAC	1013	Db	2029	TTTGGTGTCTATTTTCTCTTCCATAAAGAAAGCTGACTCCACTTCCCGCGTTTACTGAT	2088
Qy	3250	CTAATGCTTCAACTCACTCCAGTAATCTCTGGTGGTACGAACATCCCAATGAAGCACACA	3309	Qy	4285	CAAAAGGCG--TCTGAAGACGCACTTTCAAAAACCAAAACGACCGGAGCTGTAAAGCG	4343
Db	1014	CTAATGCTTCAACTCACTCCAGTAATCTCTGGTGGTACGAACATCCCAATGAAGCACACA	1073	Db	2089	TACTAGCGAAGCTGCGGGTGCAATTTTTCAGATAAAGGCAATCCCGATTTATTTCTATA	2148
Qy	3310	AGTTTGTGCTTTTGGTGCATGATTAATAATAGCTTGGCAGCAACAGGACTAGGATGAG	3369	Qy	4344	TACTAAATATTTGGAATACCGCTTCCACAAACATTTGCTCAAAAGTATCTCTTTGCTATA	4403
Db	1074	AGTTTGTGCTTTTGGTGCATGATTAATAATAGCTTGGCAGCAACAGGACTAGGATGAG	1133	Db	2149	CCGATGTGATTTGGCAATCTTTGTGAACAGAAAGTATAGCGTTGATTTCTTC-----	2204
Qy	3370	TAGCAGCAGTTCTCTTATATAGTCTTTCGACATGATTTATCTCTGTTTCTCGCAGGTTT	3429	Qy	4404	TATCTCTGTCTATATCCCTATATAACCTTACCCTTCCACCTTTTCGCTCTTTGAACTTGA	4463
Db	1134	TAGCAGCAGTTCTCTTATATAGTCTTTCGACATGATTTATCTCTGTTTCTCGGTTTC	1188	Db	2205	-ATTGGTCAAGAAATTAATGAACGGTTTCTCTATTTTGTCTCTATATACTAGTATAGGA	2263
Qy	3430	TTGTTCTGTGAGTTGGGTAAAGATACTGGGCAATTTTCACTGTTTCTTCAACTACATA	3489	Qy	4464	TCTAACTCGACCTCTACATTTTATATGTTTATCTCTAGTATTTACTCTTTAGACAAAAA	4523
Db	1189	TTGTTCTGTGAGTTGGGTAAAGATACTGGGCAATTTTCACTGTTTCTTCAACTACATA	1248	Db	2264	AATGTTTACATTTTTCGATTTGTTTTCGATTTCACTCTATGAATAGTTTCTTACTACAAATTT	2323
Qy	3490	TGCGTATATACCAATCTAAGTCTGTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	3549	Qy	4524	ATTGTAGTAGAATCTATTTCTAGAGTGAATCGAAACAAATACGAAAAATGTAACATTTCC	4583
Db	1249	TGCGTATATACCAATCTAAGTCTGTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	1308	Db	2324	TTTGTCTAAAGAGTAATACTAGAGATAACATAAAATAATGTAGAGGTGAGTTTAGATGC	2383
Qy	3550	TTACCGAATCAAAAAATTTTCAAGAAACCGAAATCAAAAAAAGAAATAAAAAATAATG	3609	Qy	4584	TATACGTAGTATATAGACAAAAATAGAAAGAAACCGTTTCATAATTTTCTTGACCAAT----	4639
Db	1309	TTACCGAATCAAAAAATTTTCAAGAAACCGAAATCAAAAAAAGAAATAAAAAATAATG	1368	Db	2384	AAAGTTCAAGGAGCGAAAGGTGATGGGTAGTTATATAGGGATATAGCACAGATATAT	2443
Qy	3610	ATGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA	3657	Qy	4640	-GAAGAAATCAACAGCTATCACTTTTCTGTTTCAAAAGTATGCGCAATCCACATCGGTAT	4698
Db				Db	2444	AGCAAGAGAGTACTTTTGTGAGCAATTTTGTGGAAGCGGTATTTCCGAATTTTGTAGTGT	2503

Db 4651 TCGGAACAGGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGTATCTTTATAGTC 4710
 Qy 6908 CTGTGGCTTTGCGCACCTCTGACTTGAGCGTCGATTTTGTGATGCTCTGTCAGGGGGC 6967
 Db 4711 CTGTGGCTTTGCGCACCTCTGACTTGAGCGTCGATTTTGTGATGCTCTGTCAGGGGGC 4770
 Qy 6968 GGAGCTATGGAAGAAAGCCAGCAAGCGGGCTTTTACGGTTCCTGGCCTTTTGTCTGGC 7027
 Db 4771 GGAGCTATGGAAGAAAGCCAGCAAGCGGGCTTTTACGGTTCCTGGCCTTTTGTCTGGC 4830
 Qy 7028 CTTTGTCTCACATGTTCTTCTCGCTTATCCCTGATTCCTGTGATAACCGTATTACCG 7087
 Db 4831 CTTTGTCTCACATGTTCTTCTCGCTTATCCCTGATTCCTGTGATAACCGTATTACCG 4890
 Qy 7088 CTTTGTAGTACTGATACCGTGCCTGCGCAGCGCAAGCGCGGAGCGAGTCACTGA 7147
 Db 4891 CTTTGTAGTACTGATACCGTGCCTGCGCAGCGCAAGCGCGGAGCGAGTCACTGA 4950
 Qy 7148 GCGAGGAAGCGGAGCGGCGCAATACGCAAGCGCTCTCCCGCGCTTGGCGGATTC 7207
 Db 4951 GCGAGGAAGCGGAGCGGCGCAATACGCAAGCGCTCTCCCGCGCTTGGCGGATTC 5010
 Qy 7208 ATTAATGCACTGGCAGCAGCAGGTTTCCGACTGGAAAGCGGGCAGTGACGCAACGCA 7267
 Db 5011 ATTAATGCACTGGCAGCAGCAGGTTTCCGACTGGAAAGCGGGCAGTGACGCAACGCA 5070
 Qy 7268 TTAATGTGATTTACCTACTACTATAGGCAACCGGCTTTACACTTTATGCTCCGGCTC 7327
 Db 5071 TTAATGTGATTTACCTACTACTATAGGCAACCGGCTTTACACTTTATGCTCCGGCTC 5130
 Qy 7328 CTATGTGTGTGGAATGTGAGCGGATAACAATTTACACAGGAAACAGCT 7378
 Db 5131 GTATGTGTGTGGAATGTGAGCGGATAACAATTTACACAGGAAACAGCT 5181

RESULT 15

AX85878
 ID AX85878 standard; DNA; 7063 BP.
 XX
 AC AX85878;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Synthetic operon comprising MSG sequence and functionl in yeast.
 XX
 KW Methylglyoxal synthase; MGS; ethanol production; 1,2-propanediol;
 KW unsaturated polyester resin; liquid laundry detergent; cosmetic;
 KW antifreeze; deicing formulation; carbon dioxide; alcohols; organic acid;
 KW animal feed; ss.
 XX
 OS Synthetic.
 OS Escherichia coli.
 XX
 XX WO9928481-Al.
 XX
 XX 10-JUN-1999.
 XX
 XX 30-NOV-1998; 98WO-US025318.
 XX
 XX 03-DEC-1997; 97US-00984717.
 XX
 XX (WISC) WISCONSIN ALUMNI RES FOUND.
 PA
 XX Cameron DC, Shaw AJ, Hoffman ML;
 PI
 XX WPI; 1999-418470/35.
 DR
 XX Production of ethanol and 1,2-propanediol.
 PT
 XX Example 21; Page 40-46; 48pp; English.
 PS
 XX The present sequence represents a synthetic operon, comprising sequences

CC encoding methylglyoxal synthase (MGS), which is functional in yeast
 CC cells. It is used in the course of the invention. The specification
 CC describes a method for the production of ethanol and 1,2-propanediol
 CC (PD) comprising using a genetically modified yeast which expresses
 CC suitable enzymes, particularly an E. coli methyl glyoxal synthase (MGS).
 CC The microbial process can use as a substrate a renewable sugar such as
 CC glucose, xylose or lactose or products from corn and cane sugar and from
 CC lignocellulosic biomass. The process produces no toxic wastes and does
 CC not involve high temperatures and pressures. The products and methods can
 CC be used for the production of 1,2-PD which can be used in the production
 CC of unsaturated polyester resins, liquid laundry detergents,
 CC pharmaceuticals, cosmetics, antifreeze and deicing formulations. They can
 CC also be used to produce ethanol. The byproducts of fermentation are
 CC carbon dioxide, alcohols, and organic acids, all of which can be purified
 CC as valuable co-products or used as animal feed
 XX
 SQ Sequence 7063 BP; 1948 A; 1592 C; 1541 G; 1982 T; 0 U; 0 Other;
 Query Match 38.9%; Score 3045.4; DB 2; Length 7063;
 Best Local Similarity 78.2%; Pred. No. 0;
 Matches 3889; Conservative 0; Mismatches 996; Indels 86; Gaps 16;
 Qy 2470 CCTGATGCGGTATTTCTCTTACGGCATCTGTGCGGTATTTTACACCGCATAGGTAATA 2529
 Db 2117 CCTGATGCGGTATTTCTCTTACGGCATCTGTGCGGTATTTTACACCGCATAGGTAATA 2176
 Qy 2530 ACTGATATATTAATTAAGCTCTAATTTGTGAGTTTAGTATATCATGCAATTTACTTATA 2589
 Db 2177 ACTGATATATTAATTAAGCTCTAATTTGTGAGTTTAGTATATCATGCAATTTACTTATA 2236
 Qy 2590 ATACAGTTTTTTAGTTTTGTGCGCGCATCTTCTCAATATATGCTTCCAGCGTCTTTTC 2649
 Db 2237 ATACAGTTTTTTAGTTTTGTGCGCGCATCTTCTCAATATATGCTTCCAGCGTCTTTTC 2296
 Qy 2650 TGTAAAGCTTACCGCTTACCTTAGCATCTTCCCTTTGCAATAGTCTCTTCCCAACA 2709
 Db 2297 TGTAAAGCTTACCGCTTACCTTAGCATCTTCCCTTTGCAATAGTCTCTTCCCAACA 2356
 Qy 2710 TAATAATGTGAGATCTGTAGAGACCATCATCCAGGTTCTATCTTGTGACCAATG 2769
 Db 2357 TAATAATGTGAGATCTGTAGAGACCATCATCCAGGTTCTATCTTGTGACCAATG 2416
 Qy 2770 CGTCTCCCTTGTCTATCTAAACCCACACCGGGTGTCTAATAATCAACCAATCGTAACCTTCAT 2829
 Db 2417 CGTCTCCCTTGTCTATCTAAACCCACACCGGGTGTCTAATAATCAACCAATCGTAACCTTCAT 2476
 Qy 2830 CTCTTCCACCGCATGCTCTTTTGTAGCAATAAAGCGGATAACAAATCTTTGTGCTCTTCG 2889
 Db 2477 CTCTTCCACCGCATGCTCTTTTGTAGCAATAAAGCGGATAACAAATCTTTGTGCTCTTCG 2536
 Qy 2890 CAATGTCAACAGTACCTTGTATATTTCTCCAGTAGATAGGAGCCCTTGCATGACAAT 2949
 Db 2537 CAATGTCAACAGTACCTTGTATATTTCTCCAGTAGATAGGAGCCCTTGCATGACAAT 2596
 Qy 2950 CTGCTAACATCAAAAGGCTCTAGGTTCTTTTGTACTTCTTCTGCGGCTCTTCAAC 3009
 Db 2597 CTGCTAACATCAAAAGGCTCTAGGTTCTTTTGTACTTCTTCTGCGGCTCTTCAAC 2656
 Qy 3010 CGCTAACATCTCTGGGCGCACACACCGGTGTGATTCGTAATGTCTGCCCATTCGTCTA 3069
 Db 2657 CGCTAACATCTCTGGGCGCACACACCGGTGTGATTCGTAATGTCTGCCCATTCGTCTA 2716
 Qy 3070 TTCTGTATACACCGCAGAGTACTGCAATTTGACTGTATTTACCAATGTGAGCAAAATTTTC 3129
 Db 2717 TTCTGTATACACCGCAGAGTACTGCAATTTGACTGTATTTACCAATGTGAGCAAAATTTTC 2776
 Qy 3130 TGTCTTCGAAGAGTAAATAATTTGACTTTGGCGGATAATGCGCTTTAGCGGCTTAACTGTC 3189
 Db 2777 TGTCTTCGAAGAGTAAATAATTTGACTTTGGCGGATAATGCGCTTTAGCGGCTTAACTGTC 2836
 Qy 3190 CTTCCATGGAAATATCATGCAAGATATCCCATGTGTTTTTAGTAAACAAATTTTGGGAC 3249
 Db 2837 CTTCCATGGAAATATCATGCAAGATATCCCATGTGTTTTTAGTAAACAAATTTTGGGAC 2896

QY 3250 CTAATGCTTCAACTAACTCAGTAATTTCTTGTGTGTGTAAGACATCCAATGAAGACACACA 3309
DB |||||
DB 2897 CTAATGCTTCAACTAACTCAGTAATTTCTTGTGTGTGTAAGACATCCAATGAAGACACACA 2956
QY |||||
QY 3310 AGTTTCTTGTCTTCTGTCATGATATTAATAGCTTGGCAGCAACAGCAGCTAGGATGAG 3369
DB |||||
DB 2957 AGTTTCTTGTCTTCTGTCATGATATTAATAGCTTGGCAGCAACAGCAGCTAGGATGAG 3016
QY |||||
QY 3370 TAGCAGCAGCTTCTTATATGTAGCTTTCGACATGATTTATCTTCTGTTCTCTGAGGTTT 3429
DB |||||
DB 3017 TAGCAGCAGCTTCTTATATGTAGCTTTCGACATGATTTATCTTCTGTTCTCTGAGGTTT 3071
QY |||||
QY 3430 TTGTTCTGTGCACTGGGTTAAGAACTAGGCAATTTCAATGTTCTTCAACACTACATA 3489
DB |||||
DB 3072 TTGTTCTGTGCACTGGGTTAAGAACTAGGCAATTTCAATGTTCTTCAACACTACATA 3131
QY |||||
QY 3490 TGGGTATATACCAATCTAAGTCTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3549
DB |||||
DB 3132 TGGGTATATACCAATCTAAGTCTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3191
QY |||||
QY 3550 TTACCGAATCAAAAAATTTCAAGAAACCGAAATCAAAAAAAGAAATCAAAAAAATG 3609
DB |||||
DB 3192 TTACCGAATCAAAAAATTTCAAGAAACCGAAATCAAAAAAAGAAATCAAAAAAATG 3251
QY |||||
QY 3610 ATGAATTTGAATTTGAAGCTGTGTGTGTGCACTCT-----CAGTACAACTCT 3657
DB |||||
DB 3252 ATGAATTTGAAGCTCTTGTGTGCACTCTTTTGAATTTTGAACATCCGAACCTGGGAGTTT 3311
QY |||||
QY 3658 GCTCTGATGCGCATAGTTAAGCCAGCCGCGACACCGCCGACACCGCTGAGCCGCCCT 3717
DB |||||
DB 3312 TCCTGAAACAGATAGTATATTTGAACCTGTATATTAATATATATAGTCTAGCGCTTTACGG 3371
QY |||||
QY 3718 GACGGCTTGTCTGCTCCGCGATCCGCTTACAGAACGCTGTGACGCTCTCCGGAGCT 3777
DB |||||
DB 3372 AGACAAATGTATGTTTGGTCTCTGGAGAACTATTGCACTATTGTCATAGTATCT 3431
QY |||||
QY 3778 -----GCATGTGTGAGAGTTTTCACCGTCATCACC--GAACCGCGGAGACGAAAG 3827
DB |||||
DB 3432 TGACGCTGCACTCCCGGTTCAATTTTCTGCTTCCATCTTGCACTTCAATAGCATCT 3491
QY |||||
QY 3828 GGCCTCGTATAGCTTATTTATAGTTAATGTCTATGATATATATGTTCTTGTAT 3887
DB |||||
DB 3492 TTGTTAACGAAGCATCTGCTTTCATTTTGTAGAACAAAAATGCAACGCGAGCGCTAA 3551
QY |||||
QY 3888 GATCCAAATCAAGGAATGATAGCATTCAGGATGAGACTAATCCAATTGAGGAGTGG 3947
DB |||||
DB 3552 TTTTTCACCAAGAACTGTGCTTCAATTTTGTAAAAACAAAAATGCAACGCGAGAGC 3611
QY |||||
QY 3948 CAGCATATAGAACAGCTAAAGGTTAGTGTGTAAGGAGCATACGATACCCCGCATGGAAT 4007
DB |||||
DB 3612 TATTTTACCAACGAAGAACTGTGCTTCAATTTTGTAAAAACAAAAATGCAACGCGAGAGC 3671
QY |||||
QY 4008 GGGATATATACAGAGGTTAGTACA--CTACCTTTTCATCTCATGATATATATGTTCTTGTAT 4066
DB |||||
DB 3672 GCTAATTTTTCACCAAGAACTGAGCTGCAATTTTACAGAACAGAAATGCAACGCGAG 3731
QY |||||
QY 4067 AGTACGATTTAAGCATTAACACGCACTATGCGCTTCTCTCATGATATATATATACAG 4126
DB |||||
DB 3732 AGCGCTATTTTACCAAGAACTATATCTTCTTTTGTCTTCAAAATGCAATGCCG 3791
QY |||||
QY 4127 GCAACACG-----CAGATATAGGTGCGAGTGGAACAGTGTATGTGCGCAGCTCG 4180
DB |||||
DB 3792 AGAGCGCTATTTTCTAAACAAAGCATCTAGATTTACTTTTCTCTCTTGTGCGCTCTA 3851
QY |||||
QY 4181 CGTTGCAATTTTCGAAGCGCTCGTT-----TTGGAACGCTTTGAAGTCTCTAT 4230
DB |||||
DB 3852 TAATGAGTCTCTGTGATACTTTTGCACCTGTAGGTCGTTAAGGTTAGAAAGAGGCTAC 3911
QY |||||
QY 4231 TCCGAAGTTCTCTATCTCT-----AGAAATATAGAACTTCAGAGCGCTTTTGAAC 4284
DB |||||
DB 3912 TTTGTTGTCTATTTTCTCTTCCATAAAAAAGCCTGACTCCACTTCCCGGTTTACTGAT 3971

QY 4285 CAAAAGCGC-TCTGAAGACGCACTTTTCAAAAAACCAAAAAACGACCGGACTGTAAACGAGC 4343
DB |||||
DB 3972 TACTAGGAAGCTGCGGGTGCAATTTTCAAGATAAAGGCAATCCCGATTTATATCTATA 4031
QY |||||
QY 4344 TACTAAAAATTTGCGAATACCGCTTCCACAAACATTTGCTCAAAAGTATCTCTTTGCTATA 4403
DB |||||
DB 4032 CGATGTGATTTGCGCATACTTTTGTGAACAGAAAGTGTAGCGTTGATGATTTCTTC--- 4087
QY |||||
QY 4404 TATCTCTGTGCTATATCCCTATATACCTACCCATCCACCTTTTCGCTTCTTGAACCTTGCA 4463
DB |||||
DB 4088 -ATTGCTCAGAAAAATTTATGAACGGTTTCTTCTATTTTGTCTCTATATACTACGTATAGGA 4146
QY |||||
QY 4464 TCTAAACTCGACCTCTACATTTTATTATTTATCTCTAGTATTTATCTCTTTAGACAAAAA 4523
DB |||||
DB 4147 AATGTTTACATTTTCTGATTTGTTTTCGATTTCTCTATGAATAGTTCTTACTACAAATTTT 4206
QY |||||
QY 4524 ATTGTAGTAAAGCACTATTTCTAGAGTGAATCGAAAAATACGAAAAATGTAACATTTTCC 4583
DB |||||
DB 4207 TTTGCTTAAAGAGTAACTACTAGAGATAAACAATAAAAAATGTAGAGTTCGAGTTTAGATGC 4266
QY |||||
QY 4584 TATACGTAGTATATAGAGACAAAAATAGAAAGAACCGTTCTATATTTTCTGACCAAT----- 4639
DB |||||
DB 4267 AGTTTCAAGGAGGAAAGGTGGTAGGTATTTATAGGGATATAGCACAGAGATATAT 4326
QY |||||
QY 4640 -GAAGAACTCATCAACGCTATCACTTTCTGTTCAAAAGTATGCGCAATCCACATCGGTAT 4698
DB |||||
DB 4327 AGCAAGAGATACTTTTGTAGCAATGTTTGTGAAGCGGTATTTGCAATATTTTAGTAGCT 4386
QY |||||
QY 4699 AGAATATATCGGGATGCTTTTCTTGAANAATGACCCGACGCTTCGTAGTAAATC 4758
DB |||||
DB 4387 CGTTACAGTCCGGTGGGTTTTTGGTTTTTGAAGTGGCTTTCAG--AGCGCTTTTGG 4443
QY |||||
QY 4759 AGTAAACGCGGAAGTGGAGTCAAGCTTTTATGGAAGAGAAAAATAGACACCAAGTA 4818
DB |||||
DB 4444 TTTTCAAGAGCGCTCTGAAGTTCTTATCTTCTAGTAGAGNATAGGAATCTCGGATTA 4503
QY |||||
QY 4819 GCTTCTTCTAACTTAAACGACCTTACAGTCAAAAGTTATCAAGAGACTGCAATATAG 4878
DB |||||
DB 4504 GGAACCTTCAAGCGTTTTCGAA-----AACGAGCGCTTCCGAAAAATGCAACGCGA 4553
QY |||||
QY 4879 AGCGCACAAAGGAGAAAAAAGTAATCTAAGATGCTTTCTTGAANAATAGCGCTCTCG 4938
DB |||||
DB 4554 GCTGCGCACATACAGCTCACTGTTACGTCGCACTTATCTGCGTGTGCTGTATATA 4613
QY |||||
QY 4939 GATGCAATTTTCTAGAACAAAAAGATATAGATTTCTTTTGTGTGTAATAAGCGCTCTC 4998
DB |||||
DB 4614 TATATACATGAGAGAACCGCATAGTGGCTGTTTATGCTTAAATGCTTATGTTGCACTC 4673
QY |||||
QY 4999 GCGTTGCAATTTTCTGTTCTGTAATAATGAGCTCAGATTTCTTTGTTGAAAAATTAG 5054
DB |||||
DB 4674 TCAGTACATCTGCTCTGATGCGCATAGTTAAGCCAGCCGCGACACCCGCAACCCCG 4733
QY |||||
QY 5055 CGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAGCAAGATTTCTTGGTTGTAAT 5114
DB |||||
DB 4734 CTGACGCGCTTACGCGGCTTGTGCTCTCCCGCATCCGCTTACAGAACGCTGTGACCG 4793
QY |||||
QY 5115 AGCGCTTTTCTGCTGCAATTTCTGTTTAAATAATGACGCTCAGATTTCTTTGTTGAAAA 5174
DB |||||
DB 4794 TCTCCGGAGCTGCTGCTGAGGTTTTTACCGCTCATCCGAAACGCGGAGAGCA 4853
QY |||||
QY 5175 ATTAGCGCTCTCGGTTGCAATTTTGTCTCAAAATGAAGCAGACAGATGCTT-----C 5227
DB |||||
DB 4854 AGGGCTCTGATGATGCGCTTATTTATAGTTAAATGTCTATGATTAATGTTTCTTAGA 4913
QY |||||
QY 5228 GTTCAGGTGGCACTTTTTCGGGAAATGTCGGGAAACCTTATTTGTTTATTTTCTTAA 5287
DB |||||
DB 4914 CGTCAAGTGGCACTTTTTCGGGAAATGTCGGGAAACCTTATTTGTTTATTTTCTTAA 4973
QY |||||
QY 5288 TACATTTCAATATGATCGCTCATGAGACAAATACCCGTGATAAATGCTTCAATAATAT 5347
DB |||||
DB 4974 TACATTTCAATATGATCGCTCATGAGACAAATACCCGTGATAAATGCTTCAATAATAT 5033
QY |||||
QY 5348 GAAAAAGGAGATAGATATTCAAACATTTCCGTGTCGCCCTTATTCCTCTTTTTCGCG 5407

Db	5034	GA	AAAAAGAAAGAGTATGAGTATTTCAACATTTCCGTGTGCGCCCTTATTCCCTCTTTTTTGCGG	5093
Qy	5408	CA	TTTTGCCCTTCCGTGTTTTTCTCACCACGAAACGCTGTGTGAAGTAAAGATGCTGAAG	5467
Db	5094	CA	TTTTGCCCTTCCGTGTTTTTCTCACCACGAAACGCTGTGTGAAGTAAAGATGCTGAAG	5153
Qy	5468	AT	CAGTTGGGTGCGACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTG	5527
Db	5154	AT	CAGTTGGGTGCGACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTG	5213
Qy	5528	AG	AGTTTTCGCCCCCGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTCGTATGTG	5587
Db	5214	AG	AGTTTTCGCCCCCGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTCGTATGTG	5273
Qy	5588	GC	CGGTATTATCCCGTATTGACGCGGGCGAAGCAACCTCGTCCGCGCATACACTATT	5647
Db	5274	GC	CGGTATTATCCCGTATTGACGCGGGCGAAGCAACCTCGTCCGCGCATACACTATT	5333
Qy	5648	CT	CAGATGACTTGGTTGAGTACTCACCGAGTCACAGAAAGCATCTTTACGGATGGGATGA	5707
Db	5334	CT	CAGATGACTTGGTTGAGTACTCACCGAGTCACAGAAAGCATCTTTACGGATGGGATGA	5393
Qy	5708	CAG	TAAGAGAAATTATGCAGTGTGCCATAACCATGATGATATACTGTGCGGCCAACTTTAC	5767
Db	5394	CAG	TAAGAGAAATTATGCAGTGTGCCATAACCATGATGATATACTGTGCGGCCAACTTTAC	5453
Qy	5768	TT	CTGCAACGANTCGGAGGACCGAAGAGCTAACCCGCTTTTGTGCAACATCGGGGATC	5827
Db	5454	TT	CTGCAACGANTCGGAGGACCGAAGAGCTAACCCGCTTTTGTGCAACATCGGGGATC	5513
Qy	5828	AT	GTAACCTCGCTTGATCTGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGC	5887
Db	5514	AT	GTAACCTCGCTTGATCTGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGC	5573
Qy	5888	GT	GACACCAACGATGCTGTATAGCAATAGCAACAAACGTTGCGCAAACTATTAACTGGCGAAC	5947
Db	5574	GT	GACACCAACGATGCTGTATAGCAATAGCAACAAACGTTGCGCAAACTATTAACTGGCGAAC	5633
Qy	5948	TAC	TACTACTAGCTTCCCGGCACAACTAATAGACTGGATGGAGCGGATAAAGTTGTCAG	6007
Db	5634	TAC	TACTACTAGCTTCCCGGCACAACTAATAGACTGGATGGAGCGGATAAAGTTGTCAG	5693
Qy	6008	GAC	CACCTTCGCGCTCGGCCCTTCCGCTCGCTGCTTTATTGTGTATAAATCTGGAGCCG	6067
Db	5694	GAC	CACCTTCGCGCTCGGCCCTTCCGCTCGCTGCTTTATTGTGTATAAATCTGGAGCCG	5753
Qy	6068	GT	GAGCGTGGGTCTCGCGGTATCATTTGACGACTGTGGGGCCAGATGGTAAAGCCCTCCCGTA	6127
Db	5754	GT	GAGCGTGGGTCTCGCGGTATCATTTGACGACTGTGGGGCCAGATGGTAAAGCCCTCCCGTA	5813
Qy	6128	TC	GATGATTATACACAGCGGGNGTCAGGCAACTATGGATGAACGNAATAGACAGATCG	6187
Db	5814	TC	GATGATTATACACAGCGGGNGTCAGGCAACTATGGATGAACGNAATAGACAGATCG	5873
Qy	6188	CT	GAGATAGTGCTCTACTGATTAAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATA	6247
Db	5874	CT	GAGATAGTGCTCTACTGATTAAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATA	5933
Qy	6248	TAC	TTTAGATTGATTTAAAACTTCATTTTTTAATTTAAAGGATCTAGGTGAAGATCCTTT	6307
Db	5934	TAC	TTTAGATTGATTTAAAACTTCATTTTTTAATTTAAAGGATCTAGGTGAAGATCCTTT	5993
Qy	6308	TT	GATAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACC	6367
Db	5994	TT	GATAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACC	6053
Qy	6368	CC	GTAGAAAAGATCAAAAGGATCTTTTGGAGATCCTTTTTTCTGCGCGTAACTCTGCTGCT	6427
Db	6054	CC	GTAGAAAAGATCAAAAGGATCTTTTGGAGATCCTTTTTTCTGCGCGTAACTCTGCTGCT	6113
Qy	6428	TG	CAAAACAAAAAACCAACCGCTACCGCGTGGTTGTTTTGCCGGATCAAGAGCTACCAA	6487

Db	6114	TGCAAA	CAAAAAA	CAACCGCTAC	CAGCGGTGGTTGTTTGC	CGATCAAGAGCTACCA	61173	
QY	6488	CTCTTTT	TCGAAAGTAA	CTGGCTTC	CAGCAGCGCAGATACCA	AACTACTGTCTTCTAG	6547	
Db	6174	CTCTTTT	TCGAAAGTAA	CTGGCTTC	CAGCAGCGCAGATACCA	AACTACTGTCTTCTAG	6233	
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QY	6668	ACTCA	GACGATAGTTAC	CCGGATAAG	CGCGTCGGGCTGAA	CGGGGGTTCGTGCA	6727	
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QY	6788	GAGAA	AGCGCACGCTTCC	GAAAGGAGAA	AGCGCGACAGGTAT	TCGGTAAGCGCGCAGG	6847	
Db	6473	GAGAA	AGCGCACGCTTCC	GAAAGGAGAA	AGCGCGACAGGTAT	TCGGTAAGCGCGCAGG	6532	
QY	6848	TCGAA	CAGGAGAGCGC	CAGGAGAGCTTCC	AGGGGAAACGGCTCGTAT	TCTTTTAGTC	6907	
Db	6533	TCGAA	CAGGAGAGCGC	CAGGAGAGCTTCC	AGGGGAAACGGCTCGTAT	TCTTTTAGTC	6592	
QY	6908	CTGT	CGGGTTTCC	CCACCTCTG	ACTTGTAGCGT	CGATTTTGTGATGCTCGTACGGGGGC	6967	
Db	6593	CTGT	CGGGTTTCC	CCACCTCTG	ACTTGTAGCGT	CGATTTTGTGATGCTCGTACGGGGGC	6652	
QY	6968	GGAG	CCCTATGG	AAAAACCG	CAGCAACCGCGCTTTT	TACGGTTCCTGGCTTTTGTCTGGC	7027	
Db	6653	GGAG	CCCTATGG	AAAAACCG	CAGCAACCGCGCTTTT	TACGGTTCCTGGCTTTTGTCTGGC	6712	
QY	7028	CTTTT	GTCTCACATGTTCTT	TTCTTCGCGTTAT	TCCCTCGATTCTGTGGAT	TAAACCGTATTACCG	7087	
Db	6713	CTTTT	GTCTCACATGTTCTT	CTTCGCGTTAT	TCCCTCGATTCTGTGGAT	TAAACCGTATTACCG	6772	
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QY	7148	GGAG	GAACGGGAAG	AGCGCCCAAT	ACGMAACCGCTCT	CCCCCGCGCTTGGCCGATTC	7207	
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QY	7208	ATTAA	TGCACTGG	CACGACGAGT	TTTCCGACGTG	GAAGCGGCGAGTGA	CGCAACGCGCA	7267
Db	6893	ATTAA	TGCACTGG	CACGAGT	TTTCCGACGTG	GAAGCGGCGAGTGA	CGCAACGCGCA	6952
QY	7268	TTAAT	GTGAGT	TACCTCACT	TTAGGCAACCG	AGGCTTTTACATTTTATGCTTCCGGCTC	7327	
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Search completed: May 16, 2004, 01:31:57
Job time : 1907.33 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 00:27:52 ; Search time 12147.4 Seconds
(without alignments)
19243.679 Million cell updates/sec

Title: US-10-067-449-9

Perfect score: 7828

Sequence: 1 atgcgctgggttcacaa.....tttttaatttaatacaaaaa 7828

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1459.2	18.6	3049	11	BC034387 Homo sapi
2	1291.4	16.5	1497	29	AY421215 Homo sapi
3	1288.2	16.5	1814	14	CD014068 90134560
4	1074.4	13.7	1497	29	AY421216 Pan trogl

C	5	1055.8	13.5	1070	9	AJ281552
C	6	1037	13.2	1497	29	AY421217
C	7	988.4	12.6	1067	9	AU081137
C	8	986.4	12.6	1013	12	BM438846
C	9	957	12.2	1089	9	AU081124
C	10	924	11.8	1004	9	AJ281480
C	11	916.8	11.7	973	14	CD458281
C	12	900.6	11.5	1025	29	CG700598
C	13	899.8	11.5	996	29	CG392995
C	14	899.4	11.5	925	14	CB686151
C	15	886.2	11.3	917	14	CD458286
C	16	884.6	11.3	1021	29	CG392916
C	17	873.6	11.2	935	12	BG838279
C	18	866	11.1	918	14	CD459092
C	19	865	11.1	1073	14	CF269652
C	20	850	10.9	1056	29	CG835880
C	21	841	10.7	841	9	AL042026
C	22	832.8	10.6	872	14	CD459085
C	23	824.6	10.5	854	12	BM438950
C	24	820.2	10.5	870	14	CD458333
C	25	820	10.5	1163	9	AU081044
C	26	819.6	10.5	1249	28	BZ572284
C	27	817	10.4	906	29	CG839354
C	28	814.4	10.4	1126	28	BZ577702
C	29	808	10.3	819	14	CD649375
C	30	807.6	10.3	966	28	BZ570738
C	31	804.8	10.3	833	14	CB686421
C	32	797.6	10.2	1011	28	BZ576726
C	33	785.4	10.0	1574	28	BZ572566
C	34	780.2	10.0	1194	28	BZ578985
C	35	777.8	9.9	800	9	AJ281449
C	36	774.8	9.9	1336	28	BZ575810
C	37	774.4	9.9	789	14	CD280920
C	38	772.4	9.9	954	9	AL044364
C	39	771	9.8	1370	28	BZ571721
C	40	770.2	9.8	922	28	BZ557830
C	41	767.6	9.8	863	14	CF752100
C	42	767.4	9.8	959	28	BZ557985
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C	44	761	9.7	857	14	CB814984
C	45	757	9.7	759	14	CD279661

ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens, Similar to solute carrier family 2 (facilitated glucose transporter), member 4, clone IMAGE:5187454, mRNA.
ACCESSION BC034387.1 GI:21706716
VERSION BC034387
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3049)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

SOURCE
ORGANISM Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
AUTHORS 1 (bases 1 to 1497)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS 2 (bases 1 to 1497)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.
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Best Local Similarity 71.8%; Pred. No. 4,7e-168;
Matches 1075; Conservative 0; Mismatches 422; Indels 0; Gaps 0;
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DB 61 GTGCTTGGCTCCCTGAGTGGTGGTACACATTTGGGTCATCATGCTCCCTCAGAAGTG 120
QY 154 ATTGAACAGAGTACAAATCAGAGCTGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGG 213
DB 121 ATTGAACAGAGTACAAATCAGAGCTGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 214 ATCCCTCCAGGACCCCTCAGCAGGAGTGAAGTGGGACCCCTGCTTGTCTGTGGG 273
DB 181 ATCCCTCCAGGACCCCTCAGCAGGAGTGAAGTGGGACCCCTGCTTGTCTGTGGG 240
QY 274 GGCATGATTTCT 333
DB 241 GGCATGATTTCT 300
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DB 301 ATGCTGGTCAACAAATCTCTGGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 394 GCTGCTCTCTATGAATGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 453
DB 361 GCTGCTCTCTATGAATGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
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DB 421 ACATCAGGCTGGTGGCCATGATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
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DB 481 CTGGGAGCCCTCAACAAATCTCTGGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540

RESULT 5
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DEFINITION
4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P6F11, mRNA sequence.
ACCESSION
AJ281552
VERSION
AJ281552.1
GI:6929432
KEYWORDS
EST.

QY 574 TTGGAGTCCCTCCTGGGCACTGCCAGCGTGTGGCCACTGCTCCTGGGCGCTCAGAGTGCTA 633
DB 541 NNN 600
QY 634 CCTGCGCTCCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 693
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DB 661 NNN 720
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QY 814 CCACATGCTCCCTGCTCCAGCTCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCGGAG 873
DB 781 CCACATGCTCCCTGCTCCAGCTCTGCGGAGCGCTGCGGAGCGCTGCGGAGCGCTGCGGAG 840
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DB 841 NNN 900
QY 934 AGCATCTTCGAGACAGCAGGAGGAGTGGCGAGCGCTGCTGCGGAGCGCTGCGGAGCGCTG 993
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QY 1294 TTCATCATTTGGCATGGGTTTCCAGTATGTTGGGAGGCTATGGGCGCTTACGCTTCTCT 1353
DB 1261 NNN 1320
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DB 1441 CAGGAGGTGAACACCGAGCAGAACTTGAGTATTTAGGCGCAGATGAGAACGACTGA 1497

SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

REFERENCE 1 (bases 1 to 1070)
 AUTHORS Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B. and Kafatos, F.C.
 TITLE Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
 MEDLINE 20300950
 PUBMED 10841561
 COMMENT Contact: Dimopoulos G
 Fotis C. Kafatos laboratory
 European Molecular Biology Laboratory
 Meyerhofstrasse 1, 69117 Heidelberg, Germany.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /lab_host="E. coli DH10B"
 /clone_lib="Anopheles gambiae immune competent 4A3A"
 /note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches to Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN
 Query Match 13.5%; Score 1055.8; DB 9; Length 1070;
 Best Local Similarity 99.7%; Pred. No. 6.4e-165;
 Matches 1068; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 DB CTGGATGAGGCGGATAAAGTTGCAGGACCACTTCTCGGCTCGG-CTTCGGCTGGCTG 952
 QY 6042 GTTATTGCTGATAAATCTGAGCGGCTGAGCGTGGGTCTCGCGGTATCATTCAGCACT 6101
 DB GTTATTGCTGATAAATCTGAGCGGCTGAGCGTGGGTCTCGCGGTATCATTCAGCACT 892
 QY 6102 GGGCCAGATGTAAGCCCTCCGATGCTAGTATCTACACGACGGGAGTCAGGCAAC 6161
 DB GGGCCAGATGTAAGCCCTCCGATGCTAGTATCTACACGACGGGAGTCAGGCAAC 832
 QY 6162 TATGATGAACGAATAGACAGATCGCTGAGATAGTGGCTCACTGATTAAAGCATTCGTA 6221
 DB TATGATGAACGAATAGACAGATCGCTGAGATAGTGGCTCACTGATTAAAGCATTCGTA 772
 QY 6222 ACTGTCAGACCAAGTTTACTCATATATATCTTAGATTGATTTAAACCTCATTTTAAAT 6281
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 QY 6282 TAAAGGATCTAGGTGAAGTCCCTTTTGAATCTCATGACCAAAATCCCTTAACGTGA 6341
 DB TAAAGGATCTAGGTGAAGTCCCTTTTGAATCTCATGACCAAAATCCCTTAACGTGA 652
 QY 6342 GTTTTCCTTCCACTGAGCGTCAGACCCCGTAGAAAGATCAAAAGATCTTTCTGAGATCC 6401

651 GTTTTCCTTCCACTGAGCGTCAGACCCCGTAGAAAGATCAAAAGATCTTTCTTGAGATCC 592
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RESULT 6
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 LOCUS Mus musculus SLC2A4 gene, VIRUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY421217
 VERSION AY421217.1 GI:39777174
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1497)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1497)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence as made by sequencing genomic exons and ordering them

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infectious hematopoietic necrosis virus"
/note=common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"

ORIGIN

Query Match      12.6%; Score 988.4; DB 9; Length 1067;
Best Local Similarity 98.7%; Pred. No. 9.4e-154; Indels 2; Gaps 2;
Matches 1017; Conservative 0; Mismatches 11;

QY 6411 GCGCTAATCTGCTGCTGCAAAACAAAACACCCGCTACACGCGTGGTGTGTTTGGC 6470
DB 1067 GCGCTAATCTGCTGCTGCAAAACAAAACACCCGCTACACGCTACACGCTGTTGTTTGGC 1010
QY 6471 GGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACCTGGCTTACGAGAGCGGAGATACC 6530
DB 1009 GGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACCTGGCTTACGAGAGCGGAGATACC 950
QY 6531 AAATACTGCTCTTAGTGAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAC 6590
DB 949 AAATACTGCTCTTAGTGAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAC 890
QY 6591 GCCTACATACCTCGCTCTGCTAACTCTGTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTC 6650
DB 889 GCCTACATACCTCGCTCTGCTAACTCTGTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTC 830
QY 6651 GTGCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGCGGAGCGGTGCGGCTG 6710
DB 829 GTGCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGCGGAGCGGTGCGGCTG 770
QY 6711 AACGGGGGTTCTGTCACACAGCCGCTGGAGGAAAGCGGAGGAGTACACCACTGAGATA 6770
DB 769 AACGGGGGTTCTGTCACACAGCCGCTGGAGGAAAGCGGAGGAGTACACCACTGAGATA 710
QY 6771 CCTACAGCGTGAGCTATGAGAAAGCGCCACCTCTCCGAAAGGAGGAGGAGGAGGAGT 6830
DB 709 CCTACAGCGTGAGCTATGAGAAAGCGCCACCTCTCCGAAAGGAGGAGGAGGAGGAGT 650
QY 6831 TCCGTAAGCGGCGAGGTCGGAACAGAGAGCGGACGAGGAGGAGTCCAGGGGGAACGC 6890
DB 649 TCCGTAAGCGGCGAGGTCGGAACAGAGAGCGGACGAGGAGGAGTCCAGGGGGAACGC 590
QY 6891 CTGGTATCTTTATAGTCTGTCGCTGTTGCGCACTCTGACTTGGAGGAGTGGATTTTGTG 6950
DB 589 CTGGTATCTTTATAGTCTGTCGCTGTTGCGCACTCTGACTTGGAGGAGTGGATTTTGTG 530
QY 6951 ATGCTCGTCAGGGGCGGAGCCTATGGAATAAGCCAGCAACCGCGGCTTTTACGGTT 7010
DB 529 ATGCTCGTCAGGGGCGGAGCCTATGGAATAAGCCAGCAACCGCGGCTTTTACGGTT 470
QY 7011 CTGGCCCTTTGCTGGCCCTTTTGTCTACATGTTCTTCTGCGGTATCCCTGATTCGT 7070
DB 469 CTGGCCCTTTGCTGGCCCTTTTGTCTACATGTTCTTCTGCGGTATCCCTGATTCGT 410
QY 7071 GGATAACCGGTATACCGCTTTGAGTGAGCTGATACCGCTCGCGGAGCGGAGCGGAGCGGA 7130
DB 409 GGATAACCGGTATACCGCTTTGAGTGAGCTGATACCGCTCGCGGAGCGGAGCGGAGCGGA 350
QY 7131 GCGCAGCGAGTCAGTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7190
DB 349 GCGCAGCGAGTCAGTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 290
QY 7191 GCGCGGTTGGCGGATTCATTAATGAGCTGGCGACAGAGGTTTCCGACTGGAAGCGGG 7250
DB 289 GCGCGGTTGGCGGATTCATTAATGAGCTGGCGACAGAGGTTTCCGACTGGAAGCGGG 230
QY 7251 CAGTGAGCGCAACCAATTAATGAGTACCTCACTCATTTAGGACCCCGAGGCTTTACA 7310
DB 229 CAGTGAGCGCAACCAATTAATGAGTACCTCACTCATTTAGGACCCCGAGGCTTTACA 170
QY 7311 CTTTATGCTTCCGGCTCCTATGTTGTGGAATTTGTGAGCGGATAACAATTTTACACAGG 7370
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169 CTTTATGCTTCCGGCTCGTATGTTGTGGAATTTGTGAGCGGATAACAATTTTACACAGG 110
7371 AACACGCTATGACCATGATTACCCAGCGCGCAATTAACCTTAAACCTTAAAGGGAACAAA 7430
109 AACACGCTATGACCATGATTACCCAGCTCGAAATTTAACCTTAAAGGGAACAAA 50
7431 GCTGGAGCTC 7440
49 GCTGGAGCTC 40

BM438846 1013 bp mRNA linear EST 31-JAN-2002
IPLV00157 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
BM438846
BM438846.1 GI:18460568
EST.
Ictalurus punctatus (channel catfish)
Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
Pang, J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.
Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
Unpublished (2002)
Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
1. 1013
/organism="Ictalurus punctatus"
/mol_type="mRNA"
/db_xref="taxon:7998"
/clone_lib="Liver cDNA library"
/note="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

FEATURES
source
1. 1013
/organism="Ictalurus punctatus"
/mol_type="mRNA"
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/clone_lib="Liver cDNA library"
/note="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

ORIGIN
Query Match      12.6%; Score 986.4; DB 12; Length 1013;
Best Local Similarity 99.5%; Pred. No. 2e-153;
Matches 1009; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 5407 GCATTTTGGCTTCTGTTTGTCTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAA 5466
DB 1 GCATTTTGGCTTCTGTTTGTCTCACCCAGAGAGCGTGGTGAAGTAAAGATGCTGAA 60
QY 5467 GATCAGTTGGTGCAACGAGTGGGTATACGAACTGATCTCAACGCGGTAAAGTCTT 5526
DB 61 GATCAGTTGGTGCAACGAGTGGGTATACGAACTGATCTCAACGCGGTAAAGTCTT 120
QY 5527 GAGAGTTTTTCCGCCCCGAAGAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 5586
DB 121 GAGAGTTTTTCCGCCCCGAAGAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 180
QY 5587 GGGCGCGTATTAATCCCGTATTGACGCGGCAAGAGCAACTCGGTGCGCGCATACATAT 5646
DB 181 GGGCGCGTATTAATCCCGTATTGACGCGGCAAGAGCAACTCGGTGCGCGCATACATAT 240
QY 5647 TCTCAGATGACTTGTTGTTGAGTACTACCACTGATCAGAAAAGCATCTTACCGATGGCATG 5706
DB 241 TCTCAGATGACTTGTTGTTGAGTACTACCACTGATCAGAAAAGCATCTTACCGATGGCATG 300
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QY 5707 ACAGTAAAGAAATATGAGTGTGCTGCAATACCATGAGTGATAACACTCGGCCCACTTAA 5766
 DB 301 ACAGTAAAGAAATATGAGTGTGCTGCAATACCATGAGTGATAACACTCGGCCCACTTAA 360
 QY 5767 CTTCTGACAAACGATCGGAGGACCGAAGGAGCTAAACCGCTTTTTCGACAAACATGGGGAT 5826
 DB 361 CTTCTGACAAACGATCGGAGGACCGAAGGAGCTAAACCGCTTTTTCGACAAACATGGGGAT 419
 QY 5827 C-ATGTAACCTCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGA 5885
 DB 420 CAATGTAACCTCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGA 479
 QY 5886 GGTTGACACGATCGCTGTAGCAATGGCAACACGTTGGCGCAAACTATTAACTGGCGA 5945
 DB 480 GGTTGACACGATCGCTGTAGCAATGGCAACACGTTGGCGCAAACTATTAACTGGCGA 539
 QY 5946 ACTACTTACTCTAGCTTCCCGCAACAATTAATAGACTCGATCGAGCGGATGAAGTTGC 6005
 DB 540 ACTACTTACTCTAGCTTCCCGCAACAATTAATAGACTCGATCGAGCGGATGAAGTTGC 599
 QY 6006 AGGACCACTTCTCGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAAATCTGGAGC 6065
 DB 600 AGGACCACTTCTCGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAAATCTGGAGC 659
 QY 6066 CGGTGAGCGTGGTCTCGCGGTATCATTCAGCACTGGGGCCAGATGGTAAAGCCCTCCCG 6125
 DB 660 CGGTGAGCGTGGTCTCGCGGTATCATTCAGCACTGGGGCCAGATGGTAAAGCCCTCCCG 719
 QY 6126 TATCGTAGTATCTACACAGCGGGAGTCAGCAACTATGGATGAACGAATAGACAGAT 6185
 DB 720 TATCGTAGTATCTACACAGCGGGAGTCAGCAACTATGGATGAACGAATAGACAGAT 779
 QY 6186 CGCTGAGTAGTGTCTCACTGATTAAGCAATGGTAACTGTGACACCAAGTTTACTCAT 6245
 DB 780 CGCTGAGTAGTGTCTCACTGATTAAGCAATGGTAACTGTGACACCAAGTTTACTCAT 839
 QY 6246 TATCTTTAGATGATTTAAACTCTCACTTTTAAATTTAAAGGATCTAGTGAAGATCT 6305
 DB 840 TATCTTTAGATGATTTAAACTCTCACTTTTAAATTTAAAGGATCTAGTGAAGATCT 899
 QY 6306 TTTTGTATCTCATGACCAAAATCCCTTAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 6365
 DB 900 TTTTGTATCTCATGACCAAAATCCCTTAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 959
 QY 6366 CCCCGTAGAAAGATCAAAAGGATCTTCTTTGAGATCTTTTCTGCGGGTAAAT 6419
 DB 960 CCCCGTAGAAAGATCAAAAGGATCTTCTTTGAGATCTTTTCTGCGGGTAAAT 1013

RESULT 9
 AU081124/c
 LOCUS
 DEFINITION
 hematopoietic necrosis virus Oncorhynchus mykiss cdna clone KG'12,
 mRNA sequence.
 AU081124
 AU081124.1 GI:6431472
 EST.
 Oncorhynchus mykiss (rainbow trout)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 1089)
 Kono, T., Sakai, M. and LaPatra, S.E.
 Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
 Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
 Hematopoietic Necrosis Virus
 Mar. Biotechnol. 2 (5), 493-498 (2001)
 Contact: Masahiro Sakai
 Faculty of Agriculture
 Miyazaki University

1-1 nishi gakukenibanadai, Miyazaki, Miyazaki 889-2192, Japan
 Email: m.sakai@cc.miyazaki-u.ac.jp.
 Location/Qualifiers
 1..1089
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="KG'12"
 /tissue_type="kidney"
 /clone_lib="Oncorhynchus mykiss kidney infected by
 infectious hematopoietic necrosis virus"
 /note="common name:rainbow trout ; infected by infectious
 hematopoietic necrosis virus"

ORIGIN

Query Match 12.2%; Score 957; DB 9; Length 1089;
 Best Local Similarity 97.0%; Pred. No. 1.5e-148;
 Matches 1018; Conservative 0; Mismatches 25; Indels 6; Gaps 4;

QY 6398 ATCCCTTTTCTCGCGCTAAATCTGC-TGCTTGGCAACAAAAA---AACCCAGCTTACCA 6453
 DB 1089 ATCCGTTTTTTCGCGGGTAAATCTGCTGCTTGGCAACAAAAAGACACCCCTTCCCAG 1030
 QY 6454 GCGGTGTTTCTTTCGCGGAT-CAAGAGCTACCAACTCTTTTTCGAAGTAACCTGGCTT 6512
 DB 1029 CGGTGTTTGTGTTTTCGCGGATCCCACTCTTTTTCGAAGTAACCTGGCTT 970
 QY 6513 CAGCAGAGCGCAGATACCAATACCTCTTCTAGTGTAGCGGTAGTGTAGGCGAC-CACT 6571
 DB 969 CAGCAGAGCGCAGATACCAATACCTCTTCTAGTGTAGCGGTAGTGTAGGCGACAACT 910
 QY 6572 TCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAACTCTGTGTGTACAGTGGCTG 6631
 DB 909 TCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAACTCTGTGTGTACAGTGGCTG 850
 QY 6632 CTGCCAGTGGCGATTAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATA 6691
 DB 849 CTGCCAGTGGCGATTAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATA 790
 QY 6692 AGGCGCAGCGGTCTGGCTGAAACGGGGTTCGTGACACAGCCAGCTTGGAGCGAACA 6751
 DB 789 AGGCGCAGCGGTCTGGCTGAAACGGGGTTCGTGACACAGCCAGCTTGGAGCGAACA 730
 QY 6752 CTTACACCGAACTGAGATACCTTACAGCGTGTAGCTATGAGAAAGCGCCAGCTTCCGGAAG 6811
 DB 729 CTTACACCGAACTGAGATACCTTACAGCGTGTAGCTATGAGAAAGCGCCAGCTTCCGGAAG 670
 QY 6812 GGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGTTGGAAACAGAGAGCGCACGAGG 6871
 DB 669 GGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGTTGGAAACAGAGAGCGCACGAGG 610
 QY 6872 AGCTTCCAGGGGGAACCGCTGTATCTTTATAGTCTGTGCGGTTTCCCACTCTGTAC 6931
 DB 609 AGCTTCCAGGGGGAACCGCTGTATCTTTATAGTCTGTGCGGTTTCCCACTCTGTAC 550
 QY 6932 TTGAGCGTCTGATTTTGTGATCTCTGTCAGGGGGCGGAGCTATGGAACAGCCAGCA 6991
 DB 549 TTGAGCGTCTGATTTTGTGATCTCTGTCAGGGGGCGGAGCTATGGAACAGCCAGCA 490
 QY 6992 AGCGGCTTTTTCAGGTTCTGGCTTTTGTGCGCTTTTGTGCTCATGTGTTCTTCTCTG 7051
 DB 489 AGCGGCTTTTTCAGGTTCTGGCTTTTGTGCGCTTTTGTGCTCATGTGTTCTTCTCTG 430
 QY 7052 CGTTATCCCTGATCTGTGGATTAACCGTATTACCGCTTTTGTGCTCATGTGTTCTTCTCTG 7111
 DB 429 CGTTATCCCTGATCTGTGGATTAACCGTATTACCGCTTTTGTGCTCATGTGTTCTTCTCTG 370
 QY 7112 GCGCAGCGCAACGACCGAGCTAGTGTAGCGGAGGAGCGAAGCGAAGCGCCCAA 7171
 DB 369 GCGCAGCGCAACGACCGAGCTAGTGTAGCGGAGGAGCGAAGCGAAGCGCCCAA 310
 QY 7172 TACGCAACCGCTCTCCCGCGGTTTGGCCGATTTAATGTGAGCTGTGCGACGAGT 7231

Db 309 TACGCAAAACCCCTCTCCCCCGCGTGGCGGATTCATTAAATGACGCTGCACGACGAGGT 250
QY 7232 TTCCCGACTGGAAGCGCGGAGTCAGCGCAACGCAATTAATGTGAGTTACTCTACTCATTT 7291
Db 249 TTCCCGACTGGAAGCGCGGAGTCAGCGCAACGCAATTAATGTGAGTTAGTACTACTCATTT 190
QY 7292 AGGCAACCCCGAGCTTACACTTTATGCTTCCGGCTCCTATGTGTGTGGAAATGTGAGCG 7351
Db 189 AGGCACCCCGAGCTTACACTTTATGCTTCCGGCTCCTATGTGTGTGGAAATGTGAGCG 130
QY 7352 GATAACAATTTACACAGGAACAGCTATGACCATGATTACGCCAAGCGGCAATTAACC 7411
Db 129 GATAACAATTTACACAGGAACAGCTATGACCATGATTACGCCAAGCTCGAAATTAACC 70
QY 7412 CTCACCTAAAGGGAACAAAGCTGAGGCTC 7440
Db 69 CTCACCTAAAGGGAACAAAGCTGAGGCTC 41

RESULT 10
AJ281480/c
LOCUS
DEFINITION
4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P4G8, mRNA sequence.
ACCESSION
AJ281480
VERSION
AJ281480.1 GI:6929360
KEYWORDS
EST.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE
1 (bases 1 to 1004)
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansong, W., Soares, M.B.
and Kafatos, F.C.
mosquito innate immunity genes from expressed sequence tags
generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
PUBMED
10841561
COMMENT
Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.
Location/Qualifiers
1..1004
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4G8"
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/lab_host="E. coli DH10B"
/clone_libs="Anopheles gambiae immune competent 4A3A"
/note=Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996). Normalization and Subtraction: Two approaches to
Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN
Query Match 11.8%; Score 924; DB 9; Length 1004;
Best Local Similarity 99.0%; Pred. No. 4.5e-143;
Matches 1001; Conservative 1; Mismatches 2; Indels 7; Gaps 7;
QY 6011 CACTTCTCGCTCGGCCCTCCGGCTGGCTGCTGTTATTGCTGATAAATCTGGAGCCGGTG 6070
Db 1004 CACTTCTCGCTCGG-CCTTCCGGCTGGCTGCTGTTATTGCTGA-AAATCTGGAGCC-GTG 948

QY 6071 AGCGTGGTCTCGCGGTATCAITTCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCG 6130
Db 947 AGCGT-GGTCCTCGGTATCAITTCAGCACT-GGGCCARATGGTAAGCCCTCCCGTATCG 890
QY 6131 TAGTTATCTACAGAGCGGGAGTCAGCAACTATGATGAACGAAATAGACAGATCGGTG 6190
Db 889 TAG-TATCTACAGAGCGGGAGTCAGCAACTATGATGAACGAAATAGACAGATCGGTG 831
QY 6191 AGATAGGTGCTCAGCTGATTAAGCATTTGTAACCTGTCAGACCAAGTTTACTCATATATAC 6250
Db 830 AGATA-GTGCTCAGCTGATTAAGCATTTGTAACCTGTCAGACCAAGTTTACTCATATATAC 772
QY 6251 TTTAGATTGATTTAAATCTTCAITTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGG 6310
Db 771 TTTAGATTGATTTAAATCTTCAITTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGG 712
QY 6311 ATAATCTCATGACCAAAATCCCTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCG 6370
Db 711 ATAATCTCATGACCAAAATCCCTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCG 652
QY 6371 TAGAAAGATCAAGGATCTTCTTGAGATCTTTTTTCTGCGGTAAATCTGCTGCTTGC 6430
Db 651 TAGAAAGATCAAGGATCTTCTTGAGATCTTTTTTCTGCGGTAAATCTGCTGCTTGC 592
QY 6431 AAACAAAAAACCACCGCTACCAAGCGGTGTTGTTTCCCGGATCAAGAGCTACCAATC 6490
Db 591 AAACAAAAAACCACCGCTACCAAGCGGTGTTGTTTCCCGGATCAAGAGCTACCAATC 532
QY 6491 TTTTTCGAAAGTAACTGGCTTCAGAGAGCGGAGATACCAATCTCTTCTAGTGT 6550
Db 531 TTTTTCGAAAGTAACTGGCTTCAGAGAGCGGAGATACCAATCTCTTCTAGTGT 472
QY 6551 AGCGGTAGTTAGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGC 6610
Db 471 AGCGGTAGTTAGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGC 412
QY 6611 TAATCTCTGTTACCAGTGGCTGCTGCCAGTGGCGATAGTCTGTCTTACCGGGTTGGACT 6670
Db 411 TAATCTCTGTTACCAGTGGCTGCTGCCAGTGGCGATAGTCTGTCTTACCGGGTTGGACT 352
QY 6671 CAAGACGATAGTTACCGGATAAGCGGAGCGGTGGCTGAACGGGGGTTCTGTCACAC 6730
Db 351 CAAGACGATAGTTACCGGATAAGCGGAGCGGTGGCTGAACGGGGGTTCTGTCANAC 292
QY 6731 AGCCAGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAGCTGAGCTATCAG 6790
Db 291 AGCCAGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAGCTGAGCTATCAG 232
QY 6791 AAAGCGCCACGCTTCCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGTGCG 6850
Db 231 AAAGCGCCACGCTTCCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGTGCG 172
QY 6851 GAACAGAGAGCGACAGAGGAGCTTCCAGGGGAAACGCGTGTATCTTTATAGTCTCTG 6910
Db 171 GAACAGAGAGCGACAGAGGAGCTTCCAGGGGAAACGCGTGTATCTTTATAGTCTCTG 112
QY 6911 TCGGGTTCCCACTCTGACTTGGAGCTCGATTTTGTGATGCTCGTCAGGGGCGCGA 6970
Db 111 TCGGGTTCCCACTCTGACTTGGAGCTCGATTTTGTGATGCTCGTCAGGGGCGCGA 52
QY 6971 GCCTATGGAAAAACGCCAGCAACGCGGCTTTTTTACGGTTCTCGCCCTTTT 7021
Db 51 GCCTATGGAAAAACGCCAGCAACGCGGCTTTTTTACGGTTCTCGCCCTTTT 1

RESULT 11
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LOCUS
DEFINITION
Eg08_08R09 R Eg08_AAFc ECORC Fusarium graminearum complex substrate
Gibberella zeae cDNA clone Eg08_08R09, mRNA sequence.
ACCESSION
CD458281
VERSION
CD458281.1 GI:31373021


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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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1..973
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/mol_type="rRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08.08h09"
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/dev_stage="Asexual"
/lab_host="E. coli DH10B"
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ubstrate"
/note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."
ORIGIN
Query Match 11.7%; Score 916.8; DB 14; Length 973;
Best Local Similarity 98.1%; Pred. No. 7e-142;
Matches 932; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
QY 5229 TTCAGTGGCACTTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAAT 5288
DB 25 TTAGTGGTGCASATTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAAT 84
QY 5289 ACATTCAATATGATCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATAATATG 5348
DB 85 ACATTCAATATGATCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATAATATG 144
QY 5349 AAAAAAGGAGATGATGAGTATTCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGC 5408
DB 145 AAAAAAGGAGATGATGAGTATTCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGC 204
QY 5409 ATTTTGCCTTCCTGTTTTCCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 5468
DB 205 ATTTTGCCTTCCTGTTTTCCTCACCAGAGACGCTGGTGAAGTAAAGATGCTGAAGA 264
QY 5469 TCAGTTGGGTGCAGAGTGGGTACATCGAATGATCTCAACAGCGGTAAAGATCCTTGA 5528
DB 265 TCAGTTGGGTGCAGAGTGGGTACATCGAATGATCTCAACAGCGGTAAAGATCCTTGA 324
QY 5529 GAGTTTTCGCCCGGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATGTGG 5588
DB 325 GAGTTTTCGCCCGGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATGTGG 384
QY 5589 CGCGGTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACATATTC 5648
DB 385 CGCGGTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACATATTC 444
QY 5649 TCAGATGACTGGTGTGAGTACTCCACGATCAGAAAGCATCTTACGGATGGCATGAC 5708
DB 445 TCAGATGACTGGTGTGAGTACTCCACGATCAGAAAGCATCTTACGGATGGCATGAC 504

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QY 5709 ACTAAGAGAAATTTATGCAGTGTGCCATTAACCATGAGTGATGAACACTGCGGCCCACTTACT 5768
DB 505 ACTAAGAGAAATTTATGCAGTGTGCCATTAACCATGAGTGATGAACACTGCGGCCCACTTACT 564
QY 5769 TCTGCAACAGTATCGGAGGACCGAAGAGGACTAACCGCTTTTTCGACAAATCGGGGATCA 5828
DB 565 TCTGCAACAGTATCGGAGGACCGAAGAGGACTAACCGCTTTTTCGACAAATCGGGGATCA 624
QY 5829 TGTAACTCGCCTTGATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 5888
DB 625 TGTAACTCGCCTTGATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 684
QY 5889 TGACACCAAGTGCCTGTAGCAATGCGCAACAACTGTCGCAAACTATTAACTGGCGAACT 5948
DB 685 TGACACCAAGTGCCTGTAGCAATGCGCAACAACTGTCGCAAACTATTAACTGGCGAACT 744
QY 5949 ACTTACTCTAGCTTCCCGGCACAAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGG 6008
DB 745 ACTTACTCTAGCTTCCCGGCACAAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGG 804
QY 6009 ACCACTTCTGCGCTCGGCCCTTCCCGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGG 6068
DB 805 ACCACTTCTGCGCTCGGCCCTTCCCGCTGGCTGTTTATTGCTGATAAATCTGGAGSCGG 864
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DB 865 TGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAG-CCVCCGTTAT 923
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DB 924 CGTACTTATCTACAGACGGGGAGTCAGGCACTATGATGAACGAAATA 973

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RESULT 12
LOCUS CG700598/c
DEFINITION ZMMBBC0120G04f ZMMBBC (EcoRI) Zea mays subsp. mays genomic clone
ACCESSION CG700598
VERSION 1
KEYWORDS Zea mays subsp. mays (maize)
SOURCE Zea mays subsp. mays
ORGANISM Zea mays subsp. mays
REFERENCE 1. (bases 1 to 1025)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PGIR (2003c)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 24.
Location/Qualifiers
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Query Match 11.5%; Score 900.6; DB 29; Length 1025;
Best Local Similarity 98.2%; Pred. No. 3.3e-139;
Matches 932; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

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 CB686151
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Brassica napus
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 1 (bases 1 to 925)
 Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A., Chagnon, J., Farah, S., Couroux, P. and Hattori, J.
 Expressed Sequence Tags from Constitutively Frost Tolerant transgenic Brassica napus overexpressing BNCBF17
 Unpublished (2002)
 Contact: Singh, J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA 0C6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@em.agr.ca.
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FEATURES
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ORIGIN

Query Match 11.5%; Score 899.4; DB 14; Length 925;
 Best Local Similarity 98.5%; Pred. No. 5.5e-139;
 Matches 911; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

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VERSION
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REFERENCE
  1 (bases 1 to 917)
AUTHORS
  Watson,R.J., Heyls,R., Chapados,J., Couroux,P., Harris,L.J.,
  Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
  Sprott,D. and Tinker,N.A.
TITLE
  A cDNA library prepared from Fusarium graminearum grown on a
  complex plant substrate
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Watson, Robert.J.
  Eastern Cereal and Oilseed Research Centre
  Agriculture and Agri-food Canada
  Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
  CANADA
  Tel.: (613) 759-1655
  Fax: (613) 759-1701
  Email: watsonrj@agr.gc.ca.

FEATURES
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ORIGIN
Query Match      11.3%; Score 886.2; DB 14; Length 917;
Best Local Similarity 99.7%; Pred. No. 8.4e-137;
Matches 888; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	2207.2	28.2	7432	4	US-09-367-891A-6
C 6	2206.2	28.2	5534	1	US-08-452-267-3
C 7	2206.2	28.2	5534	3	US-09-123-644-3
C 8	2204.6	28.2	12479	4	US-09-318-138-13
C 9	2204.6	28.2	12494	3	US-08-335-312-13
C 10	2204.6	28.2	12494	3	US-08-848-760B-33
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C 13	2203.8	28.2	2961	3	US-08-446-935-6
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C 15	2203.8	28.2	4145	3	US-08-358-928-62
C 16	2203.8	28.2	4277	3	US-08-651-472-63
C 17	2203.8	28.2	4277	3	US-08-358-928-63
C 18	2203.8	28.2	5356	3	US-08-446-935-1
C 19	2203.8	28.2	5352	3	US-08-651-472-72
C 20	2203.8	28.2	5352	3	US-08-358-928-72
C 21	2203.8	28.2	6811	3	US-08-651-472-67
C 22	2203.8	28.2	6811	3	US-08-358-928-67
C 23	2203.8	28.2	6926	3	US-08-651-472-69
C 24	2203.8	28.2	6926	3	US-08-358-928-69
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C 39	2203.6	28.2	7379	3	US-08-675-566-13	Sequence 13, Appl
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C 41	2203.6	28.2	8792	3	US-08-675-566-2	Sequence 25, Appl
C 42	2203.6	28.2	10281	2	US-08-816-155B-1	Sequence 1, Appl
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ALIGNMENTS

RESULT 1

US-09-845-917A-28/c

; Sequence 28, Application US/09845917A

; Patent No. 6653529

; GENERAL INFORMATION:

; APPLICANT: Bogaert, Thierry

; APPLICANT: Vandekerckhove, Joel

; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH

; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR

; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR

; FILE REFERENCE: P/14-1

; CURRENT APPLICATION NUMBER: US/09/845,917A

; CURRENT FILING DATE: 2001-04-30

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 28

; LENGTH: 10288

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (8456)

; OTHER INFORMATION: "N is A, C, G, or T"

; OTHER INFORMATION: Description of Artificial Sequence: artificial

; OTHER INFORMATION: plasmid

US-09-845-917A-28

Query Match	57.4%;	Score 4492.6;	DB 4;	Length 10288;
Best Local Similarity	87.3%;	Pred. No. 0;		
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QY	1739	ACGCATGTAACATTTACTGAAACCTTGTCTGAGAGGTTTGGGACCGCTCGAAGCCTT	1798	
Db	7698	ACGCATGTAACATTTACTGAAACCTTGTCTGAGAGGTTTGGGACCGCTCGAAGCCTT	7639	
QY	1799	TAATTTGGCGCGGTATCCCAATTCGCCCTTATAGTGTGTATTAACGGCGCTCACTGGC	1858	

Db	7638	TAATTTG-----CAAGCTCGGATCTCGAGTCGCGAAGACTTGGACGACTGGC	7589
Qy	1859	CGTCGTTTTACACGTCGTGACTGGGAAAACCTGGGCTTACCCAACTTAATCGCCTTGC	1918
Db	7588	CGTCGTTTTACACGTCGTGACTGGGAAAACCTGGGCTTACCCAACTTAATCGCCTTGC	7529
Qy	1919	AGCACATCCCCCTTTGCGCAGCTGGCGTAATAGCGAGAGAGCGCGACCGATCGCCCTTC	1978
Db	7528	AGCACATCCCCCTTTGCGCAGCTGGCGTAATAGCGAGAGAGCGCGACCGATCGCCCTTC	7469
Qy	1979	CCAACAGTTGGCAGCTGAAATGCGGAATGCGCGAAGCGCGCCCTGTAGCGCGCATTAAG	2038
Db	7468	CCAACAGTTGGCAGCTGAAATGCGGAATGCGCGAAGCGCGCCCTGTAGCGCGCATTAAG	7409
Qy	2039	CGCGCGGGTGTGGTGTATCGCGCAGCGTACCGCTACACTTCCGACGCGCCCTAGCGCC	2098
Db	7408	CGCGCGGGTGTGGTGTATCGCGCAGCGTACCGCTACACTTCCGACGCGCCCTAGCGCC	7349
Qy	2099	CGCTCCTTTGCGCTTTCTCCCTTCTCCCTTCTCGCCACGTTGCGCGCTTTCCCGTCAAGC	2158
Db	7348	CGCTCCTTTGCGCTTTCTCCCTTCTCCCTTCTCGCCACGTTGCGCGCTTTCCCGTCAAGC	7289
Qy	2159	TCTAAATCGGGGGCTCCCTTTAGGGTTCGGAATTTAGTGTCTTTACGGCACCTCGACCCCAA	2218
Db	7288	TCTAAATCGGGGGCTCCCTTTAGGGTTCGGAATTTAGTGTCTTTACGGCACCTCGACCCCAA	7229
Qy	2219	AAACCTGATTTAGGGTGTATGTTTACGCTAGTGGGCGATCGCCCTGTAGACGGTTTTTCG	2278
Db	7228	AAACCTGATTTAGGGTGTATGTTTACGCTAGTGGGCGATCGCCCTGTAGACGGTTTTTCG	7169
Qy	2279	CCCTTTGAGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTTGTTCCAACTCGAAACAAC	2338
Db	7168	CCCTTTGAGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTTGTTCCAACTCGAAACAAC	7109
Qy	2339	ACTCAACCTAFTCTCGGCTATTTCTTTGATTTAATAGGGATTTTCCGGAFTTCCGGCCTA	2398
Db	7108	ACTCAACCTAFTCTCGGCTATTTCTTTGATTTAATAGGGATTTTCCGGAFTTCCGGCCTA	7049
Qy	2399	TTGGTTAAAAATGAGCTGATTTAACAATAATTTAAACGCGAATTTTAAACAATAATTAAC	2458
Db	7048	TTGGTTAAAAATGAGCTGATTTAACAATAATTTAAACGCGAATTTTAAACAATAATTAAC	6989
Qy	2459	GTTTACAAATTTCTCATCGGTATTTTCTCTTACGCAATCTGCGGTATTTTACACCGC	2518
Db	6988	GTTTACAAATTTCTCATCGGTATTTTCTCTTACGCAATCTGCGGTATTTTACACCGC	6929
Qy	2519	ATAGGGTAATACTGATATAATTAATTTGAATTTAATAGGGATTTTCCGGAFTTCCGGCCTA	2578
Db	6928	ATAGATCGGCAAGTGCACAAACATACCTAAATAAATACTACTCAGTAATAACCTATTTTC	6869
Qy	2579	ATTTACTTATAATACAGTTTATTTTGTGTCGCGCATCTTCTCAATATGCTTCCCA	2638
Db	6868	TTAGCATTTTGGACGAAATTTGCTATTTTGTAGAGTCTTTTACACCAATTTGTCTCCACA	6809
Qy	2639	GCTGCTTTCTGTAAAGTTTACCCCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCC	2698
Db	6808	CTTCGCTTTACATCAAC-----ACCAATTAAGC	6781
Qy	2699	TCTTCCCAACAATAATATGTCAGATCTGTAGAGACCAATCATCTCCAGGTTCTPATCTG	2758
Db	6780	CATTTAATCTAAGCGCATCACCAACATTTCTTGGGCTCAGTCCACCAGCTAACATAAAT	6721
Qy	2759	TTGACCCCAATGCGTCTCCCTGTGATCTAAACCCACACCGGGTGTCTAATCAACCAATC	2818
Db	6720	GTAAGCTTTTCGGGGCTCTCTGCGCTT-----CCAAACCAAGTTCAGAAATTCGAGTTCCAATC	6666
Qy	2819	GTAACCTTCATCTCTTCCACCCATCTCTTTGTAGCAATAAAGCGGATAACAAATCTTT	2878
Db	6665	CAAAAGTTTCACTGTCCAC-----CTGCTTCTGMAATCAACAAGGGAATAAACGAATG	6612
Qy	2879	GTGCTCTTTCGCAATGTCAACAGTACCTTAGTATTTCTCCAGTAGATAGGGAGCCCTT	2938
Db	6511	AGGTTTCTGTGAAGCTGCACTGAGTAGTAGTGTTCGACTCTTTTGGAAATACGAGTCTTTT	6552
Qy	2939	GCATGCAAAATTCGTAACTCAAAAGCGCTCTAGGTTCTTTGTTACTTCTTTCGCGC	2998
Db	6551	-----AATACTGCAAAACCGAGAACTCTTTGGTATTTCTTGCACGACTCATCTCCA	6500
Qy	2999	CTGCTTCAAAACCGCTTAAACAATACCTGGGCCCCACACACCGGTGTGCATTTGTAATGTGCG	3058
Db	6499	TGCAGT-----TGGAGGATATCAATGCGCTAATCATTTGACGAGAGCAAAACATCCTC	6447
Qy	3059	CCATTTCTGTATTTCTGTATACACCCGAGAGTACTGCAATTTTGTAGTGTATTTACCAATGTC	3118
Db	6446	CTTAGGTTGATTTAGAAACACGCAACCAAGTATTTGCGAGTGTCTGAACTATTTTATA	6387
Qy	3119	AGCAAAATTTTCTGTCTTTCGAAGAGTAAATAATCTGCTTTCGCGGATATGCTTTAGGG	3178
Db	6386	TG-----CTTTTCAAGACTTGAATTTTCTTTCGAATTAACCGGGTCAATGT	6339
Qy	3179	CTTAACTGTGCCCTCCATGGAAAATCAGTCAAGATATCCAATGTGTTTTTAGTAAACA	3238
Db	6338	TCCTTTCTATTGGGCACACATATAATACCCAGCAAGTCAGCATCGGAATCTAG--AGCA	6281
Qy	3239	AATTTTGGGACCTTAATGCTTCAACTACTCCAGTAAATCTCTTGGTGGTAC--GAAATCCA	3297
Db	6280	CAITTCGGGCTCTGTGCTCTGCAAGCCGCAAACTTTTCAACAATGGACCAAACTACCT	6221
Qy	3298	ATGAAGCACACAAGTTTGTGCTTTTTCGTCATGATATTAATAGCTTGGCAGCAACAG	3357
Db	6220	GTGAAATTAATAACAGACATACCTCAAGCTGCTTGTGTCTTAATACGCTATACTAC	6161
Qy	3358	GACTAGATGAGTAGCAGCAGCTTCTTATATATGATGCTTTCGACATGATTTATCTTCGTT	3417
Db	6160	GTGCTCAATAGTACCAATGCTTCTTGGCCCTCTCC-----TTTTCCTT	6112
Qy	3418	TCCTGCAAGTTTGTGCTGTGAGTTGGTTGAAGATATCTGCGGCAATTCATGTTTCTT	3477
Db	6111	TTTCGACCGAATTAATTTCTTAATCGGCAAAAGAAAGCTCCGGA-----T	6064
Qy	3478	CAACACTACATATGCTGATATATATACCAATCTTAAGTCTGTGCTCTCTCTCTCTCTCT	3537
Db	6063	CAAGTTGTACGTAAGGTGACAGCTATTTTCAATAAGAAATATCTTCCACTACTGCCA	6004
Qy	3538	TCTGTTTCGGAGATTACCGAATCAAAAAATTTTCAAAGAAACCGAAATCAAAAAAGAAAT	3597
Db	6003	TCTGGCGTCATACTGCAAGATCACATATATTA-----CGATGCTGTCTATTAAT	5952
Qy	3598	AAAAAAAATGATGAATTTGAAAGCTGTGGTATGCTGCACTCTCAGTACAATCT	3657
Db	5951	GCTTCTTATATATATATATATATGTAATGCTGCTGATCTATGCTGCACTCTCAGTACAATCT	5892
Qy	3658	GCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCAACCCGCAACCCGCTGACGCGCCT	3717
Db	5891	GCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCAACCCGCTGACGCGCCT	5832
Qy	3718	GACGGCTTGTGCTCTCCGCAATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGAGCT	3777
Db	5831	GACGGCTTGTGCTCTCCGCAATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGAGCT	5772
Qy	3778	GCATGTGTAGAGTTTTCACCGCTCATCCGAAACCGCGAGAGCAAAAGGCGCTCGTGA	3837
Db	5771	GCATGTGTAGAGTTTTCACCGCTCATCCGAAACCGCGAGAGCAAAAGGCGCTCGTGA	5712
Qy	3838	TAGCCCTATTTTATAGTTAAATGTCATGATAATAATGTTTTTCTAGTATGATCAATAT	3897
Db	5711	TAGCCCTATTTTATAGTTAAATGTCATGATAATAATGTTTTTCTAGTATGATCAATAT	5652
Qy	3898	CAAGGAAATGATGACATTTGAAGGATGAGACTAATCCAATTTGAGGAGTGGCAGCATATAG	3957
Db	5651	CAAGGAAATGATGACATTTGAAGGATGAGACTAATCCAATTTGAGGAGTGGCAGCATATAG	5592
Qy	3958	AACAGCTTAAAGGGTAGTGTGAAGGAAGCATACCATACCCCGCATGGAATGGATAATAT	4017
Db	5591	AACAGCTTAAAGGGTAGTGTGAAGGAAGCATACCATACCCCGCATGGAATGGATAATAT	5532

Db 3371 AGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCAATTGGTAACCTGTACAGCAAGTT 3312
QY TACTCATATATATCTTTAGATGATTTAAACCTCATTTTAAATTTTAAAGGATCTAGGTG 6297
Db 3311 TACTCATATATATCTTTAGATGATTTAAACCTCATTTTAAATTTTAAAGGATCTAGGTG 3252
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RESULT 2
US-09-845-917A-27/c
; Sequence 27, Application US/09845917A
; Patent No. 6653529
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845.917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13414
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11582)
; OTHER INFORMATION: "N is A, G, C or T"
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-845-917A-27
Query Match 57.4%; Score 4492.6; DB 4; Length 13414;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
QY 1559 TCATGTAATTAGTTATGTCAGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 1618
Db 11004 TCATGTAATTAGTTATGTCAGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 10945
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Db 10654 AGCATCTCCCTTTTCCGCACTGGCGTAAATAGGAGAGCGCCGACCGCTCGCCCTTC 10595
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QY 4078 AAGCATAAACACGCACTATGCCGTTCTTCTCATGTATATATATACAGCAACACGAG 4137
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Db 8417 TAGGAACCTTCAGAGCGCTTTTGAACACCAAAAGCGCTCTGAAGACGCACTTTTCAAAAAC 8358
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QY 4618 CGTTCAATATTTCTGACCAATGAAGAACTCAACGCTATCACTTTCTGTTTCAAAAAGT 4677
Db 8057 CGTTCAATATTTCTGACCAATGAAGAACTCAACGCTATCACTTTCTGTTTCAAAAAGT 7998
QY 4678 ATGCGCAATCCACATCGGTATAGAAATATAATCGGGATGCTTTATCTTTGAAAAAATGCA 4737
Db 7997 ATGCGCAATCCACATCGGTATAGAAATATAATCGGGATGCTTTATCTTTGAAAAAATGCA 7938
QY 4738 CCGCAGCTTCCTAGTAACTAGTAAACCGGGAGTGGAGTCAAGCTTTTATGGA 4797
Db 7937 CCGCAGCTTCCTAGTAACTAGTAAACCGGGAGTGGAGTCAAGCTTTTATGGA 7878
QY 4798 GAGAAAAATAGACACCAAAAGTAGCTTTCTTAACTTAAACGAGACCTACAGTGCAAAAAGT 4857
Db 7877 GAGAAAAATAGACACCAAAAGTAGCTTTCTTAACTTAAACGAGACCTACAGTGCAAAAAGT 7818
QY 4858 TATCAAGAGACTGCATATATAGAGCGCACAAAGAGAAAAAAGTAATCTAAGATGCTTTG 4917
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QY 4918 TTAGAAAAATAGCGCTCTCGGATGCATTTTGTAGAACAAAAAGAGATAGATCTT 4977
Db 7757 TTAGAAAAATAGCGCTCTCGGATGCATTTTGTAGAACAAAAAGAGATAGATCTT 7698
QY 4978 TGTGTAAAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAAAAAATCAGCTCAGATTC 5037
Db 7697 TGTGTAAAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAAAAAATCAGCTCAGATTC 7638
QY 5038 TTTGTTGAAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAAGCACAGA 5097
Db 7637 TTTGTTGAAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAAGCACAGA 7578
QY 5098 TTCTTGTGTTGAAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAGCTCA 5157
Db 7577 TTCTTGTGTTGAAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAGCTCA 7518
QY 5158 GATTTCTTTGTTGAAAAATTAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAAGCA 5217
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QY 5218 CAGATGCTTTGTTGAGGTGCACTTTTTCGGGGAATATGTCGGGAAACCCCTATTGTTTGA 5277
Db 7457 CAGATGCTTTGTTGAGGTGCACTTTTTCGGGGAATATGTCGGGAAACCCCTATTGTTTGA 7398

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Db 7337 CAATAATATTGAAAAAGGAAGATATGAGTATTCAACAATTTCCGTGTGCCCTTATTCCC 7278
QY 5398 TTTTTCGCGCATTTTTCCTTCTGTTTTCCTCACCAGAAACGCTGCTGTAAGTAAAA 5457
Db 7277 TTTTTCGCGCATTTTTCCTTCTGTTTTCCTCACCAGAAACGCTGCTGTAAGTAAAA 7218
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Db 7217 GATGCTGAAAGATCAAGTTGGGTGCAAGAGTGGTTTACATCGAACTGGATCTCAACAGCGT 7158
QY 5518 AAGATCTTCAGAGTTTTTTCGCGCGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTT 5577
Db 7157 AAGATCTTCAGAGTTTTTTCGCGCGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTT 7098
QY 5578 CTGCTATGTCGCGGTATTATCCCGTATTGACGCGGCAAGAGCAACTCGTCCGCGC 5637
Db 7097 CTGCTATGTCGCGGTATTATCCCGTATTGACGCGGCAAGAGCAACTCGTCCGCGC 7038
QY 5638 ATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACAGTCAACAGAAAGCATCTTACG 5697
Db 7037 ATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACAGTCAACAGAAAGCATCTTACG 6978
QY 5698 GATGGCATGACAGTAAGAAATTAAGCAGTGTCTGCCATAACCATGAGTGAATAACTGGG 5757
Db 6977 GATGGCATGACAGTAAGAAATTAAGCAGTGTCTGCCATAACCATGAGTGAATAACTGGG 6918
QY 5758 GCCAACTATTCTTGACAAACGATCGGAGGACCGAAGAGCTTAAACGCTTTTTCGACAAAC 5817
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Db 6257 ATCTGCTGCTTGCACAAACAAACACACCGCTACACGCGGTGTTTGTGTTGCGGATCAA 6198
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Db 6077 TACTCTGCTCTGCTTAATCTCTGTTTACAGTGGCTGCTGCCAGTGGCGATAGTGTGCTT 6018
Qy 6658 ACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGCGGTGCGGCTGAACGGGG 6717
Db 6017 ACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGCGGTGCGGCTGAACGGGG 5958
Qy 6718 GGTCTGTCACACAGCCAGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAG 6777
Db 5957 GGTCTGTCACACAGCCAGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAG 5898
Qy 6778 CGTGAGCTATGAGAAAGCGCCAGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGGTA 6837
Db 5897 CGTGAGCTATGAGAAAGCGCCAGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGGTA 5838
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Db 5777 CTTTATAGTCTGCTGCGGTTTCCGACCTCTGACTTGAAGGTCGATTTTGTGATGCTCG 5718
Qy 6958 TCAGGGGGGCGAGCCTATGGAAGAAACGCCAGCAACCGGCGCTTTTACGGTTTCTTGCC 7017
Db 5717 TCAGGGGGGCGAGCCTATGGAAGAAACGCCAGCAACCGGCGCTTTTACGGTTTCTTGCC 5658
Qy 7018 TTTTGTGCTGCTTTTGTCTACATGTTCTTTCTGCGGTTATCCCTCGATTCGTGGATAAC 7077
Db 5657 TTTTGTGCTGCTTTTGTCTACATGTTCTTTCTGCGGTTATCCCTCGATTCGTGGATAAC 5598
Qy 7078 CGTATTACCGCTTTTGTAGTGAGTGATACCGCTGCGCGAGCGGAGCGAAGCGGAGCGAGC 7137
Db 5597 CGTATTACCGCTTTTGTAGTGAGTGATACCGCTGCGCGAGCGGAGCGAAGCGGAGCGAGC 5538
Qy 7138 GAGTCAGTGAGCGGAGGAGCGGAGCGGCCCAATAGCAAAACCGCTCTCCCGCGCGT 7197
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Db 5477 TGSCCGATTCATTAATGACGTGCGACGAGGTTTCCGACCTGGAAGCGGCGAGTGAG 5418
Qy 7258 CGCAACGCAATTAATGAGTGATCTCACTCATTTAGGCAACCGAGGCTTTTACATTTATG 7317
Db 5417 CGCAACGCAATTAATGAGTGATCTCACTCATTTAGGCAACCGAGGCTTTTACATTTATG 5358
Qy 7318 CTTCCGCTCCTATGTTGTGAGTGTGAGTGTGAGCGGATTAACAAATTTACACAGGAACAGC 7377
Db 5357 CTTCCGCTCCTATGTTGTGAGTGTGAGTGTGAGCGGATTAACAAATTTACACAGGAACAGC 5298
Qy 7378 TATGACCATGATTACGCCAAGCGGCA 7404
Db 5297 TATGACCATGATTACGCCAAGCTTGA 5271

US-08-801-344-5
; Sequence 5, Application US/08801344
; Patent No. 6087140
; GENERAL INFORMATION:
; APPLICANT: Cameron, Douglas C.
; APPLICANT: Shaw, Anita J.
; APPLICANT: Altaras, Nedim E.
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,344
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REFERENCE/DOCKET NUMBER: 09820.037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Yeast shuttle vector YEp352
; US-08-801-344-5

Query Match 39.1%; Score 3057.4; DB 3; Length 5181;
Best Local Similarity 78.3%; Pred. No. 0;
Matches 3890; Conservative 0; Mismatches 996; Indels 85; Gaps 15;

Qy 2470 CCTGATGCGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATAGGTAATA 2529
Db 234 CCTGATGCGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATAGGTAATA 293
Qy 2530 ACTGATATAATTAATTAAGCTCTAATTTGTGAGTTAGTAGTATACATGATTTACTTATA 2589
Db 294 ACTGATATAATTAATTAAGCTCTAATTTGTGAGTTAGTAGTATACATGATTTACTTATA 353
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Db 354 ATACAGTTTTTGTGTTTTGTGCGCGCATCTTCTCAAAATATGTTCCACGCTGCTTTTC 413
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Qy 2710 TAATAATGTCAGATCTCTGTAGACACCATCATCCAGGTTCTATCTGTTGACCCGATG 2769
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Qy 2770 CGTCTCCCTTGTCTCATCTTAACCCACACCGGCTGTCAATAATCAACCAATCGTAACCTTCAT 2829
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654 CAATGTCACAGTACCCCTTAGTATATCTCCAGTAGATAGGAGCCCTTGCATGCAAT 713
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714 CTGCTAAACATCAAAAGGCTCTAGTCTCTTTGTTGTTCTTTCTGCGCCCTGCTTCAAC 773
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894 TGTCTTCGAAGAGTAAAAATTTGACTTTGGCGGATAATGCCCTTTAGCGGCTTAACTGTC 953
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3190 CTTCCATGGAAAAATCAGTCAAGATATCCACATGTGTTTTAGTAAACAAATTTGGGAC 3249
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3610 ATGAATGAATGAAGAGTGTGTATGGTGCACTCT-----CAGTACAAATCT 3657
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1369 ATGAATGAAGAGTGTGTATGGTGCACTCT-----CAGTACAAATCT 1428
Qy
3658 GCTCTGATGCGCATAGTTAAGCAGCCCGACACCCGCCCAACCCGCTGACGCGCCT 3717
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1429 TCCCTGAACAGATAGTATATTTGAACCTGTATTAATATATATAGTCTAGCGCTTTACGG 1488
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3718 GACGGGCTGTGCTCCCGCATCCGCTTACAGACAGCTGTGACCGCTCTCCGGAGCT 3777
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1609 TTGTTAAGCAAGCATCTGTGCTTCAATTTGTAGCAAAATGCAACCGGAGCGCTAA 1668
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3888 GATCCAATATCAAGGAATGATAGCATTTGAAGGATGAGACTAATCCAATTTGAGGAGTGG 3947

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4008 GGGATATATACAGGAGGTACTAGA-CTACCTTTTCATCTTACATAAATAGACGCATATA 4066
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1789 GCTAATTTTTCAACAAAGAAATCTGAGCTGCATTTTTTACAGAACAGAAATGCAACGCGAG 1848
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4067 AGTACGCAATTTAAGCATATAACACGCACTATGCGCTTCTTCTCATGTATATATATACAG 4126
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1849 AGCGTATTTTACCAACAAAGAAATCTATCTCTTTTTTGTCTACAAAAATGCAATCCG 1908
Qy
4127 GCAACAG-----CAGATATAGTGTGCGAGTGAACAGTGTGTATGTGGCAGCTCG 4180
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4181 CGTTGCAATTTTCGAAGCGCTCGTT-----TTCCGAAACGCTTTGAAGTTCTCTAT 4230
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1969 TAATGCACTCTCTTGATACTTTTTTGGCAGCTGTAGTCCGTTAAGTTAGAGAGGCTTAC 2028
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4231 TCCGAACTTCTTATCTCT-----AGAAAGTATAGGAATCTTCAGAGCGCTTTTGAAG 4284
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2029 TTTGGTGTCTATTTCTCTTCCATAAAAGAAAGCTGACTCCACTTCCCGCGCTTACTGAT 2088
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4285 CAAAGGCG-TCGTGAGACGCACTTTCAAAACCAAAACGCAACGCACTGTACGAGC 4343
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4344 TACTAAATATTTGCAATAGCGCTTCCACAAACATGCTCAAAAGTATCTCTTTGCTATA 4403
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2149 CCGATGGAATTTGGCATACTTTGTGAACAGAAAGTATAGCGTTGATGTTCTTC----- 2204
Qy
4404 TATCTCTGTCTATATCCCTATATAACCTACCCATCCCACTTCCGCTCTGCTTGAACCTGCA 4463
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2205 -ATTGGTCAGAAATATTAAGACGGTCTTCTATTTGTCTCTATATATAGCTATAGCA 2263
Qy
4464 TCTAACTGCACTCTACATTTTTTATGTTTATCTCTAGTATTACTCTTTAGACAAAAA 4523
Db
2264 AATGTTTACATTTTCGTAATTTTTCGATTTCACTCTATGAATAGTCTTCTTACATACTTT 2323
Qy
4524 ATTGTAGTAAAGAACTATTCTAGAGTGAATCGAAACAAATACGAAATGTAAACATTTCC 4583
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2324 TTTGTCTAAGAGTATACTAGAGATAAACAATAAAATGTAGAGTGTAGTTAGATGC 2383
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4640 -GAAGATCATCAACGCTATCACTTTCTGTTCAAAAGTATGCCATCCCATCGGTAT 4698
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2444 AGCAAGAGATACCTTTTGAAGCAATGTTTGGAAAGCGGTATTCGCAATATTTTAGTAGCT 2503
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4699 AGAATAAATCGGGGATGCGCTTTATCTTGAATAATGCACCGCAGCTTCGCTAGTAATC 4758
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4819 GCCTTCTCTTAACTTAAACGAGCTCAGTGTCAAAAGTATCAAGAGACTGCAATATAG 4878
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Db
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Qy
4939 GATGCAATTTTGTAGAAACAAAAAGAGTATAGATTCTTTGTTGTTAAATATAGCGCTCTC 4998

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Qy 4999 GCGTTGCAAT-----TCGTCTCTGTAAATAATGACGCTCAGATTCCTTTGTTGAAAAATTAG 5054
Db 2791 TCAGTACAACTGCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCAACCCG 2850
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Qy 5468 ATCAGTTGGTGCAGAGTGGTTTACATCGAATGCTGATCTCAACAGCGGTAAGATCCTTG 5527
Db 3271 ATCAGTTGGTGCAGAGTGGTTTACATCGAATGCTGATCTCAACAGCGGTAAGATCCTTG 3330
Qy 5528 AGAGTTTTCGCCCCGGAAGACGTTTTCATATGATGAGCACTTTTAAAGTTCTGCTATGTG 5587
Db 3331 AGAGTTTTCGCCCCGGAAGACGTTTTCATATGATGAGCACTTTTAAAGTTCTGCTATGTG 3390
Qy 5588 GCGCGGTATTTATCCGTTATTTGACGCGGGAAGAGCAACCTCGGTGCGCGGATACATATT 5647
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Qy 5648 CTGAGATGACTTGGTTGAGTACTCACAGTTCACAGAAAGCATCTTACGGATGGCATGA 5707
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Db 3511 CAGTAAGAGAAATATGAGTGTGCTGCCATAACCATGATGATACACTTGCAGCCCACTTAC 3570
Qy 5768 TTCTGCAACAGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCGCAACATCGGGGATC 5827
Db 3571 TTCTGCAACAGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCGCAACATCGGGGATC 3630
Qy 5828 ATGTAACCTCGCTGATCGTTGGGAACCGAGCTGTAATGAAGCATACCAACGAGGAC 5887
Db 3631 ATGTAACCTCGCTGATCGTTGGGAACCGAGCTGTAATGAAGCATACCAACGAGGAC 3690
Qy 5888 GTGACACCAAGATCGCTGTAGCAATGGCAACAAACGTTTGCAGAACTATTAACTGGCGAAC 5947
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Qy 5948 TACTTACTTACTGCTTCCCGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGCAG 6007
Db 3751 TACTTACTTACTGCTTCCCGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGCAG 3810
Qy 6008 GACCACTTCTGCGCTCGGCTTCCGCTGGCTGGTTTATGCTGATTAATCTGGAGCGG 6067
Db 3811 GACCACTTCTGCGCTCGGCTTCCGCTGGCTGGTTTATGCTGATTAATCTGGAGCGG 3870

Qy 6068 GTGAGCGTGGGTCTCCGCGTATCATTTGCAGCACTCGGGGCGAGATGTAAGCCCTCCCGTA 6127
Db 3871 GTGAGCGTGGGTCTCCGCGTATCATTTGCAGCACTCGGGGCGAGATGTAAGCCCTCCCGTA 3930
Qy 6128 TCGTAGTTATCTACAGAGCGGGAGTCAAGCACTATGATGTAAGCAAGATAGACAGATCG 6187
Db 3931 TCGTAGTTATCTACAGAGCGGGAGTCAAGCACTATGATGTAAGCAAGATAGACAGATCG 3990
Qy 6188 CTGAGATAGTGCCTCACTGATTAAGCAATGTTGTAACCTGTGAGACCAAGTTTACTCATATA 6247
Db 3991 CTGAGATAGTGCCTCACTGATTAAGCAATGTTGTAACCTGTGAGACCAAGTTTACTCATATA 4050
Qy 6248 TACTTTAGATGATTTTAAACCTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTT 6307
Db 4051 TACTTTAGATGATTTTAAACCTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTT 4110
Qy 6308 TTGATTAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAAGCC 6367
Db 4111 TTGATTAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAAGCC 4170
Qy 6368 CGGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTGCT 6427
Db 4171 CGGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTGCT 4230
Qy 6428 TGCAAAACAAAAAACCAACCGCTACCAAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAA 6487
Db 4231 TGCAAAACAAAAAACCAACCGCTACCAAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAA 4290
Qy 6488 CTCCTTTTCGAAAGTAACTGCGCTTACAGAGCGGAGATACCAAAATCTGCTCTCTAG 6547
Db 4291 CTCCTTTTCGAAAGTAACTGCGCTTACAGAGCGGAGATACCAAAATCTGCTCTCTAG 4350
Qy 6548 TGTAGCGGTAGTTAGGCGCAACCTCAAGAACTCTGTAGCACCGCTACATACCTGCTC 6607
Db 4351 TGTAGCGGTAGTTAGGCGCAACCTCAAGAACTCTGTAGCACCGCTACATACCTGCTC 4410
Qy 6608 TGTAAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAGTCTGCTTACCGGGTTGG 6667
Db 4411 TGTAAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAGTCTGCTTACCGGGTTGG 4470
Qy 6668 ACTCAAGACGATAGTTTACCGGATAGCGGCGAGCGGTGCGGCTGAAAGGGGGTTCGTGCA 6727
Db 4471 ACTCAAGACGATAGTTTACCGGATAGCGGCGAGCGGTGCGGCTGAAAGGGGGTTCGTGCA 4530
Qy 6728 CACAGCCAGCTTGGAGCGAAACGACCTACAACGAACTGAGATACCTACAGCGTGAATAT 6787
Db 4531 CACAGCCAGCTTGGAGCGAAACGACCTACAACGAACTGAGATACCTACAGCGTGAATAT 4590
Qy 6788 GAGAAAGCCCAAGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGG 6847
Db 4591 GAGAAAGCCCAAGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGG 4650
Qy 6848 TCGGAAACAGAGAGCGCACAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTTATAGTC 6907
Db 4651 TCGGAAACAGAGAGCGCACAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTTATAGTC 4710
Qy 6908 CTGTCGGGTTTTCGCCACTCTGACTTGAAGTGGATTTTGTGATGCTCTGAGGGGGG 6967
Db 4711 CTGTCGGGTTTTCGCCACTCTGACTTGAAGTGGATTTTGTGATGCTCTGAGGGGGG 4770
Qy 6968 GGAGCCTATGGAAAAACCGCAGCAACCGCGCTTTTACGGTTCTTGGCTTTTGTGCG 7027
Db 4771 GGAGCCTATGGAAAAACCGCAGCAACCGCGCTTTTACGGTTCTTGGCTTTTGTGCG 4830
Qy 7028 CTTTGTCTCAGATGCTTTCTTGTGCGTTATCCCTGATTTCTGTTGATTAACCGTATTACCG 7087
Db 4831 CTTTGTCTCAGATGCTTTCTTGTGCGTTATCCCTGATTTCTGTTGATTAACCGTATTACCG 4890
Qy 7088 CTTTGTGAGTGAAGTACCGCTCGCGGAGCGGAAACGAGCCGAGCGAGTCAAGTGA 7147
Db 4891 CTTTGTGAGTGAAGTACCGCTCGCGGAGCGGAAACGAGCCGAGCGAGTCAAGTGA 4950

QY	7148	GCAGAGNACGGGAAGAGCGCCCAATATAGCAACCGCTCTCTCCCGCGCGTGTGCCCAATTC	7207
Db	4951	GCAGGAAAGCGGAAGAGCGCCCAATATAGCAACCGCTCTCTCCCGCGCGTGTGCCCAATTC	5010
QY	7208	ATTAAATGCAGCTGGCAGCAGCAGGTCTTCCGACATGGAAAGCGGCGACGTGTAGCGCAACGCGAA	7267
Db	5011	ATTAAATCCAGCTGGCAGCAGCAGGTCTTCCGACATGGAAAGCGGCGACGTGTAGCGCAACGCGAA	5070
QY	7268	TTAATGTGAGTATACCTCACTCATTTAGGCGACCCCGAGGCTTTTACACTTTTATGCTTTCGGGCTC	7327
Db	5071	TTAATGTGAGTATACCTCACTCATTTAGGCGACCCCGAGGCTTTTACACTTTTATGCTTTCGGGCTC	5130
QY	7328	CTATGTTGTGTGGAAATGTGAGCGGATACAAATTTTCACAGAGAAACAGCT	7378
Db	5131	GTAATGTTGTGTGGAAATGTGAGCGGATACAAATTTTCACAGAGAAACAGCT	5181

RESULT 4

```

US-09-498-599-5
; Sequence 5, Application US/09498599
; Patent No. 630352
; GENERAL INFORMATION:
; APPLICANT: Cameron, Douglas C.
; APPLICANT: Shaw, Anita J.
; APPLICANT: Altaras, Nedin B.
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF
; TITLE OF INVENTION: 1,2-PROPANEDIOL FROM SUGAR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,599
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REFERENCE/DOCKET NUMBER: 09820.037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGIN:
; ORGANISM: Yeast shuttle vector YEp352
US-09-498-599-5

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	Query Match	39.1%	Score 3057.4	DB 4	Length 5181
	Best Local Similarity	78.3%	Pred. No. 0		
	Matches 3890	Conservative	0	Mismatches 996	Indels 85
	Gaps	15			
Qy	2470	CCTGATGCGGTATTTCTCTCTTACGGCATCTGCGGTAATTTTACACGCCATACGGTAATA	2529		
Db	234	CCTGATGCGGTATTTCTCTCTTACGGCATCTGCGGTAATTTTACACGCCATACGGTAATA	293		
Qy	2530	ACTGATATAATTAATTTGAAGCTCTAATTTGTGAGTTTAGTATACATGCATTTTACTTATA	2589		

[illegible]

Db 3571 TTCTGACCAACGATCGAGGACCGAAGGAGCTTAACCGCTTTTTCACAAACATGGGGATC 3630
Qy 5828 ATGTAACCTCGCTTATGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAAACGACGAGC 5887
Db 3631 ATGTAACCTCGCTTATGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAAACGACGAGC 3690
Qy 5888 GTGACACCAACGATGCTGTAGCAATGGCAACACAGTTTTCGCAAACTATTAACTGGCGAAC 5947
Db 3691 GTGACACCAACGATGCTGTAGCAATGGCAACACAGTTTTCGCAAACTATTAACTGGCGAAC 3750
Qy 5948 TACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGGAGCGGATGAAGTTTCAG 6007
Db 3751 TACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGGAGCGGATGAAGTTTCAG 3810
Qy 6008 GACCACTTCTGGCTCGGCTTCCCGCTGGCTGGCTGGTTTATTGCTGATAAATCTGAGCGG 6067
Db 3811 GACCACTTCTGGCTCGGCTTCCCGCTGGCTGGCTGGTTTATTGCTGATAAATCTGAGCGG 3870
Qy 6068 GTGAGCGTGGGTCTCGCGGTATCAATGACGACCTGGGCGCAGATGGTAAGCCCTCCCGTA 6127
Db 3871 GTGAGCGTGGGTCTCGCGGTATCAATGACGACCTGGGCGCAGATGGTAAGCCCTCCCGTA 3930
Qy 6128 TCGTAGTTATCTACGACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATCG 6187
Db 3931 TCGTAGTTATCTACGACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATCG 3990
Qy 6188 CTGAGATAGTGCCTCACTGATTAAAGCAATGCTAGCAACCAAGTTTACTCATATA 6247
Db 3991 CTGAGATAGTGCCTCACTGATTAAAGCAATGCTAGCAACCAAGTTTACTCATATA 4050
Qy 6248 TACTTTAGATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTT 6307
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Qy 6308 TTGATAATCTCANGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACC 6367
Db 4111 TTGATAATCTCANGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACC 4170
Qy 6368 CCGTAGAAGATCAAGGATCTCTTCAGATCCCTTTTCTGGCGTAACTCGTCT 6427
Db 4171 CCGTAGAAGATCAAGGATCTCTTCAGATCCCTTTTCTGGCGTAACTCGTCT 4230
Qy 6428 TCGAAACAAAAAACCCACCGCTTACAGCGGTGTTGTTTCCCGGATCAAGAGCTACCAA 6487
Db 4231 TCGAAACAAAAAACCCACCGCTTACAGCGGTGTTGTTTCCCGGATCAAGAGCTACCAA 4290
Qy 6488 CTCCTTTTCCGAAGTAACTGCTTTCAGCAGCGCAGATACCAAAATCTGCTTCTAG 6547
Db 4291 CTCCTTTTCCGAAGTAACTGCTTTCAGCAGCGCAGATACCAAAATCTGCTTCTAG 4350
Qy 6548 TGTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTC 6607
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Qy 6608 TCGTAATCTGTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTACCGGGTTG 6667
Db 4411 TCGTAATCTGTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTGTCTTACCGGGTTG 4470
Qy 6668 ACTCAAGCAGTATGTTACCGGATAAGCGCAGCGTGGGCTGAAACGCGGGGTTGTCGA 6727
Db 4471 ACTCAAGCAGTATGTTACCGGATAAGCGCAGCGTGGGCTGAAACGCGGGGTTGTCGA 4530
Qy 6728 CACAGCCAGCTTGGAGGACGACCTACCGACTGAGATACCTACAGCGTGAAGCTAT 6787
Db 4531 CACAGCCAGCTTGGAGGACGACCTACCGACTGAGATACCTACAGCGTGAAGCTAT 4590
Qy 6788 GAGAAAGCGCCACGCTTCCGAGGAGGAAAGCGGACAGGTATCCGCTAAGCGCGAGG 6847
Db 4591 GAGAAAGCGCCACGCTTCCGAGGAGGAAAGCGGACAGGTATCCGCTAAGCGCGAGG 4650
Qy 6848 TCGGAACAGGAGCGCAGAGGAGCTTCCAGGGGAAACCGCTTGTATCTTTATAGTC 6907

Db 4651 TCGAAACAGGAGCGCACGAGGAGCTTCCAGGGGAAACGCTTGTATCTTTATAGTC 4710
Qy 6908 CTGTGCGGTTTTCGCCACCTCTGACTTGAAGCGTCAATTTTGTGATGCTGTCGTCAGGGGCGC 6967
Db 4711 CTGTGCGGTTTTCGCCACCTCTGACTTGAAGCGTCAATTTTGTGATGCTGTCGTCAGGGGCGC 4770
Qy 6968 GAGACCTATGAAAAAAGCGCAGCAACCGCGCTTTTACGGTTCTTGGCCCTTTGCTGCGC 7027
Db 4771 GAGACCTATGAAAAAAGCGCAGCAACCGCGCTTTTACGGTTCTTGGCCCTTTTGGCTGCGC 4830
Qy 7028 CTTTTGTCTACATGTTCTTCTTCCCTGCTATCCCTGATTTCTGTGATAACCGTATTACCG 7087
Db 4831 CTTTTGTCTACATGTTCTTCTTCCCTGCTATCCCTGATTTCTGTGATAACCGTATTACCG 4890
Qy 7088 CTTTGTAGTGAAGTATACCGCTCGCGCAGCCGAAACGACGAGCGCAGCGAGTCAGTGA 7147
Db 4891 CTTTGTAGTGAAGTATACCGCTCGCGCAGCCGAAACGACGAGCGCAGCGAGTCAGTGA 4950
Qy 7148 GCGAGGAAGCGGAAGAGCGGCCAATACGAAAACCGCTCTCCCGCGCGTTGGCCGATTC 7207
Db 4951 GCGAGGAAGCGGAAGAGCGGCCAATACGAAAACCGCTCTCCCGCGCGTTGGCCGATTC 5010
Qy 7208 ATTAATGACGCTGCGCAGCAGAGTTTCCCGACTCGMAAGCGGCGAGTCGAGCGCAACGAA 7267
Db 5011 ATTAATGACGCTGCGCAGCAGAGTTTCCCGACTCGMAAGCGGCGAGTCGAGCGCAACGAA 5070
Qy 7268 TTAATGTAGTTACTCTCACTCATTAGGACCCCGAGGCTTTACACTTTATGCTTCCGGCTC 7327
Db 5071 TTAATGTAGTTACTCTCACTCATTAGGACCCCGAGGCTTTACACTTTATGCTTCCGGCTC 5130
Qy 7328 CTATGTTGTGGAATTTGTGAGCGGATAACAATTTTCACAGGAAACAGCT 7378
Db 5131 GTATGTTGTGGAATTTGTGAGCGGATAACAATTTTCACAGGAAACAGCT 5181

RESULT 5
US-09-367-891A-6/c
; Sequence 6, Application US/09367891A
; Patent No. 6524816
; GENERAL INFORMATION:
; APPLICANT: RASMUSSEN, PREBEN
; TITLE OF INVENTION: EXPRESSION ELEMENT
; FILE REFERENCE: 078883/0111
; CURRENT APPLICATION NUMBER: US/09/367,891A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: PCT/IB98/00312
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7432
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: pPR70 plasmid
US-09-367-891A-6

Query Match 28.2%; Score 2207.2; DB 4; Length 7432;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2209; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5229 TTCAAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAAT 5288
Db 2247 TTAGGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAAT 2188
Qy 5289 ACATTCAATATGATCCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATATATTG 5348
Db 2187 ACATTCAATATGATCCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATATATTG 2128
Qy 5349 AAAAAGCAAGTATGATTTCAACATTTCCGTTGCGCCCTTATCCCTTTTTCGCGC 5408
Db 2127 AAAAAGCAAGTATGATTTCAACATTTCCGTTGCGCCCTTATCCCTTTTTCGCGC 2068

QY 5409 ATTTTGGCTTCTGTTTCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 5468
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QY 5469 TCAGTTGGGTGACAGAGTGGTTACATCGAAGTGAATCTCAACAGCGGTAAAGATCCTTGA 5528
DB 2007 TCAGTTGGGTGACAGAGTGGTTACATCGAAGTGAATCTCAACAGCGGTAAAGATCCTTGA 1948
QY 5529 GAGTTTTCGCCCCGAAGAGCTTTTCCAAATGATGAGCACTTTTAAAGTCTCTGCTATGTGG 5588
DB 1947 GAGTTTTCGCCCCGAAGAGCTTTTCCAAATGATGAGCACTTTTAAAGTCTCTGCTATGTGG 1888
QY 5589 CGCGGTATTTATCCCGTATTGAACGCGGGCAAGAGCAATCGGTGCGCGGATACATATTC 5648
DB 1887 CGCGGTATTTATCCCGTATTGAACGCGGGCAAGAGCAATCGGTGCGCGGATACATATTC 1828
QY 5649 TCAGATGACTTGGTTGAGTACTCACAGTACAGAAAGCACTTTACGGATGGCATGAC 5708
DB 1827 TCAGATGACTTGGTTGAGTACTCACAGTACAGAAAGCACTTTACGGATGGCATGAC 1768
QY 5709 AGTAAGAGAAATATGAGTCTGCCATAACCATGAGTGATACTGCGGCGCAACTTACT 5768
DB 1767 AGTAAGAGAAATATGAGTCTGCCATAACCATGAGTGATACTGCGGCGCAACTTACT 1708
QY 5769 TCTGACAAAGATCGGAGGACCGAAGAGCTAACCGCTTTTGTGCAAAATGCGGGATCA 5828
DB 1707 TCTGACAAAGATCGGAGGACCGAAGAGCTAACCGCTTTTGTGCAAAATGCGGGATCA 1648
QY 5829 TGTAACTCCGCTTGATCGTTGGGAACCGGAGCTGAATGAGCATCAACAGACGAGCG 5888
DB 1647 TGTAACTCCGCTTGATCGTTGGGAACCGGAGCTGAATGAGCATCAACAGACGAGCG 1588
QY 5889 TGACACCAAGATCGCTGTAGCAATGCAACAAAGTTCGCGCAAACTTAACTGCGCAACT 5948
DB 1587 TGACACCAAGATCGCTGTAGCAATGCAACAAAGTTCGCGCAAACTTAACTGCGCAACT 1528
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DB 1527 ACTTACTCTAGCTTCCCGGCAACAATAATAGACTGGATGGAGCGGATAAAGTTTCAGG 1468
QY 6009 ACCACTTCTCGCTCGGCTTCCGCTGCTGTTTATGCTGATTAATCTGAGCGCG 6068
DB 1467 ACCACTTCTCGCTCGGCTTCCGCTGCTGTTTATGCTGATTAATCTGAGCGCG 1408
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QY 6129 CGTAGTTATCTACACGCGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC 6188
DB 1347 CGTAGTTATCTACACGCGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC 1288
QY 6189 TGAGATAGTGGCTCTACTGATTAAGCATTTGGTAACTGTGAGCAAGTTTACTCATATAT 6248
DB 1287 TGAGATAGTGGCTCTACTGATTAAGCATTTGGTAACTGTGAGCAAGTTTACTCATATAT 1228
QY 6249 ACTTTAGATTGATTTAAACCTTCATTTTAAATTTAAAGGATCTAGTGAAGATCCTTTT 6308
DB 1227 ACTTTAGATTGATTTAAACCTTCATTTTAAATTTAAAGGATCTAGTGAAGATCCTTTT 1168
QY 6309 TGATAATCTCATGACCAAAATCCCTTAAAGTGGTGTGTTTCCCTACTGAGCGTCAAGCC 6368
DB 1167 TGATAATCTCATGACCAAAATCCCTTAAAGTGGTGTGTTTCCCTACTGAGCGTCAAGCC 1108
QY 6369 CGTAGAAGATCAAGAGTCTCTTTCAGATCTTTTCTGCGGTAACTGCTGCTT 6428
DB 1107 CGTAGAAGATCAAGAGTCTCTTTCAGATCTTTTCTGCGGTAACTGCTGCTT 1048
QY 6429 GCAACAAAAACCAACCGCTACAGCGGTGTTGTTTGGCGGATCAAGAGCTACCAAC 6488
DB 1047 GCAACAAAAACCAACCGCTACAGCGGTGTTGTTTGGCGGATCAAGAGCTACCAAC 988

QY 6489 TCTTTTTCGAAAGTAACTGGCTTCAGCAGAGCGGAGATACCAAACTACTGTCTCTTAGT 6548
DB 987 TCTTTTTCGAAAGTAACTGGCTTCAGCAGAGCGGAGATACCAAACTACTGTCTCTTAGT 928
QY 6549 GTAGCGTATGTTAGGCGCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCT 6608
DB 927 GTAGCGTATGTTAGGCGCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCT 868
QY 6609 GCTAATCTCTGTTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTCTGTTTACCGGGTTGA 6668
DB 867 GCTAATCTCTGTTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTCTGTTTACCGGGTTGA 808
QY 6669 CTCAGAAGCATAGTTTACCGGATAAGCGCGAGCGGTGGCTGAAACGGGGGTTCTGTCAC 6728
DB 807 CTCAGAAGCATAGTTTACCGGATAAGCGCGAGCGGTGGCTGAAACGGGGGTTCTGTCAC 748
QY 6729 ACAGCCCACTTGGAGCGAAGCACTTACACCGAACTGAGATACCTACAGCGTACGCTATG 6788
DB 747 ACAGCCCACTTGGAGCGAAGCACTTACACCGAACTGAGATACCTACAGCGTACGCTATG 688
QY 6789 AGAAAGCGCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGCGAGGT 6848
DB 687 AGAAAGCGCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGCGAGGT 628
QY 6849 CGGAAACAGAGAGCGCACAGGAGGCTTCCAGGGGAAACGCGCTGTATCTTTATAGTCC 6908
DB 627 CGGAAACAGAGAGCGCACAGGAGGCTTCCAGGGGAAACGCGCTGTATCTTTATAGTCC 568
QY 6909 TGTGCGGTTTCCCACTCTGACTTGGAGCTCGATTTTGTGATGCTCGTACAGGGGCG 6968
DB 567 TGTGCGGTTTCCCACTCTGACTTGGAGCTCGATTTTGTGATGCTCGTACAGGGGCG 508
QY 6969 GAGCTTATGAAAAACGCGCAGCAACGCGGCTTTTACGGTTCCTGGCTTTTGTGCGCC 7028
DB 507 GAGCTTATGAAAAACGCGCAGCAACGCGGCTTTTACGGTTCCTGGCTTTTGTGCGCC 448
QY 7029 TTTTGTCTCATGTTCTTTCCTGCTTATCCCGTATTCCTGTGATAACCGTATACCGC 7088
DB 447 TTTTGTCTCATGTTCTTTCCTGCTTATTCCTGCTATTCCTGTGATAACCGTATACCGC 388
QY 7089 CTTTGTAGTCACTGATACCGCTCGCGCAGCGAAGCGAGCGGAGTCACTGAG 7148
DB 387 CTTTGTAGTCACTGATACCGCTCGCGCAGCGAAGCGAGCGGAGTCACTGAG 328
QY 7149 CGAGGAAGCGGAGAGCGCCCAATACGCAAAACCGCTCTCCCGCGCTTGGCCGATTCA 7208
DB 327 CGAGGAAGCGGAGAGCGCCCAATACGCAAAACCGCTCTCCCGCGCTTGGCCGATTCA 268
QY 7209 TTAATGCACTGGCAGCAGAGGTTTCCGACTGGAAAGCGGGGAGTGGAGCAACGCAAT 7268
DB 267 TTAATGCACTGGCAGCAGAGGTTTCCGACTGGAAAGCGGGGAGTGGAGCAACGCAAT 208
QY 7269 TAACTGAGTTACCTCACTTATAGCACCCCGAGCTTTACACTTTATGCTTCCGGCTCC 7328
DB 207 TAACTGAGTTACCTCACTTATAGCACCCCGAGCTTTACACTTTATGCTTCCGGCTCC 148
QY 7329 TATGTTGTGTAATTTGTGAGCGGATAACAAATTTTACAGGAAACAGCTATGACCATGA 7388
DB 147 TATGTTGTGTAATTTGTGAGCGGATAACAAATTTTACAGGAAACAGCTATGACCATGA 88
QY 7389 TTACGCAAGCGCGCAATTTAACTCTCACTAAAGGGAAACAAAGCTGGAGCTC 7440
DB 87 TTACGCAAGCGCGCAATTTAACTCTCACTAAAGGGAAACAAAGCTGGAGCTC 36

RESULT 6

US-08-452-267-3
; Sequence 3, Application US/08452267
; Patent No. 5801027
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Ramsay, Nichola

TITLE OF INVENTION: Control of Genes in Transgenic Plants

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & Thornburg
STREET: 11 South Meridian
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/452,267
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 6653-25744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pUMIGIT
US-08-452-267-3

Query Match 28.2%; Score 2206.2; DB 1; Length 5534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2208; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	5229	TTACGTTGGGCACTTTTCGGGGAATGTGCGGGAACCTTATTTGTTTATTTTCTAAAT	5288
DB	3324	TTTAGTGGCACTTTTCGGGGAATGTGCGGGAACCTTATTTGTTTATTTTCTAAAT	3383
QY	5289	ACATTCAAATATGTATCCGCTCATGAGCAATAACCCCTGATAATGCTTCAATAATTTG	5348
DB	3384	ACATTCAAATATGTATCCGCTCATGAGCAATAACCCCTGATAATGCTTCAATAATTTG	3443
QY	5349	AAAAAGGAGATATGATATTCACATTTCCGTTGCGCCCTTATCCCTTTTTCGGGC	5408
DB	3444	AAAAAGGAGATATGATATTCACATTTCCGTTGCGCCCTTATCCCTTTTTCGGGC	3503
QY	5409	ATTTTTCCTTCTGTTTGTCTACCCAGAAACGCTGTTGAAAGTAAAGATGCTGAAGA	5468
DB	3504	ATTTTTCCTTCTGTTTGTCTACCCAGAAACGCTGTTGAAAGTAAAGATGCTGAAGA	3563
QY	5469	TCAGTTGGGTGACAGATGGGTATCATCGAACTGATCTCAACAGCGTAAAGATCTTTGA	5528
DB	3564	TCAGTTGGGTGACAGATGGGTATCATCGAACTGATCTCAACAGCGTAAAGATCTTTGA	3623
QY	5529	GAGTTTTCGCCCGGAAGACGTTTTCGAATGATGAGCACTTTTAAAGTTCGCTATGGG	5588
DB	3624	GAGTTTTCGCCCGGAAGACGTTTTCGAATGATGAGCACTTTTAAAGTTCGCTATGGG	3683
QY	5589	CCGCGTATTATCCCGTATTGACCGCGGCAAGAGCACTCCGTCGCCCATACACTATTC	5648
DB	3684	CCGCGTATTATCCCGTATTGACCGCGGCAAGAGCACTCCGTCGCCCATACACTATTC	3743
QY	5649	TCAGAAATGACTGGTTGAGTACTCAACAGTACAGAAAGCATCTTACGGATGCGATGAC	5708
DB	3744	TCAGAAATGACTGGTTGAGTACTCAACAGTACAGAAAGCATCTTACGGATGCGATGAC	3803

QY	5709	AGTAAGAGAAATATGAGTCTGCCATAACCATGAGTGAATAAAGTGGCGCAACTTACT	5768
DB	3804	AGTAAGAGAAATATGAGTCTGCCATAACCATGAGTGAATAAAGTGGCGCAACTTACT	3863
QY	5769	TCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTGTGACAAACATGGGGATCA	5828
DB	3864	TCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTGTGACAAACATGGGGATCA	3923
QY	5829	TGTAACCTCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACAAAGCAGGCG	5888
DB	3924	TGTAACCTCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACAAAGCAGGCG	3983
QY	5889	TGACACCAACGATCGCTGAGCAATGCGCAACAAACCTGCGCAAACTATTAACTGGCGAAT	5948
DB	3984	TGACACCAACGATCGCTGAGCAATGCGCAACAAACCTGCGCAAACTATTAACTGGCGAAT	4043
QY	5949	ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGG	6008
DB	4044	ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGG	4103
QY	6009	ACCACTTCTCGGCTCGGCCCTTCCGGCTGGCTGGTATTGCTGATTAATCTGGAGCGG	6068
DB	4104	ACCACTTCTCGGCTCGGCCCTTCCGGCTGGCTGGTATTGCTGATTAATCTGGAGCGG	4163
QY	6069	TGAGCGTGGGTCTCGCGGTATCATTTGACGACCTGCGGCGCAGATGGTAAGCCCTCCGAT	6128
DB	4164	TGAGCGTGGGTCTCGCGGTATCATTTGACGACCTGCGGCGCAGATGGTAAGCCCTCCGAT	4223
QY	6129	CGTAGTTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCG	6188
DB	4224	CGTAGTTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCG	4283
QY	6189	TGAGATAGGTGCTCCTGATTAAGCAATGGTAACTGTTCAGACCAAGTTTACTCATATAT	6248
DB	4284	TGAGATAGGTGCTCCTGATTAAGCAATGGTAACTGTTCAGACCAAGTTTACTCATATAT	4343
QY	6249	ACTTTAGATTGATTTAAACCTTCAATTTTAAAGGATCTAGTGAAGATCCTTTT	6308
DB	4344	ACTTTAGATTGATTTAAACCTTCAATTTTAAAGGATCTAGTGAAGATCCTTTT	4403
QY	6309	TGATAATCTCATGACCAAAATCCCTTAAACGAGTTCGTTCCACTGAGCGTCAGACCC	6368
DB	4404	TGATAATCTCATGACCAAAATCCCTTAAACGAGTTCGTTCCACTGAGCGTCAGACCC	4463
QY	6369	CGTAGAAAAGATCAAGGATCTTCTGAGATCCCTTTTCTGCGCGTAATCTGCTGCTT	6428
DB	4464	CGTAGAAAAGATCAAGGATCTTCTGAGATCCCTTTTCTGCGCGTAATCTGCTGCTT	4523
QY	6429	GCAACAAAAAACCACCGCTTACCAGCGGTGTTTGTGCGGATCAAGAGCTACCAAC	6488
DB	4524	GCAACAAAAAACCACCGCTTACCAGCGGTGTTTGTGCGGATCAAGAGCTACCAAC	4583
QY	6489	TCTTTTCCGAAGGTAACTGGCTTTCAGCAGCGCAGATACCAATACTGTCTCTAGT	6548
DB	4584	TCTTTTCCGAAGGTAACTGGCTTTCAGCAGCGCAGATACCAATACTGTCTCTAGT	4643
QY	6549	GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTT	6608
DB	4644	GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTT	4703
QY	6609	GCTAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTTCTTACCGGGTGA	6668
DB	4704	GCTAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTTCTTACCGGGTGA	4763
QY	6669	CTCAAGACGATAGTTTACCGGATAAGGCGCAGCGTCCGGCTGAAACCGGGGTTCGTCAC	6728
DB	4764	CTCAAGACGATAGTTTACCGGATAAGGCGCAGCGTCCGGCTGAAACCGGGGTTCGTCAC	4823
QY	6729	ACAGCCAGCTTGGAGCGAAGCACTACACCGAAGTGAATACCTACAGCGTGAAGTATG	6788
DB	4824	ACAGCCAGCTTGGAGCGAAGCACTACACCGAAGTGAATACCTACAGCGTGAAGTATG	4883

6789 AGAAGCGCCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGACAGGT 5848
Db AGAAGCGCCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGACAGGT 4943
Qy CGAAGCAGGAGAGCGACGAGGAGCTCCAGGGGAAACGCTGCTATCTTATAGTCC 6908
Db CGAAGCAGGAGAGCGACGAGGAGCTCCAGGGGAAACGCTGCTATCTTATAGTCC 5003
Qy TGTGGGTTTGGCACCCTCTGACTTGGAGGCTCGAATTTTGTGATGCTCGTCAAGGGGGGG 6968
Db TGTGGGTTTGGCACCCTCTGACTTGGAGGCTCGAATTTTGTGATGCTCGTCAAGGGGGGG 5063
Qy GAGCCTATGAAAAAGCGCAGAACCGGGCTTTTACGGTCTCTGGCCTTTTGTGGCC 7028
Db GAGCCTATGAAAAAGCGCAGAACCGGGCTTTTACGGTCTCTGGCCTTTTGTGGCC 5123
Qy TTTTGTCTACATGCTTCTTCTCGGTATCCCTGATTCCTGATTCCTGGATTAACCGTATTACCGC 7088
Db TTTTGTCTACATGCTTCTTCTCGGTATTCCTGATTCCTGGATTAACCGTATTACCGC 5183
Qy CTTTGTGAGTGTGATACCGCTCGCGCAGCCGAAACGCGAGCGCAGCGAGTCACTGAG 7148
Db CTTTGTGAGTGTGATACCGCTCGCGCAGCCGAAACGCGAGCGCAGCGAGTCACTGAG 5243
Qy CGAGGAAGCGGAAGAGCGCCAAATACGAAACCGCCTCTCCCGCGGCTTGGCCGATTCA 7208
Db CGAGGAAGCGGAAGAGCGCCAAATACGAAACCGCCTCTCCCGCGGCTTGGCCGATTCA 5303
Qy TTAATGCAGCTGCGACGAGGTTTCCGACTGGAAGCGGCGAGTGAAGCAACCAAT 7268
Db TTAATGCAGCTGCGACGAGGTTTCCGACTGGAAGCGGCGAGTGAAGCAACCAAT 5363
Qy TAAATGTGAGTGTACTCACTCATTAGGACCCCGAGGCTTTTACACTTTTATGCTTCCGGCTCC 7328
Db TAAATGTGAGTGTACTCACTCATTAGGACCCCGAGGCTTTTACACTTTTATGCTTCCGGCTCC 5423
Qy TATGTTGTGTGAAATGTGAGCGGATTAACATTTTCAACAGGAAACAGCTATGACCATGA 7388
Db TATGTTGTGTGAAATGTGAGCGGATTAACATTTTCAACAGGAAACAGCTATGACCATGA 5483
Qy TTACGCCAGCGCGCAATTAACCTCACTAAAGGAAACAAAGCTGGAGCT 7439
Db TTACGCCAGCGCGCAATTAACCTCACTAAAGGAAACAAAGCTGGAGCT 5534

RESULT 7

US-09-123-644-3
; Sequence 3, Application US/09123644
; Patent No. 6127606
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Rangay, Nicola
; TITLE OF INVENTION: Method of Using Transactivation Proteins to
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 South Meridian
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,644
; FILING DATE: 28-JUL-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P.

REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 6653-60788
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pUMIGIT
US-09-123-644-3

Query Match 28.2%; Score 2206.2; DB 3; Length 5534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2208; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5229 TTCAGGTGCACTTTTCGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 5288
Db 3324 TTTAGGTGCACTTTTCGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 3383
Qy 5289 ACATTCAAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATG 5348
Db 3384 ACATTCAAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATG 3443
Qy 5349 AAAAAAGAAAGATGAGTATTTCAACATTTCCGTGTCGCGCTTATTTCCCTTTTTCGGGC 5408
Db 3444 AAAAAAGAAAGATGAGTATTTCAACATTTCCGTGTCGCGCTTATTTCCCTTTTTCGGGC 3503
Qy 5409 ATTTTGCCTTCTGTTTGTCTCACCCAGAAACGCTGTAAGTAAAGATGCTCAAGA 5468
Db 3504 ATTTTGCCTTCTGTTTGTCTCACCCAGAAACGCTGTAAGTAAAGATGCTCAAGA 3563
Qy 5469 TCAGTTGGGTGACGAGTGGGTTTACATCGAACTGATCTCAACAGCGGTAAGATCCTTGA 5528
Db 3564 TCAGTTGGGTGACGAGTGGGTTTACATCGAACTGATCTCAACAGCGGTAAGATCCTTGA 3623
Qy 5529 GAGTTTTCGCCCGGAAGAACGTTTTCATGATGAGCACTTTTAAAGTCTGCTATGTGG 5588
Db 3624 GAGTTTTCGCCCGGAAGAACGTTTTCATGATGAGCACTTTTAAAGTCTGCTATGTGG 3683
Qy 5589 CGCGGTATTTATCCGTTGAGCGCGGCAAGCAACTCGGTGCGCGCATACACTATTTC 5648
Db 3684 CGCGGTATTTATCCGTTGAGCGCGGCAAGCAACTCGGTGCGCGCATACACTATTTC 3743
Qy 5649 TCAGAATGACTTGGTTGAGTACTCACCACTCAGAAAAAGCATCTTACGGATGGCATGAC 5708
Db 3744 TCAGAATGACTTGGTTGAGTACTCACCACTCAGAAAAAGCATCTTACGGATGGCATGAC 3803
Qy 5709 AGTAAGAAATATGCAAGTGTGCTAATACCATGATGATTAACATCGCGGCAACTTACT 5768
Db 3804 AGTAAGAAATATGCAAGTGTGCTAATACCATGATGATTAACATCGCGGCAACTTACT 3863
Qy 5769 TCTGCAACGATCGGAGGACCGAAGGAGCTTAACCGCTTTTTCACAACAATGGGGATCA 5828
Db 3864 TCTGCAACGATCGGAGGACCGAAGGAGCTTAACCGCTTTTTCACAACAATGGGGATCA 3923
Qy 5829 TGTAACTCGCTTGTGTTGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 5888
Db 3924 TGTAACTCGCTTGTGTTGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 3983
Qy 5889 TGACACCAAGTCTGTAGCAATGCAACAAGTTTGGCAACTATTAATCTGGGCAACT 5948
Db 3984 TGACACCAAGTCTGTAGCAATGCAACAAGTTTGGCAACTATTAATCTGGGCAACT 4043
Qy 5949 ACTTACTTAGCTTCCCGCAACAAATTAATAGCTGAGGCGGATTAAGTTTCAGG 6008
Db 4044 ACTTACTTAGCTTCCCGCAACAAATTAATAGCTGAGGCGGATTAAGTTTCAGG 4103

Matches 2207; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	5230	TCAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATA	5289
DB	10160	TCAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATA	10219
QY	5290	CATTCAATATGTATCGGCTCATGAGCAGCATATCCCTGATAAATGCTTCAATATATGA	5349
DB	10220	CATTCAATATGTATCGGCTCATGAGCAGCATATCCCTGATAAATGCTTCAATATATGA	10279
QY	5350	AAAAGGAAGATATGAGTATTCACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCA	5409
DB	10280	AAAAGGAAGATATGAGTATTCACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCA	10339
QY	5410	TTTTGCCCTTCCTGTTTTCCTCCACCCAGAAACGCTGCTGAAAGTAAAGATGCTGAAGAT	5469
DB	10340	TTTTGCCCTTCCTGTTTTCCTCCACCCAGAAACGCTGCTGAAAGTAAAGATGCTGAAGAT	10399
QY	5470	CAGTTGGGTGCAGAGTGGGTTATCATGAACTGGAATCTCAACAGCGGTAAAGTCTTGAG	5529
DB	10400	CAGTTGGGTGCAGAGTGGGTTATCATGAACTGGAATCTCAACAGCGGTAAAGTCTTGAG	10459
QY	5530	AGTTTTGCGCCCGGAAGAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGC	5589
DB	10460	AGTTTTGCGCCCGGAAGAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGC	10519
QY	5590	GCGGTATTATCCGGTATTGACGCGGCAAGAGCAACTCGGTGCGCGCATACATATTCT	5649
DB	10520	GCGGTATTATCCGGTATTGACGCGGCAAGAGCAACTCGGTGCGCGCATACATATTCT	10579
QY	5650	CAGATGACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGGATGACA	5709
DB	10580	CAGATGACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGGATGACA	10639
QY	5710	GTAAAGAAATATGCAAGTCTGCTGCAATACCATGAGTGATAACTGCGGCAACTTACTT	5769
DB	10640	GTAAAGAAATATGCAAGTCTGCTGCAATACCATGAGTGATAACTGCGGCAACTTACTT	10699
QY	5770	CTGACAAACGATCGGAGACCGAAGGAGCTAACCGCTTTTTTGACAAACATGGGGGATCAT	5829
DB	10700	CTGACAAACGATCGGAGACCGAAGGAGCTAACCGCTTTTTTGACAAACATGGGGGATCAT	10759
QY	5830	GTAACTCGCCTTGATCTGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGAGCGGT	5889
DB	10760	GTAACTCGCCTTGATCTGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGAGCGGT	10819
QY	5890	GACACCAAGTCTGCTAGCAATGGCAACCACTGCGCAAACTATTAACTGCGGAACTA	5949
DB	10820	GACACCAAGTCTGCTAGCAATGGCAACCACTGCGCAAACTATTAACTGCGGAACTA	10879
QY	5950	CTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGAGTGGAGCGGATAAAGTTGACGA	6009
DB	10880	CTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGAGTGGAGCGGATAAAGTTGACGA	10939
QY	6010	CCACTTCTGCGCTCGGCCCTTCGCGCTGGCTGTTTATGCTGATAAATCTGAGCGGCT	6069
DB	10940	CCACTTCTGCGCTCGGCCCTTCGCGCTGGCTGTTTATGCTGATAAATCTGAGCGGCT	10999
QY	6070	GAGGTGGGTCTCGCGTATCATGAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATC	6129
DB	11000	GAGGTGGGTCTCGCGTATCATGAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATC	11059
QY	6130	GTAGTTATCTACAGCAGCGGAGTCAGGCAACTATGATGAAACGAATAGACAGATCGCT	6189
DB	11060	GTAGTTATCTACAGCAGCGGAGTCAGGCAACTATGATGAAACGAATAGACAGATCGCT	11119
QY	6190	GAGATAGGTCCTCACTGATTAAGCAATGTTAACTGTGACCAAGTTTACTCATATATA	6249
DB	11120	GAGATAGGTCCTCACTGATTAAGCAATGTTAACTGTGACCAAGTTTACTCATATATA	11179
QY	6250	CTTTAGATGATTTAAACCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT	6309
DB	11180	CTTTAGATGATTTAAACCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT	11239

QY	6310	GATAATCTCATGAGCAAAATCCCTTAAACGTGAGTTTTTCTGTTCCACTGAGCGTCAGACCCC	6369
DB	11240	GATAATCTCATGAGCAAAATCCCTTAAACGTGAGTTTTTCTGTTCCACTGAGCGTCAGACCCC	11299
QY	6370	GTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTCTGCGCGTAAATCTGCTGCTTG	6429
DB	11300	GTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTCTGCGCGTAAATCTGCTGCTTG	11359
QY	6430	CAAAACAAAAACCAACCGCTTACAGCGGTGTTTTGTTGCGGATCAAGAGCTACCAACT	6489
DB	11360	CAAAACAAAAACCAACCGCTTACAGCGGTGTTTTGTTGCGGATCAAGAGCTACCAACT	11419
QY	6490	CTTTTTCGGAAGTAACTGCGCTTACAGAGCGCAGATACCAATACTGTCCTTCTAGTG	6549
DB	11420	CTTTTTCGGAAGTAACTGCGCTTACAGAGCGCAGATACCAATACTGTCCTTCTAGTG	11479
QY	6550	TAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTG	6609
DB	11480	TAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTG	11539
QY	6610	CTAATCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGTTGGAC	6669
DB	11540	CTAATCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGTTGGAC	11599
QY	6670	TCAAGACGATAGTTACCGGATAAAGCGCAGCGTCCGGCTGAAACGGGGGTTCTGTCACA	6729
DB	11600	TCAAGACGATAGTTACCGGATAAAGCGCAGCGTCCGGCTGAAACGGGGGTTCTGTCACA	11659
QY	6730	CAGCCAGCTTGGAGCGAAGCACTACACCGAATCTGATACCTACAGCGTGAAGTATGA	6789
DB	11660	CAGCCAGCTTGGAGCGAAGCACTACACCGAATCTGATACCTACAGCGTGAAGTATGA	11719
QY	6790	GAAAGCGCAGCTTCCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	6849
DB	11720	GAAAGCGCAGCTTCCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	11779
QY	6850	GGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	6909
DB	11780	GGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	11839
QY	6910	GTGCGGTTCGCCACCTCTGACTTGAGCGTGCATTTTGTGATGCTGCTGAGGGGGCG	6969
DB	11840	GTGCGGTTCGCCACCTCTGACTTGAGCGTGCATTTTGTGATGCTGCTGAGGGGGCG	11899
QY	6970	AGCTATGAAAACCCGAGCAACCGCGCTTTTACCGGTTCTGCGCTTTTGTGCGCT	7029
DB	11900	AGCTATGAAAACCCGAGCAACCGCGCTTTTACCGGTTCTGCGCTTTTGTGCGCT	11959
QY	7030	TTTGTCTCAGATGTTCTTCTGCGTTATCCCTGATTTCTGTGATAAACCGTATTACCGCC	7089
DB	11960	TTTGTCTCAGATGTTCTTCTGCGTTATCCCTGATTTCTGTGATAAACCGTATTACCGCC	12019
QY	7090	TTTGTGTAGTATGATACCGCTCCCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	7149
DB	12020	TTTGTGTAGTATGATACCGCTCCCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	12079
QY	7150	GAGGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	7209
DB	12080	GAGGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	12139
QY	7210	TAAATGAGCTGGCAGCAGAGGTTTCCCGACTGGAAGCGGCGAGTGAAGCGCAATTT	7269
DB	12140	TAAATGAGCTGGCAGCAGAGGTTTCCCGACTGGAAGCGGCGAGTGAAGCGCAATTT	12199
QY	7270	AATGTAGTATCTCACTCAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	7329
DB	12200	AATGTAGTATCTCACTCAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	12259
QY	7330	ATGTTGTGGAATGTGAGCGGATTAACAAATTTTACACAGGAAACAGCTATGACCATGAT	7389
DB	12260	ATGTTGTGGAATGTGAGCGGATTAACAAATTTTACACAGGAAACAGCTATGACCATGAT	12319

QY 7390 TACGCCAAGCGCGCAATTAACCTCACTAAAGGGAACAAAGCTCGAGCTC 7440
Db 12320 TACGCCAAGCTCGAATTAACCTCACTAAAGGGAACAAAGCTCGAGCTC 12370

RESULT 9

US-08-935-312-13
; Sequence 13, Application US/08935312
; Patent No. 6207455
; GENERAL INFORMATION:
; APPLICANT: CHANG, Lung-Ji
; TITLE OF INVENTION: LENTIVIRAL VECTORS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,312
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG-112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-935-312-13

Query Match 28.2%; Score 2204.6; DB 3; Length 12494;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5230 TCAGGTGGCACATTTTCGGGGAAATGTGCGGAAACCCCTATTCTTTTCTAAATA 5289
Db 10165 TCAGGTGGCACATTTTCGGGGAAATGTGCGGAAACCCCTATTCTTTTCTAAATA 10224
QY 5290 CATTCAATATATATATCCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATGA 5349
Db 10225 CATTCAATATATATATCCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATGA 10284
QY 5350 AAAAGGAAGATGAGATGATTAACAATTCGCTGTCGCCCTTATTCCTTTTTCGGGCA 5409
Db 10285 AAAAGGAAGATGAGATGATTAACAATTCGCTGTCGCCCTTATTCCTTTTTCGGGCA 10344
QY 5410 TTTTCCCTTCCTGTTTTCCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGAT 5469
Db 10345 TTTTCCCTTCCTGTTTTCCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGAT 10404
QY 5470 CAGTTGGGTGACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAG 5529
Db 10405 CAGTTGGGTGACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAG 10464
QY 5530 AGTTTTCGCCCGAAGAACGTTTTCCTCAATGATGAGCACTTTTAAAGTTCTGCTATGTCG 5589
Db 10465 AGTTTTCGCCCGAAGAACGTTTTCCTCAATGATGAGCACTTTTAAAGTTCTGCTATGTCG 10524

QY 5590 GCGTATTATCCGTTATTGACGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCT 5649
Db 10525 GCGTATTATCCGTTATTGACGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCT 10584
QY 5650 CAGAATGACATTGGTTGAGTACTACACAGTCAAGAAAGCACTTTACGGATGGCATGACA 5709
Db 10585 CAGAATGACATTGGTTGAGTACTACACAGTCAAGAAAGCACTTTACGGATGGCATGACA 10644
QY 5710 GTAAGAGAATTATGCACTGCTGCCATAAACATAGTATTAACACTGCGGCGCAACTTCTT 5769
Db 10645 GTAAGAGAATTATGCACTGCTGCCATAAACATAGTATTAACACTGCGGCGCAACTTCTT 10704
QY 5770 CTGACAAACGATCGGAGGACCGAAGAGCTAACCCCTTTTGGCAACAATGGGGGATCAT 5829
Db 10705 CTGACAAACGATCGGAGGACCGAAGAGCTAACCCCTTTTGGCAACAATGGGGGATCAT 10764
QY 5830 GTAACTCGCCTTGATCGTTGGGAAACCGAGCTGAATGAAGCCATACCAAAACGACGAGT 5889
Db 10765 GTAACTCGCCTTGATCGTTGGGAAACCGAGCTGAATGAAGCCATACCAAAACGACGAGT 10824
QY 5890 GACACACGATGCTGTAGCAATGGCAACACGTTGGCAAACTATTAACTGGCGCAACTA 5949
Db 10825 GACACACGATGCTGTAGCAATGGCAACACGTTGGCAAACTATTAACTGGCGCAACTA 10884
QY 5950 CTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGA 6009
Db 10885 CTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGA 10944
QY 6010 CCACCTCTGCGCTCGGCGCTTCCGCGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGCT 6069
Db 10945 CCACCTCTGCGCTCGGCGCTTCCGCGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGCT 11004
QY 6070 GAGCGTGGTCTCGCGGTATCATTTGACGACTGCGGCGCAGATGGTAAGCCCTCCCGTATC 6129
Db 11005 GAGCGTGGTCTCGCGGTATCATTTGACGACTGCGGCGCAGATGGTAAGCCCTCCCGTATC 11064
QY 6130 GTAGTTATCTACAGCGGGGAGTCAGGCAACTATGATGAACGAAATAGACAGATCGCT 6189
Db 11065 GTAGTTATCTACAGCGGGGAGTCAGGCAACTATGATGAACGAAATAGACAGATCGCT 11124
QY 6190 GAGATAGTGCCTCAGCTGATTAAGCACTGTAACCTGTGACACCAAGTTTACTCATATATA 6249
Db 11125 GAGATAGTGCCTCAGCTGATTAAGCACTGTAACCTGTGACACCAAGTTTACTCATATATA 11184
QY 6250 CTTTAGATTGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 6309
Db 11185 CTTTAGATTGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 11244
QY 6310 GATAATCTCATGACCAAAATCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCC 6369
Db 11245 GATAATCTCATGACCAAAATCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCC 11304
QY 6370 GTAGAAAGATCAAAAGGATCTTTTGAGATCTTTTTCGCGGTAATCTGCTGCTTG 6429
Db 11305 GTAGAAAGATCAAAAGGATCTTTTGAGATCTTTTTCGCGGTAATCTGCTGCTTG 11364
QY 6430 CAAACAAAAAACCACGCTACAGCGGTGTTTTCGCGGATCAAGAGTACCAACT 6489
Db 11365 CAAACAAAAAACCACGCTACAGCGGTGTTTTCGCGGATCAAGAGTACCAACT 11424
QY 6490 CTTTTCCTGAGGTAATCTGCTTACAGCAGCGCAGATACCAAAATCTGCTTCTAGTG 6549
Db 11425 CTTTTCCTGAGGTAATCTGCTTACAGCAGCGCAGATACCAAAATCTGCTTCTAGTG 11484
QY 6550 TAGCGGTAGTTAGGCCCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTG 6609
Db 11485 TAGCGGTAGTTAGGCCCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTG 11544
QY 6610 CTAATCTGTTACAGTGGCTGCTGCGAGTGGCGATAGTCTGCTTACCGGGTTGAC 6669
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6670 TCAAGACGATAGTACCGGATAGGCGGACGCGTCCGGCTGTAACGGGGGGTTCGTGCACA 6729
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6730 CAGCCAGCTTGGAGCGGACGCTACCGAACTGAGTACTCAGCGTGAGCTATGA 6789
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6850 GGAACAGGAGAGCGCAGCGAGGAGCTTCCAGGGGAAACGCCCTGGTATCTTTATAGTCCT 6909
Db GGAACAGGAGAGCGCAGCGAGGAGCTTCCAGGGGAAACGCCCTGGTATCTTTATAGTCCT 11844
6910 GTCCGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGG 6969
Db GTCCGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGG 11904
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7090 TTTGAGTGAGCTATACCGCTCCGCGAGCGGAGCGGAGCGGAGCGGAGTCACTGAGC 7149
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7210 TAATGAGCTGGGACGAGCGGAGTTCGCGACTGGAAGCGGCGAGTGAAGCGCAACGCAAT 7269
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7390 TACGCCAAGCGCGCAATTAACCTCTACTAAAGGGAACAAAGCTGGAGCTC 7440
Db TACGCCAAGCTCGAAATTAACCTCTACTAAAGGGAACAAAGCTGGAGCTC 12375

RESULT 10

US-08-848-760B-33

Sequence 33, Application US/08848760B

Patent No. 6248721

GENERAL INFORMATION:

APPLICANT: Chang, Lung-Ji

TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: United States of America

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 12494 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-848-760B-33

Query Match 28.2%; Score 2204.6; DB 3; Length 12494;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5230 TCAGGTGGGACATTTTCGGGGAATGTCGGGGAACCCCTATTGTTTATTTCTTAATA 5289
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QY 5530 AGTTTTTCGCCCCGGAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGATGTCG 5589
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Db 10525 GCGGTATTATCCGTTATGACGCGGGGCAAGCAACTCGGTCGCGCATACACTATTCT 10584
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QY 5710 GTAAGAGAATTTATGAGTGTGCTCCATAACCATGAGTGATAAACAATCGCGCAACTTACTT 5769
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QY 5830 GTAACTCGCTTCATCGTTGGGAACCGGAGCTGAATGAAGCCCATACCAACGACGAGCGT 5889
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10885 CTTACTCTAGCTTCCGCGCAAAATTAATAGACTGGATGGAGCGGATAAAGTTGACGGA 10944
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10945 CCACCTCTGCGCTGGCGCTTCCGCGCTGGCTGGTTATTGCTGATATAATCTGGAGCCGCT 11004
6070 GAGCGTGGGTCTCGCGGTATCAITGACGACTGGGGCCAGATGGTAAGCCCTCCCGTATC 6129
11005 GAGCGTGGGTCTCGCGGTATCAITGACGACTGGGGCCAGATGGTAAGCCCTCCCGTATC 11064
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11065 GTAGTTTCTACAGCGGGGAGTTCAGGCAACTATGATGATGAACGAATATGACAGATCGCT 11124
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11125 GAGATAGTGGCTCACTGATTAAGCATTTGTAAGTGTGTCAGACCAAGTTTACTCATATATA 11184
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11245 GATAATCTCATGACCAAAATCCCTTAACGTGAGTTTCTGTTCCACTGAGCGGTGAGACCC 11304
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11485 TAGCGGTAGTTAGGCGCACCTTCAAGAACTCTGAGCAGCGCTACATACCTGCTCTG 11544
6610 CTAATCTCTGTTACCAAGTGGCTGCTGCCAGTGGCGATAGTCTGCTTTACCGGTTGGAC 6669
11545 CTAATCTCTGTTACCAAGTGGCTGCTGCCAGTGGCGATAGTCTGCTTTACCGGTTGGAC 11604
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11605 TCAAGACGATGTTACCGGATAAGCGGAGCGGCTGGGCTGAAACGGGGGTTCTGTGACA 11664
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11725 GAAAGCGCACCTTCCCGAAGGAGGAGGAGGAGCGGATGATGATGATGATGATGATGATG 11784
6850 GAAAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6909
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11845 GTCGGGTTTCGCCCTCTGCTTACGAGCGTCAATTTTGTGATGCTGCTCAGGGGGCGG 11904
6970 AGCCTATGAAAAACGCCAGCAACCGCGGCTTTTACGCTTCTGCGCTTTTGTGCGCT 7029

11905 AGCTATGAAAAACGCCAGCAACCGCGCTTTTACGGTTCTTGGCTTTTGTGGCT 11964
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11965 TTTGCTCACATGTTCTTTCTGCTGTTATCCCTGATTCCTGTTGGATAACCGTATTACCGC 12024
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12025 TTTGAGTGAGCTGATACCGCTCGCGCAGCGCAACAGACCGAGCGAGTCACTGAGC 12084
7150 GAGAAAGCGGAGCGCGCAATATAGCAACCGCTCTTCCCGCGCTTGGCCGATTCAT 7209
12085 GAGAAAGCGGAGCGCGCAATATAGCAACCGCTCTTCCCGCGCTTGGCCGATTCAT 12144
7210 TAATGAGCTGGCAGCAGCGTTTCCCGACTGGAAAGCGGCGAGTGAAGCGCAACCAAT 7269
12145 TAATGAGCTGGCAGCAGCGTTTCCCGACTGGAAAGCGGCGAGTGAAGCGCAACCAAT 12204
7270 AATGAGTTTACCTCACTTACCTAGCGACCCAGCGCTTTACACTTTATGCTTCCGCTCT 7329
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7330 AATGAGTTTACCTCACTTACCTAGCGACCCAGCGCTTTACACTTTATGCTTCCGCTCT 7389
12265 AATGAGTTTACCTCACTTACCTAGCGACCCAGCGCTTTACACTTTATGCTTCCGCTCT 12324
7390 TAGCCAAAGCGCGCAATTAACCTCACTTAAGGGAACAAAGCTGGAGCTC 7440
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RESULT 11
US-09-608-730B-21
; Sequence 21, Application US/09608730B
; Patent No. 6423544
; GENERAL INFORMATION:
; APPLICANT: Hardy, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING RECOMBINANT
; TITLE OF INVENTION: VIRIONS
; FILE REFERENCE: PP01569.101
; CURRENT APPLICATION NUMBER: US/09/608,730B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/476,299
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 21
; LENGTH: 4883
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pBS CP
US-09-608-730B-21

Query Match 28.2%; Score 2204; DB 4; Length 4883;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

5229 TTCAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTCTTAAT 5288
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5289 ACATTCAATATGATCGCTCATGACATACCCCTGATAATGCTTCAATAATATG 5348
2690 ACATTCAATATGATCGCTCATGACATACCCCTGATAATGCTTCAATAATATG 2749
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Db 3050 TCAGAATGACTGGTTGAGTACTCACAGTCAAGAAAGACATCTTACCGATGCGCATGAC 3109
Qy 5709 AGTAAGAGAAATATGCACTGCTGCCATTAACCATGAGTAACTGCGCGCAACTTACT 5768
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Db 3470 TGAGCGTGGTCTCGCGGTATCATTTGACGACACTGGGGCCAGATGGTAAGCCCTCCGTTAT 3529
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Db 3530 CGTAGTTATCTACACGACGGGAGTCAGGCAACTATGATGAACGAAATAGACAGATCGC 3589
Qy 6189 TGAGATAGGTGCCTCACTGATTAAAGCAATGGTAACCTGTACAGACCAAGTTTACTCATATAT 6248
Db 3590 TGAGATAGGTGCCTCACTGATTAAAGCAATGGTAACCTGTACAGACCAAGTTTACTCATATAT 3649
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Db 3650 ACTTTAGATTGATTAAACCTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTT 3709
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Qy 6669 CTCAGACGATAGTTTACCGGATAAGCGCGAGCGGTCTGAGCTGAAACGGGGGTTCTGTCAC 6728
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Qy 7029 TTTTGTCTACATGTTCTTCTCGCTTATCCCGTGTATCTGTGATAACCGGTATTACCGC 7088
Db 4430 TTTTGTCTACATGTTCTTCTCGCTTATCCCGTGTATCTGTGATAACCGGTATTACCGC 4489
Qy 7089 CTTTGTAGTGAAGTATACCGCTCGCGAGCGGAAACGACGCGGAGCGAGTCAAGTGAAG 7148
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RESULT 12

US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
; GENERAL INFORMATION:
; APPLICANT: Rakhmievich, Alexander
; TITLE OF INVENTION: IL-12 Gene Therapy of Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles & Brady
; STREET: 1 South Pinckney Street

CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,206A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 110229.91144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7287 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Plasmid DNA"
CLONE: pWRG3169
IMMEDIATE SOURCE:
FEATURE:
NAME/KEY: promoter
LOCATION: 1..628
FEATURE:
NAME/KEY: idNA
LOCATION: 629..810
FEATURE:
NAME/KEY: CDS
LOCATION: join(953..1258, 1332..1673)
OTHER INFORMATION: /product= "p35 gene product"
FEATURE:
NAME/KEY: polyA site
LOCATION: 1797..2024
FEATURE:
NAME/KEY: promoter
LOCATION: 2110..2737
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NAME/KEY: idNA
LOCATION: 2738..2919
FEATURE:
NAME/KEY: CDS
LOCATION: 2983..3990
OTHER INFORMATION: /product= "p40 gene product"
FEATURE:
NAME/KEY: polyA site
LOCATION: 4075..4306
US-08-659-206A-1

Query Match 28.2%; Score 2204; DB 2; Length 7287;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 5; Indels 0; Gaps 0;
QY 5229 TTTCAGTGGCCTTTTCGGGGAAATGTCGGGAAACCCCTATTGTTTATTTTCTAAAT 5288
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QY 5529 GAGTTTGGCCCGAAGAAAGCTTTTCCATGATGAGCACTTTTAAAGTTCTGCTATGCG 5588
DB 5301 GAGTTTGGCCCGAAGAAAGCTTTTCCATGATGAGCACTTTTAAAGTTCTGCTATGCG 5360
QY 5589 CGCGTATTATCCGCTATTGACGCGCGGCAAGAGCAACTCGTGGCCGCATACATTATTC 5648
DB 5361 CGCGTATTATCCGCTATTGACGCGCGGCAAGAGCAACTCGTGGCCGCATACATTATTC 5420
QY 5649 TCAGAATGACTTGGTTGAGTACTCACCAAGTCAAGAAAAGCATCTTACGGATGGCATGAC 5708
DB 5421 TCAGAATGACTTGGTTGAGTACTCACCAAGTCAAGAAAAGCATCTTACGGATGGCATGAC 5480
QY 5709 AGTAAGAGAATTATGCAAGTGGTGCCTAATCAATGATGATTAACACTGCGGCCAATCTTACT 5768
DB 5481 AGTAAGAGAATTATGCAAGTGGTGCCTAATCAATGATGATTAACACTGCGGCCAATCTTACT 5540
QY 5769 TCTGACAAACGATCGAGGACCGAAGGAGCTAACCGCTTTTGGCAACAATGGGGGATCA 5828
DB 5541 TCTGACAAACGATCGAGGACCGAAGGAGCTAACCGCTTTTGGCAACAATGGGGGATCA 5600
QY 5829 TGTAACCTCGCTTGGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 5888
DB 5601 TGTAACCTCGCTTGGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 5660
QY 5889 TGACACCAAGATGCTGAGCAATGGCAACCACTTGGGCAAACTATTAACTGGCGNACT 5948
DB 5661 TGACACCAAGATGCTGAGCAATGGCAACCACTTGGGCAAACTATTAACTGGCGNACT 5720
QY 5949 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGG 6008
DB 5721 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGG 5780
QY 6009 ACCACTTCTGCGTGGCCCTTCCGCTGGCTGGCTGTTTATCTGATATAATCTGGAGCGCG 6068
DB 5781 ACCACTTCTGCGTGGCCCTTCCGCTGGCTGGCTGTTTATCTGATATAATCTGGAGCGCG 5840
QY 6069 TGACGTTGGGTCTGCGGCTATCATTTGAGCACTGGGCGCAGATGTAAGCCCTCCCGTAT 6128
DB 5841 TGACGTTGGGTCTGCGGCTATCATTTGAGCACTGGGCGCAGATGTAAGCCCTCCCGTAT 5900
QY 6129 CGTAGTTTATCTACACGACGGGAGTCAAGGCAACTATGGATGAACGAAATAGACAGATCGC 6188
DB 5901 CGTAGTTTATCTACACGACGGGAGTCAAGGCAACTATGGATGAACGAAATAGACAGATCGC 5960
QY 6189 TGAGATAGGTGCTCTACTGATTAAGCAATGGTAACTGTGACACCAAGTTTACTATATAT 6248
DB 5961 TGAGATAGGTGCTCTACTGATTAAGCAATGGTAACTGTGACACCAAGTTTACTATATAT 6020
QY 6249 ACTTTAGATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 6308
DB 6021 ACTTTAGATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 6080
QY 6309 TGATAATCTCATGACCAAAATCCCTTAAACGAGTGTTCGTTTCCACTGAGCGCTCAGACCC 6368
DB 6081 TGATAATCTCATGACCAAAATCCCTTAAACGAGTGTTCGTTTCCACTGAGCGCTCAGACCC 6140
QY 6369 CGTAGAAAAGATCAAGGATCTCTTGAGATCTCTTTTCTGCGCGTAATCTGCTGCTT 6428
DB 6141 CGTAGAAAAGATCAAGGATCTCTTGAGATCTCTTTTCTGCGCGTAATCTGCTGCTT 6200
QY 6429 GCAACAAAAGAACCCGCTTACCAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAAC 6488
DB 6201 GCAACAAAAGAACCCGCTTACCAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAAC 6260

QY 6489 TCCTTTTCCGAGGTACTCGCTTCAGCAGCGCAGATACCAATACTGTCTCTTAGT 6548
Db 6261 TCCTTTTCCGAGGTAACTGGCTTCAGCAGCGCAGATACCAATACTGTCTCTTAGT 6320
QY 6549 GTAGCCGTAGTGTAGCCACCACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCT 6608
Db 6321 GTAGCCGTAGTGTAGCCACCACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCT 6380
QY 6609 GCTAAATCTCTTACCAAGTGTCTGCTGACGTGCGATAAGTCTGTCTTACCGGGTTGGA 6668
Db 6381 GCTAAATCTCTTACCAAGTGTCTGCTGACGTGCGATAAGTCTGTCTTACCGGGTTGGA 6440
QY 6669 CTCAGACGATAGTACCGGATAGCGGACGCGCTGGGCTGAACGGGGGTTCTGTCAC 6728
Db 6441 CTCAGACGATAGTACCGGATAGCGGACGCGCTGGGCTGAACGGGGGTTCTGTCAC 6500
QY 6729 ACAGCCAGCTTCGAGCGAAGCACTTACACCGAATCTAGATACCTACAGCGTCACTATG 6788
Db 6501 ACAGCCAGCTTCGAGCGAAGCACTTACACCGAATCTAGATACCTACAGCGTCACTATG 6560
QY 6789 AGAAGCGCCACGCTTCCGAGGAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGTT 6848
Db 6561 AGAAGCGCCACGCTTCCGAGGAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGTT 6620
QY 6849 CGAAGCAGGAGCGACGAGGAGCTTCCAGGGGAGAAAGCGCTGTATCTTTATAGTCC 6908
Db 6621 CGAAGCAGGAGCGACGAGGAGCTTCCAGGGGAGAAAGCGCTGTATCTTTATAGTCC 6680
QY 6909 TGTGCGGTTTCGCACTCTGACTGAGCTGCTGATCTTTTGTGATGCTCGTACGGGGGGG 6968
Db 6681 TGTGCGGTTTCGCACTCTGACTGAGCTGCTGATCTTTTGTGATGCTCGTACGGGGGGG 6740
QY 6969 GAGCCTATGGAAGAAAGCGCAGCAACGCGCTTTCAGCGTCTCTGCGCTTTTGTGCGCC 7028
Db 6741 GAGCCTATGGAAGAAAGCGCAGCAACGCGCTTTCAGCGTCTCTGCGCTTTTGTGCGCC 6800
QY 7029 TTTTGTCTACATGTTCTTCTCGGTTATCCCTGATTCCTGTGATACCGTAAACCGTATACCG 7088
Db 6801 TTTTGTCTACATGTTCTTCTCGGTTATCCCTGATTCCTGTGATACCGTAAACCGTATACCG 6860
QY 7089 CTTTGTAGTGTAGTATACCGCTCGCGCAGCCGACGAGCGGAGCGAGTCACTGAG 7148
Db 6861 CTTTGTAGTGTAGTATACCGCTCGCGCAGCCGACGAGCGGAGCGAGTCACTGAG 6920
QY 7149 CGAGGAAGCGGAAGAGCGCCCAATAGCAAAACCGCTCTCCCGCGCGTTGGCCGATTC 7208
Db 6921 CGAGGAAGCGGAAGAGCGCCCAATAGCAAAACCGCTCTCCCGCGCGTTGGCCGATTC 6980
QY 7209 TTAATGAGCTGGACGACAGGTTTCCGACTGGAAGCGGGGAGTGAAGCGCAACGCAAT 7268
Db 6981 TTAATGAGCTGGACGACAGGTTTCCGACTGGAAGCGGGGAGTGAAGCGCAACGCAAT 7040
QY 7269 TAAATGAGTGTAGTGTAGCGGATTAACCTTACCTTAAGGGAACAAAGCTGGAGCTC 7328
Db 7041 TAAATGAGTGTAGTGTAGCGGATTAACCTTACCTTAAAGGGAACAAAGCTGGAGCTC 7100
QY 7329 TATGTTGTGTGGAATGTAGCGGATTAACCTTACCTTAAGGGAACAAAGCTGGAGCTC 7388
Db 7101 TATGTTGTGTGGAATGTAGCGGATTAACCTTACCTTAAAGGGAACAAAGCTGGAGCTC 7160
QY 7389 TTAAGCAGCGCGCAATTAACCTTACCTTAAGGGAACAAAGCTGGAGCTC 7440
Db 7161 TTAAGCAGCGCGCAATTAACCTTACCTTAAAGGGAACAAAGCTGGAGCTC 7212

RESULT 13

US-08-446-935-6/c
; Sequence 6, Application US/08446935
; Patent No. 6187991
; GENERAL INFORMATION:
; APPLICANT: Soeller, Walter C.
; APPLICANT: Carty, Maynard D.
; APPLICANT: Kreutter, David K.

; TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II
; TITLE OF INVENTION: DIABETES MELLITUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pfizer Inc.
; STREET: 235 East 42nd Street, 20th Floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-5755
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,935
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheyke, Robert F.
; REGISTRATION NUMBER: 31,304
; REFERENCE/DOCKET NUMBER: PC8153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 573-1189
; TELEFAX: (212) 573-1939
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2961 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; US-08-446-935-6

Query Match 28.2%; Score 2203.8; DB 3; Length 2961;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2205; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5234 GTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTTGTTTCTTAATACATT 5293
Db 2961 GTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTTGTTTCTTAATACATT 2902
QY 5294 CAAATATGATCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATAATATGAAAA 5353
Db 2901 CAAATATGATCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATAATATGAAAA 2842
QY 5354 GGAAGATGATGATTAACAATTTCCGTGCGCCCTTATTCCTTTTTCGCGCATTTT 5413
Db 2841 GGAAGATGATGATTAACAATTTCCGTGCGCCCTTATTCCTTTTTCGCGCATTTT 2782
QY 5414 GCCTTCCTCTTTTTCGCTCACCAGAAACGCTGCTGGAAGTAAAGATGCTGAAGTCACT 5473
Db 2781 GCCTTCCTCTTTTTCGCTCACCAGAAACGCTGCTGGAAGTAAAGATGCTGAAGTCACT 2722
QY 5474 TGGGTGCACGAGTGGGTATCATCGAACTCGATCTCAACAGCGGTAAGATCTTTGAGAGTT 5533
Db 2721 TGGGTGCACGAGTGGGTATCATCGAACTCGATCTCAACAGCGGTAAGATCTTTGAGAGTT 2662
QY 5534 TTCGCCCCGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTTCTGTATGTGGCGCG 5593
Db 2661 TTCGCCCCGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTTCTGTATGTGGCGCG 2602
QY 5594 TATATCCGCTATGACGCGGCAAGCACTCGTTCGCGCATACACTATTTCTCAGA 5653
Db 2601 TATATCCGCTATGACGCGGCAAGCACTCGTTCGCGCATACACTATTTCTCAGA 2542
QY 5654 ATGACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCATGACAGTAA 5713
Db 2541 ATGACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCATGACAGTAA 2482
QY 5714 GAGAATTATGCAAGTGTGCTCCATAACCATGATGATAACACTGCGGCCAACTTACTTCTGA 5773

APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pS29pt-S4
US-08-651-472-62

Query Match 28.2%; Score 2203.8; DB 3; Length 4145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2205; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	5234	GTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATT	5293
DB	1	GTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATT	60
QY	5294	CAAAATGATGATCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTGAAAA	5353
DB	61	CAAAATGATGATCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTGAAAA	120
QY	5354	GGAAAGATGATGATTTCAACATTTTCGTTGTCGCCCTTATTCCTTTTTTTCGGGCAATTT	5413
DB	121	GGAAAGATGATGATTTCAACATTTTCGTTGTCGCCCTTATTCCTTTTTTTCGGGCAATTT	180
QY	5414	GCCTTCTGTTTTGCTCACCAGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGT	5473
DB	181	GCCTTCTGTTTTGCTCACCAGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGT	240
QY	5474	TGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTT	5533
DB	241	TGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTT	300
QY	5534	TTCCGCCCCGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCG	5593
DB	301	TTCCGCCCCGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCG	360
QY	5594	TATTATCCGCTATTGAGCGCGGCAAGAGCACTCGGTGCGCCGATACACTATTCTCAGA	5653
DB	361	TATTATCCGCTATTGAGCGCGGCAAGAGCACTCGGTGCGCCGATACACTATTCTCAGA	420
QY	5654	ATGACTTGGTTGAGTACTCACCAGTCAAGAAAGCATCTTACGGATGGCATGACAGATAA	5713
DB	421	ATGACTTGGTTGAGTACTCACCAGTCAAGAAAGCATCTTACGGATGGCATGACAGATAA	480
QY	5714	GAGAAATTATGCACTGTGCGCATTAACCATGATGATAAACAATCGCGCCAACTTACTCTGA	5773
DB	481	GAGAAATTATGCACTGTGCGCATTAACCATGATGATAAACAATCGCGCCAACTTACTCTGA	540
QY	5774	CAACGATCGGAGACCGAAGAGCACTAACCGTTTTTTTGCAACAATGCGGGGATCATGTAA	5833
DB	541	CAACGATCGGAGACCGAAGAGCACTAACCGTTTTTTTGCAACAATGCGGGGATCATGTAA	600
QY	5834	CTCGCTTGTATCTGTGGAAACCGAGCTGAATGAAGCCATACCAACACGACGAGCGTGACA	5893
DB	601	CTCGCTTGTATCTGTGGAAACCGAGCTGAATGAAGCCATACCAACACGACGAGCGTGACA	660

QY	5894	CCACGATGCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTA	5953
DB	661	CCACGATGCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTA	720
QY	5954	CTCTAGCTTCCCGGCAACAATTAATAGACTGAGTGGAGCGGTAAGTTGCAAGGACAC	6013
DB	721	CTCTAGCTTCCCGGCAACAATTAATAGACTGAGTGGAGCGGTAAGTTGCAAGGACAC	780
QY	6014	TTCTGCGCTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGCTGAGC	6073
DB	781	TTCTGCGCTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGCTGAGC	840
QY	6074	GTGGGTCTCGGGTATCATTTGAGCACTCGGGGCGAGATGGTAAGCCTCCCGTATCGTAG	6133
DB	841	GTGGGTCTCGGGTATCATTTGAGCACTCGGGGCGAGATGGTAAGCCTCCCGTATCGTAG	900
QY	6134	TTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAATACAGACATCGCTGAGA	6193
DB	901	TTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAATACAGACATCGCTGAGA	960
QY	6194	TAGGTGCTCTCACTGATTAAAGCAATTTGTAACCTGTGAGCAACAAAGTTTACTCATATATCTTT	6253
DB	961	TAGGTGCTCTCACTGATTAAAGCAATTTGTAACCTGTGAGCAACAAAGTTTACTCATATATCTTT	1020
QY	6254	AGATTGATTTAAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGTATA	6313
DB	1021	AGATTGATTTAAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGTATA	1080
QY	6314	ATCTCATGACCAAAATCCCTTAACGTTGAGTCTTCCACTGAGCGTCAGACCCGCTAG	6373
DB	1081	ATCTCATGACCAAAATCCCTTAACGTTGAGTCTTCCACTGAGCGTCAGACCCGCTAG	1140
QY	6374	AAAAAGATCAAGGATCTTCTTGAGATCTTTTCTGCGCGTAATCTGCTGCTGCAAA	6433
DB	1141	AAAAAGATCAAGGATCTTCTTGAGATCTTTTCTGCGCGTAATCTGCTGCTGCAAA	1200
QY	6434	CAAAAAACAACCGCTACAGCGGTGGTTGTTTGGCGGATCAAGAGTACCAACTCTTT	6493
DB	1201	CAAAAAACAACCGCTACAGCGGTGGTTGTTTGGCGGATCAAGAGTACCAACTCTTT	1260
QY	6494	TTCCGGAAGTAACTGGCTTCAGAGAGCGAGATACCAATCTGCTTCTAGTGTAGC	6553
DB	1261	TTCCGGAAGTAACTGGCTTCAGAGAGCGAGATACCAATCTGCTTCTAGTGTAGC	1320
QY	6554	CGTAGTTAGGCCAACCACTTCAAGAACTGTGTAGCACCGCTCATATACCTCTGCTAA	6613
DB	1321	CGTAGTTAGGCCAACCACTTCAAGAACTGTGTAGCACCGCTCATATACCTCTGCTAA	1380
QY	6614	TCTGTTTACAGTGGCTGTGCGAGTGGCGATAAGTGTGTTTACCGGGTTGGAATCAA	6673
DB	1381	TCTGTTTACAGTGGCTGTGCGAGTGGCGATAAGTGTGTTTACCGGGTTGGAATCAA	1440
QY	6674	GACGATAGTTACCGGATAGGCGCAGCGGTGGGCTGAACGGGGGTTCTGTCACACAGC	6733
DB	1441	GACGATAGTTACCGGATAGGCGCAGCGGTGGGCTGAACGGGGGTTCTGTCACACAGC	1500
QY	6734	CCAGCTTGGAGCGGAAACGACTACCGAACTGAGATACCTACAGCGTGAAGTATGAGAA	6793
DB	1501	CCAGCTTGGAGCGGAAACGACTACCGAACTGAGATACCTACAGCGTGAAGTATGAGAA	1560
QY	6794	GGCCACAGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGCTCGGAA	6853
DB	1561	GGCCACAGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGCTCGGAA	1620
QY	6854	CAGGAGCGCAGGAGGAGCTTCCAGGGGAAACGCTGTTATCTTTATGCTCTGTCG	6913
DB	1621	CAGGAGCGCAGGAGGAGCTTCCAGGGGAAACGCTGTTATCTTTATGCTCTGTCG	1680
QY	6914	GGTTTTCGCACTCTGACCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	6973
DB	1681	GGTTTTCGCACTCTGACCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1740
QY	6974	TATGAAAAACCGCAGCAACCGCGCTTTTACGGTTCTGCGCTTTTCTGCGCTTTTGG	7033

Db 1741 TATGAAAAACCCAGCAACGGCGCTTTTACGGCTTCTGGCTTCTGGCTTTTG 1800
Qy 7034 CTCACATGTTCTTCTCGGTATCCCTGATTCCTGTGATAACCGTATACCGCTTTG 7093
Db 1801 CTCACATGTTCTTCTCGGTATCCCTGATTCCTGTGATAACCGTATACCGCTTTG 1860
Qy 7094 AGTGAGCTGATACCGCTCGCGCAGCGCAACGACCGAGCGAGCGAGTCACTGAGCGAGG 7153
Db 1861 AGTGAGCTGATACCGCTCGCGCAGCGCAACGACCGAGCGAGCGAGTCACTGAGCGAGG 1920
Qy 7154 AAGCGGAAGAGCGCCCAATACGCAAAACCGCTCTCTCCCGCGCTTGCGCCGATCATTAAT 7213
Db 1921 AAGCGGAAGAGCGCCCAATACGCAAAACCGCTCTCTCCCGCGCTTGCGCCGATCATTAAT 1980
Qy 7214 GCAGCTGCGACGACGATTTCCCGACTGGAAGCGGCGAGTGAAGCAACGCAATTAATG 7273
Db 1981 GCAGCTGCGACGACGATTTCCCGACTGGAAGCGGCGAGTGAAGCAACGCAATTAATG 2040
Qy 7274 TCAGTTTACTCTACTCATTTAGGCAACCCAGGCTTTTACACTTTTATGCTTCCGCTCTCTATGT 7333
Db 2041 TGAGTTAGCTCACTCATTTAGGCAACCCAGGCTTTTACACTTTTATGCTTCCGCTCTCTATGT 2100
Qy 7334 TGTGTGGAATTTGTGAGCGGATAACAAATTTTCAACAGGAAACAGCTATGACCATGATTACG 7393
Db 2101 TGTGTGGAATTTGTGAGCGGATAACAAATTTTCAACAGGAAACAGCTATGACCATGATTACG 2160
Qy 7394 CCAAGCGGCAATTAACCTCTCACTAAGGGAACAAAGCTGGAGCTC 7440
Db 2161 CCAAGCGGCAATTAACCTCTCACTAAGGGAACAAAGCTGGAGCTC 2207

RESULT 15

US-08-358-928-62
; Sequence 62, Application US/08358928
; Patent No. 6265183
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/358,928
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
TELEX: 904136
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: pS2gpt-S4
; US-08-358-928-62

Query Match 28.2%; Score 2203.8; DB 3; Length 4145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2203; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5234 GTGCGACTTTTTCGGGGAAATGTGCGCGAAACCCCTATTGTTTATTTTCTAAATACATT 5293
Db 1 GTGCGACTTTTTCGGGGAAATGTGCGCGAAACCCCTATTGTTTATTTTCTAAATACATT 60
Qy 5294 CAAATATGATCCGCTCATGAGACAATAACCTGATAAATCTTCAATAATATTGAAAAA 5353
Db 61 CAAATATGATCCGCTCATGAGACAATAACCTGATAAATCTTCAATAATATTGAAAAA 120
Qy 5354 GGAAGAGTATGATTAATCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCAATTT 5413
Db 121 GGAAGAGTATGATTAATCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCAATTT 180
Qy 5414 GCCTTCCTGTTTTCCTCACCAGAAACGCTGTGGAAGTAAAGATCTGGAAGATCAGT 5473
Db 181 GCCTTCCTGTTTTCCTCACCAGAAACGCTGTGGAAGTAAAGATCTGGAAGATCAGT 240
Qy 5474 TGGGTGACAGTGGGTTTACATCGAACTGATCTCAACAGCGGTAAAGATCTTGAAGATT 5533
Db 241 TGGGTGACAGTGGGTTTACATCGAACTGATCTCAACAGCGGTAAAGATCTTGAAGATT 300
Qy 5534 TTGCGCCCGGAAGAACGTTTTCCTAATGATGACACTTTTAAAGTTCTGCTATGTGCGCGG 5593
Db 301 TTGCGCCCGGAAGAACGTTTTCCTAATGATGACACTTTTAAAGTTCTGCTATGTGCGCGG 360
Qy 5594 TATTATCCGTTATGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGA 5653
Db 361 TATTATCCGTTATGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGA 420
Qy 5654 ATGACTTGGTTGAGTACTCACCAGTACAGAAAGATCTTACCGATGCGCATGACAGTAA 5713
Db 421 ATGACTTGGTTGAGTACTCACCAGTACAGAAAGATCTTACCGATGCGCATGACAGTAA 480
Qy 5714 GAGAAATATGCGTGCCTAATACCATGATTAACACTGCGGCCCAACTTACTTCTGA 5773
Db 481 GAGAAATATGCGTGCCTAATACCATGATTAACACTGCGGCCCAACTTACTTCTGA 540
Qy 5774 CAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCACAACAATGGGGGATCATGTA 5833
Db 541 CAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCACAACAATGGGGGATCATGTA 600
Qy 5834 CTCGCCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACA 5893
Db 601 CTCGCCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACA 660
Qy 5894 CCAGATGCGCTGTAGCAATGGCAACAAGTTGCGCAAACTATTAACTGCGCAACTACTTGA 5953
Db 661 CCAGATGCGCTGTAGCAATGGCAACAAGTTGCGCAAACTATTAACTGCGCAACTACTTGA 720
Qy 5954 CTCTAGCTTCCCGCAACAATTAATAGACTGAGTGGAGCGGATAAAGTTGAGGACCAAC 6013
Db 721 CTCTAGCTTCCCGCAACAATTAATAGACTGAGTGGAGCGGATAAAGTTGAGGACCAAC 780
Qy 6014 TTCTGCGCTCGGCCCTTTCGGCTGGCTGTTTATGCTGATAAATCTGGAGCCGCTGAGC 6073
Db 781 TTCTGCGCTCGGCCCTTTCGGCTGGCTGTTTATGCTGATAAATCTGGAGCCGCTGAGC 840

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QY 6074 GTGGGTCTCGCGGTATCAATTGACAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAG 6133
Db 841 GTGGGTCTCGCGGTATCAATTGACAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAG 900
QY 6134 TTATCTACACGCGGGAGTCAAGCACTACTGATGAAGCAATAGACAGATCGCTGAGA 6193
Db 901 TTATCTACACGCGGGAGTCAAGCACTACTGATGAAGCAATAGACAGATCGCTGAGA 960
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Search completed: May 16, 2004, 13:09:22
Job time : 377.412 secs

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11	3318.6	42.4	9210	15	US-10-228-785-9	Sequence 9, Appli
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QY 7801 AAAAGTCTTTTAAATTTTAAATCAAAAA 7828
Db 7801 AAAAGTCTTTTAAATTTTAAATCAAAAA 7828

RESULT 2

US-10-067-449-11
; Sequence 11, Application US/10067449
; Publication No. US20030166258A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wiczorko, Roman
; APPLICANT: Dlugai, Silke
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; TITLE OF INVENTION: GLUT Promoter
; FILE REFERENCE: DE4V2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: DE 101 06 718.6
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 7777
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-449-11

Query Match 89.1%; Score 6975.2; DB 15; Length 7777;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 7297; Conservative 0; Mismatches 478; Indels 15; Gaps 2;

QY 39 GGACCCCTCAGCAGCAGTGAAGTGGGACCTGGTCTTCTGCTGCTTCTCTGCGGTGCT 98
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QY 99 TGGCTCCCTGCAAGTTGGGTACAAATTTGGGTGCTCAATGCGCTCAGAAAGTGA 158
Db 63 TGGCTCCCTGCAAGTTGGGTACAACTGAGTCAATGCGCTCAGAAAGTGA 122
QY 159 ACAGAGCTACAATGAGACGTGGCTGGGAGGAGGCGCTGAGGAGCCAGCTTCAATCC 218
Db 123 GGAGTTCTACACAGACATGGTCCACCGCTATGGG-----GAGAGCATCT 170
QY 219 TCCAGGACCTTCAACACCTCTGGGCTCTGCGGCTCTGCGGCTCTTTCGTGGGCGCAT 278
Db 171 GCGCACCAGCTCACCACGCTCTGGTCTCTCATGTGGGCTCTTCTGTTGGGCGCAT 230
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Db 231 GATTTCTCTTCTCATTTGGGCTCTTCTGTTAAAGCTTTGGCGGCGGAAATCAATGCT 290
QY 339 GGTCAACAAATGCTCTGGGCTGCTGGGCGGAGCTCATGGGCTGGGCGGCAACGCTGCTG 398
Db 291 GATGATGAACCTGCTGGCTTCTGTCGCCGCTGCTCATGGGCTTCTCGAAATCGGCAA 350
QY 399 CTCCTATGAATGCTCATCTTGGAGGATTCCTCATTTGGGCTCTACTAGGCGCTGACATC 458
Db 351 GTCCTTTGAGATGCTGATCTGGGCGCTTCTCATCGGTGTGTACTGCGGCTGAGCCAC 410
QY 459 AGGGCTGGTGGCGCTGCTGGGAGATTTGCTCCACTCATCTCGGGGCGGCTTGGG 518
Db 411 AGGCTTGGTGGCGCTGCTGGGAGATTTGCTGGGCTTCTGTTGGGCGGCTTGGG 470
QY 519 GAGCTCAACCAAGTGGCAATTTGTTATCGGCAATTTGATCGGCTGCTGCGGCTTGA 578
Db 471 CACCTTGCACAGCTGGGCTGCTGCTGCGCATCTCTCATCGGCTGCTGCTGCGCTGGA 530
QY 579 GTCCCTCTCGGCACTGCCAGCTGTCCTGCGGCTCAGAGTGTACTCTGCT 638

Db	531	CTCCATCATGGGCAACAAGGACCTGTGGCCCTGCTGCTGAGCATCATCTTTCATCCCGC	590	Qy	1719	TTTTCTGTACAGCGCGTGTACGATGTAAACATTATATCTGAAAAACCTTGTCTTGAGAAGGT	1778
Qy	639	CTCTCTGACGTGGTCTCTGTGCGCTTCTGTCCGAGAGCCCCGCTACCTCTACATCAT	698	Db	1668	TTTTCTGTACAGAGCGGTGTACGATGTAAACATTATATCTGAAAAACCTTGTCTTGAGAAGGT	1727
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Qy	699	CCAGAAATCTGAGGGGCTGCGAGAAAGAGTCTGAAGCGCTGTGACAGCTGGGCGGATGT	758	Db	1728	TTTGGGACGTCTGAAGGCTTTAAATTTGGGCGGTGTACCCAAATTCGCCCTATAGTAGTGG	1787
Db	651	CCGCAACGAGGAGAACCGGCGCAAGAGTGTCTAAAGAAAGCTGCGCGGACAGCTGACGT	710	Qy	1839	TATTTACGCGCGCTACCTGCGCGTGTCTTAAACAGTGTGACTGGGAAAAACCTTGGCGGT	1898
Qy	759	TTCTGAGTGTCTGGCTGAGCTGAGGATGAGAGCGGAAGCTGAGCGTGTAGCGGCCACT	818	Db	1788	TATTTACGCGCGCTACCTGCGCGTGTCTTAAACAGTGTGACTGGGAAAAACCTTGGCGGT	1847
Db	711	GACCATGACCTGCGAGGAGTGAAGAAAGAGTGTGCGAGATGATGCGGGAGAAAGGT	770	Qy	1899	ACCCAACTTAATCGCCTTTCGAGCACATCCCTTTCGCCAGCTGGCGTAATAGCGAAGAG	1958
Qy	819	GTCCCTGTCTCAGCTCTCTGGGAGCGGTACACCGGAGCCCTGTATTTGCGGTGCT	878	Db	1848	ACCCAACTTAATCGCCTTTCGAGCACATCCCTTTCGCCAGCTGGCGTAATAGCGAAGAG	1907
Db	771	GACCATCTGAGAGCTTCTCCGCTCCCGCGCTACCGCGAGCCCATCTCATCGCTGTGGT	830	Qy	1959	GCCCGCACCGATCGCCTTCCCAAACAGTTGGCGAGCTGAAATGGCGAATGGCGGACGCG	2018
Qy	879	GCTGACGCTGAGCCAGCAGCTCTCTGGCATCAATGCTGTCTTTATTTATTCGACACGAT	938	Db	1908	GCCCGCACCGATCGCCTTCCCAAACAGTTGGCGAGCTGAAATGGCGAATGGCGGACGCG	1967
Db	831	GCTGACGCTGTCCAGCAGCTGTCTGGCATCAAGCTGTCTTCTATTACTCCACGAGCAT	890	Qy	2019	CCCTGTAGCGCGCATTAAGCGCGGCGGTGTGGTGTGTTACGCGCAGCTGTACCGCTACA	2078
Qy	939	CTTCGAGACAGAGGGGTAGGCGAGCTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT	998	Db	1968	CCCTGTAGCGCGCATTAAGCGCGGCGGTGTGGTGTGTTACGCGCAGCTGTACCGCTACA	2027
Db	891	CTTCGAGAGGGGGGTGACAGCAGCTGTGTATGCCACCAATTTGGCTCCGGTATCTGCAA	950	Qy	2079	CTTGCCAGCGCCTTAGCGCGCGCTCTTTCGCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC	2138
Qy	999	CACAGTCTTACCTTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT	1058	Db	2028	CTTGCCAGCGCCTTAGCGCGCGCTCTTTCGCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC	2087
Db	951	CACGGCTTTCATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT	1010	Qy	2139	GCGCGCTTTCCTCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGGAATTAAGTGT	2198
Qy	1059	TCTCTGGGCTTGGCGGGCATGTGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT	1118	Db	2088	GCGCGCTTTCCTCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGGAATTAAGTGT	2147
Db	1011	CTCATAGGCTCGCTGCGATGGCGGGTGTGGCATCTCATGACCATCGCGCTAGCAT	1070	Qy	2199	TTACGGCACCTCGACCCCAAAACCTTGAATTTAGGGTGTGCTTACAGTGTGGGCGCATCG	2258
Qy	1119	GCTGAGGAGGTTTCAGGCCATGAGCTAGCTGTCTCATTTGTGGCATCTTTTGGCTTCTGGC	1178	Db	2148	TTACGGCACCTCGACCCCAAAACCTTGAATTTAGGGTGTGCTTACAGTGTGGGCGCATCG	2207
Db	1071	GCTGAGGAGGTTTCAGGCCATGAGCTAGCTGTCTCATTTGTGGCATCTTTTGGCTTCTGGC	1130	Qy	2259	CCCTGTAGACGGTTCCTTTCGCGCTTTCGAGCTGTGAGTCCAGCTTCTTAAATAGTGGACTC	2318
Qy	1179	ATTTTTCGAGTGTGGCTGGCGCCATTTCTTGTGTTTCTTGTGTTTCTTGTGTTTCTTGTG	1238	Db	2208	CCCTGTAGACGGTTCCTTTCGCGCTTTCGAGCTGTGAGTCCAGCTTCTTAAATAGTGGACTC	2267
Db	1131	CTTCTTTGAGTGTGGCTGGCGCCATTTCTTGTGTTTCTTGTGTTTCTTGTGTTTCTTGTG	1190	Qy	2319	TTGTTTCAAACTGTGAAACAACTCAACCTTATCTCGGTCTATCTTTTGAATTAAGGG	2378
Qy	1239	GGGACCCCGCGGAGCCATGGCTGTGGCTGTGGCTTCTTCAACCTGGAGGACAACTTCAT	1298	Db	2268	TTGTTTCAAACTGTGAAACAACTCAACCTTATCTCGGTCTATCTTTTGAATTAAGGG	2327
Db	1191	GGTCCAGCTGAGCTGCGCTGCGCTTTCAGGCTTCTTCAACCTGGACCTCAAAATTCAT	1250	Qy	2379	ATTTTTCGCGATTCGCGCTTAAAGAAATGAGCTGATTTTAAACAAAAATTTTAAACGCG	2438
Qy	1299	CATTGGCATGGTTCAGATATGTTGGGAGGCTATGGGGGCTTACGCTTCTTCTTCTAT	1358	Db	2328	ATTTTTCGCGATTCGCGCTTAAAGAAATGAGCTGATTTTAAACAAAAATTTTAAACGCG	2387
Db	1251	TGTGGGCATGTCTTCCAGTATGTGGAGCAACTGTGTGGTTCCTTACGCTTTCATCATCT	1310	Qy	2439	AAATTTTAAACAAAAATTTTAAAGCTTTCCTGATGCGGTATTTTCTCTTACGCGATC	2498
Qy	1359	TGCGGTCTCTGCTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1418	Db	2388	AAATTTTAAACAAAAATTTTAAAGCTTTCCTGATGCGGTATTTTCTCTTACGCGATC	2447
Db	1311	CATGTGCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1370	Qy	2499	TGTGCGGTATTTTCAACCGCATAGGTAAATTAATTAATTAATTAATTAATTAATTAATTA	2558
Qy	1419	CCGACGTTTTCAGATCTCAGCTGCTTCCACCGGACACCTCTCTTCTTCTTCTTCTTCTT	1478	Db	2448	TGTGCGGTATTTTCAACCGCATAGGTAAATTAATTAATTAATTAATTAATTAATTAATTA	2507
Db	1371	CCGACCTTCGATGAGTCTTCCGCTTCCGCTTCCGCGAGGGGAGC---CAGCCAAAGTGA	1427	Qy	2559	TGTGAGTTTGTATATACATGATTTTACTTAAATTAATTAATTAATTAATTAATTAATTAAT	2618
Qy	1479	GGTGAACCCAGACAGAACTTGTAGTATTTAGGGCCAGATGAGAACGACTGATAGCTTA	1538	Db	2508	TGTGAGTTTGTATATACATGATTTTACTTAAATTAATTAATTAATTAATTAATTAATTAAT	2567
Db	1428	TAAGACCCCGAGGAGCTGTTCATCCCTCGGGGCTGTATTTCCCAAGTGTGATAAGCTTA	1487	Qy	2619	CTTCTCAAAATATGCTTCCAGCGCTTCTTCTGTAACCGTTCACCTCTACCTTAGCATCC	2678
Qy	1539	TGATACCGTCCAGCTCGAGTCAATGATTTAGTATGTCAGCTTACATTCACGCGCTCC	1598	Db	2568	CTTCTCAAAATATGCTTCCAGCGCTTCTTCTGTAACCGTTCACCTCTACCTTAGCATCC	2627
Db	1488	TGATACCGTCCAGCTCGAGTCAATGATTTAGTATGTCAGCTTACATTCACGCGCTCC	1547	Qy	2679	CTTCTCAAAATATGCTTCCAGCGCTTCTTCTGTAACCGTTCACCTCTACCTTAGCATCC	2738
Qy	1599	CCCCACATCCGCTCTAACCCGAAAGAGAGGTATAGACAACTGAAAGTCTAGGTCCTTAT	1658	Db	2628	CTTCTCAAAATATGCTTCCAGCGCTTCTTCTGTAACCGTTCACCTCTACCTTAGCATCC	2687
Db	1548	CCCCACATCCGCTCTAACCCGAAAGAGAGGTATAGACAACTGAAAGTCTAGGTCCTTAT	1607	Qy	2739	TCATCCAGGTTCTATATGTTGACCCAAATGCGCTTCTTCTGTAACCGTTCACCTCTACCT	2798
Qy	1659	TTATTTTTTATAGTTATGTTAGTATTAAGAACGTTATTTATTTTAAATTTTCTTTT	1718	Db	2688	TCATCCAGGTTCTATATGTTGACCCAAATGCGCTTCTTCTGTAACCGTTCACCTCTACCT	2747
Db	1608	TTATTTTTTATAGTTATGTTAGTATTAAGAACGTTATTTATTTTAAATTTTCTTTT	1667				

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QY 2859 AAGCCGATACAAATCTTTGTCGCTCTTCGCAATGTCAACAGTACCCCTTAGTATATCT 2918
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QY 3759 GTGACCGTCTCCGGAGCTGCATGTGTGACAGGTTTTTCAACGTCATCACCGAACCGCG 3818
DB 3708 GTGACCGTCTCCGGAGCTGCATGTGTGACAGGTTTTTCAACGTCATCACCGAACCGCG 3767
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DB 3768 AGACGAAAGGCCCTCGTGATACGCTATTTTATAGGTTAATGTCTATGATAAATAGGTT 3827
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DB 3828 TCTTAGTATGATCCAAATATCAAGGAAATGATAGCAATTTGAAGATGAGACTAATCCAATT 3887
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DB 3948 GCATGGAATGGGATAATATCACAGGAGGTACTAGACTACCTTTTCATCATATAAATAGA 4007
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DB 4008 CGCATATAAGTAGCGATTTAAGCATATAACACGCACTATGCGGTTCTTCTCATGTATATAT 4067
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DB 4068 ATATACAGCAACACGCGAGATATAGGTGCGAGCTGAACTGAGTGAAGTGTATGTCGCGAGCT 4127
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DB 4128 CGCGTTGCAATTTTCGGAAGCGCTCGTTTTCGGAACGCTTTTGAAGTTCCTTATTCGGAAGT 4187
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Db 335 CTTCCCGCTCTATGTTGTGTGAATTTGAGCGGATTAACAATTTTACACAGGAAACAGC 276
QY 7378 TATGACCATGATTACGCCAGCGCGCA 7404
Db 275 TATGACCATGATTACGCCAGCTTGCA 249

RESULT 5
US-09-945-917-28/c
; Sequence 28, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945, 917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10288
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8456)
; OTHER INFORMATION: "N is A, C, G, or T"
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-945-917-28

Query Match 57.4%; Score 4492.6; DB 10; Length 10288;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

QY 1559 TCATGTAATTAATGATGTCACGCTACATTCACGCGCTCCGCCACATCGGCTCTAACCG 1618
Db 7878 TCATGTAATTAATGATGTCACGCTACATTCACGCGCTCCGCCACATCGGCTCTAACCG 7819
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Db 7818 AAAAGGAAGGAGTTAGACAACTGAAGTCTAGGTCCTATTTATTTTATATGTTATGT 7759
QY 1679 TAGTATTAGAACGTTATTATATTTTCAATTTTCTTTTCTTTCTGTACAGACGGGTGT 1738
Db 7758 TAGTATTAGAACGTTATTATATTTTCAATTTTCTTTTCTTTTCTGTACAGACGGGTGT 7699
QY 1739 ACCGATGTAACATTATATCTGAAACCTTGCTTGAGAAAGGTTTGGGACGCTCGAAGGCTT 1798
Db 7698 ACCGATGTAACATTATATCTGAAACCTTGCTTGAGAAAGGTTTGGGACGCTCGAAGGCTT 7639
QY 1799 TAATTTGCGCGGTATACCAATTCGCCCTATATAGTGAGTCGTATTAACGCGGCTCACTGCG 1858

Db 7638 TAAATTTG-----CAAAGCTCGGATCTCGAGCTCGCGAAAGCTTGGACGACTGCG 7589
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Db 7588 CGTCTGTTTACAAAGCTGCTGACCTGGGAAACCTCTGCGTTTACCAACTTAATCGCTTGC 7529
QY 1919 AGCACATCCCCCTTTTCGCGAGCTGGCGTAAATAGCGAAGAGGCCCGCACCGATCGCCCTTC 1978
Db 7528 AGCACATCCCCCTTTTCGCGAGCTGGCGTAAATAGCGAAGAGGCCCGCACCGATCGCCCTTC 7469
QY 1979 CCNACAGTTGCGGAGCTGAAATGGCGGAGCGCGCTCTAGCGGCGCATTAAG 2038
Db 7468 CCNACAGTTGCGGAGCTGAAATGGCGGAGCGCGCTCTAGCGGCGCATTAAG 7409
QY 2039 CGCGGCGGCTGCTGCTTACCGCGAGCTGACCGCTACACTTGGCAGCGCCCTAGCGCC 2098
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Db 7348 CGCTCCCTTTTCGCTTTCTCCCTTTCTCGCACGTTTCGCGGCTTTCCCGCTCAAGC 7289
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Db 7288 TCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTAGTGTCTTACGGGACCTCGACCCCAA 7229
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Db 7228 AAAACTTGAATAGGGTGATGTTTACGTAAGTGGCCCATCGCTGATAGCGGTTTTTCG 7169
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Db 7108 ACTCAACCTATCTCGTCTATTTCTTTGATTTAAGGGAATTTTCGCGGCTTACCGCTA 7049
QY 2399 TTGGTTAAAAAATGAGCTGATTTTAAACAAATTTTAAACGGAATTTTAAACAAATTTAAC 2458
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QY 2579 ATTTACTTATAATACAGTTTATTTTGTGCGCGCATCTTCTCAATATGCTTTCCCA 2638
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QY 2639 GCGTCTTTCTGTAACTGTTTACCTCTTACCTTACCTTACCTTCCCTTTCGCAATAGTCC 2698
Db 6808 CTTCCGCTTACATCAAC-----ACCAATTAACGC 6781
QY 2699 TCTTCCAAACAATAATGTCAGATCTCTGAGACCAATCATCATCGGTTCTATATG 2758
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QY 2819 GTAACTTTCATCTCTTCCACCCATGCTCTTTTGTAGCAATAAAGCCGATTAACAAATCTTT 2878
Db 6665 CAAAAGTTTCACTGTCCAC-----CTGCTTCTGAATCAACAAGGGAATAAAGCAATG 6612
QY 2879 GTGCTCTTTGCGAATGTCACAGTACCTTATATTTCTTCCAGTAGATAGGAGGCCCTT 2938

Db 6611 AGTTTCTGTGAAGCTGCACTGAGTAGTATGTTGCACTCTTTTGGAAATACGAGTCTTTT 6552
Qy 2939 GCATGACAAATCTGCTACATCAAAAGCCCTAGGTTCCCTTTGTACTTCTTCTGCGC 2998
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Qy 2999 CTGCTTTCAAACCGCTAAACAATACCTTGGGCCCAACACACACCGTGTGCATTCGTAAATGTCG 3058
Db 6499 TGCAGT-----TGGACGATCAATGATCGCTATCATTTGACGAGACCAACATCCTC 6447
Qy 3059 CCAATCTGCTATTCGTATATACACCGGAGAGTACTGCAATTTGACTGTATTAACCAATGTC 3118
Db 6446 CTTAGGTTGATTAAGAAACACGCAACCAAGTATTTGGAGTGCTGAACTATTTTATA 6387
Qy 3119 AGCAATTTTCTGCTTCGAAGAGTAAATAATGCTTGTGGCGATTAATGCCTTTAGCGG 3178
Db 6386 TG-----CTTTTCAAGACTTGAATAATTTCTTGCAATACCGGGTCAATGTT 6339
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Qy 3298 ATGAAGCACACAAAGTTTGTCTTTTGTGTCATGATATTAATAGCTTGGCAGCAACAG 3357
Db 6220 GTGAATTAATAACAGACATACTCAAGCTGCCCTTGTGCTTAAATCAAGTATACTCAC 6161
Qy 3358 GACTAGGATGAGTAGCAGCAGTTCCTTATATGATGCTTTTCGACATGATTTATCTCGTT 3417
Db 6160 GTGCTCAATAGTCAACCAATGCCCTCCCTCTTGGCCCTCTCC-----TTTTCTTT 6112
Qy 3418 TCCCTCAGGTTTTGTTCTGTGCAATTTGAAAGTGTGTTAAGATPACTGGGCAATTCATGTTTCTT 3477
Db 6111 TTTGACCGAATTAATTTCTTAATCGGCAAAAAAGAAAGCTCCGGA-----T 6064
Qy 3478 GAACACTACATATGCTATATATACCAATCTAAGTCTGTGCTCTTCTTCTGTTCTTCTT 3537
Db 6063 CAAGATTGACGTAAGGTGACAAGCTATTTTCAATAAAGAAATATCTTCCACTACTGCCA 6004
Qy 3538 TCTGTTTCGGAGATTACCGAATCAAAAAATTTCAAAGAAACCGAAATCAAAAAAAGAAT 3597
Db 6003 TCTGGCGTCATRACTGCAAGTACACATATATTA-----CGATGCTGTCTATTAAAT 5952
Qy 3598 AAAAAAAATGATGAATTTGAATTTGAAGTGTGTTAGTGTCACCTCTCAGTACAATCT 3657
Db 5951 GCTTCTATATATATATATATATGTTGATGTTGATCTATGTTGCACTCTCAGTACAATCT 5892
Qy 3658 GCTCTGATGCCGATAGTTAAGCCAGCCCGACACACCCGCAACACCCGCTGACGCGCCT 3717
Db 5891 GCTCTGATGCCGATAGTTAAGCCAGCCCGACACACCCGCAACACCCGCTGACGCGCCT 5832
Qy 3718 GACGGGCTTGTCTGCTCCGGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 3777
Db 5831 GACGGGCTTGTCTGCTCCGGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 5772
Qy 3778 GCATGTGCAGAGGTTTTCCGCTCATCACCGAAACCGCGAGACGAAAGGGCTCTGTGA 3837
Db 5771 GCATGTGCAGAGGTTTTCCGCTCATCACCGAAACCGCGAGACGAAAGGGCTCTGTGA 5712
Qy 3838 TACGCTATTTTATAGTTAATGTCATGATTAATGTTTCTTCTAGTATGATCCAATAT 3897
Db 5711 TACGCTATTTTATAGTTAATGTCATGATTAATGTTTCTTCTAGTATGATCCAATAT 5652
Qy 3898 CAAAGGAATGATAGCATTTGAAGGATGAGATTAATCCAAATTTGAGGAGTGGCAGCATATAG 3957
Db 5651 CAAAGGAATGATAGCATTTGAAGGATGAGATTAATCCAAATTTGAGGAGTGGCAGCATATAG 5592
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Db 5591 AACAGCTAAGGGTAGTGTGAAGGAAGCATACGATACCCCGCATGGAAATGGGATATAT 5532

Qy 4018 CACAGGAGTACTAGACTACCTTTTCATCTACATAAATAGACGCATATAAGTACGCAATTT 4077
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Qy 4078 AAGCATAAACACGCACTATGCGCTTCTTCTCATGTATATATATATACAGGCAACACGAG 4137
Db 5471 AAGCATAAACACGCACTATGCGCTTCTTCTCATGTATATATATATACAGGCAACACGAG 5412
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Qy 4198 CGCTCGTTTTTCGGAACCGCTTTGAAAGTCTTATTTCCGAAGTTCCTATTTCTAGAAAATG 4257
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Qy 4258 TAGGAATCTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAAGACGCACTTTTCAAAAAC 4317
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Qy 4498 TCTAGTATTTACTCTTTTACAAAATAATTTCTAGTAAGAACTATTTTCATAGAGTGAATCGAA 4557
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Qy 4558 AACAACTACGAAATTTGTAACATTTCTTATACGTAGTATATAGAGACAAAATAGAGAANAAC 4617
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Qy 4738 CCGCGAGCTTCGCTAGTAAATCAGTAAACCGGGAGTGGAGTCAAGCTTTTATATGGA 4797
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QY 5638 ATACACTATTCTCAGAAATGATGTTGGTTGATCTACACAGTACAGAAAGATCTTACG 5697
DB 3911 ATACACTATTCTCAGAAATGATGTTGGTTGATCTACACAGTACAGAAAGATCTTACG 3852
QY 5698 GATGGATGACAGTAAGAGAAATATGACGCTGCTGCAATACCATGATGATGATACCTGCG 5757
DB 3851 GATGGATGACAGTAAGAGAAATATGACGCTGCTGCAATACCATGATGATGATACCTGCG 3792
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QY 5818 ATGGGGATCATGTAATCTGCTGCTGATCGTTGGGAAACCGGAGCTGAATGAGCCATACCA 5877
DB 3731 ATGGGGATCATGTAATCTGCTGCTGATCGTTGGGAAACCGGAGCTGAATGAGCCATACCA 3672
QY 5878 AACGACGAGCTGACACGATGCTGTAGCAATGCAACACGTTGCGCAAACTATTTA 5937
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QY 6298 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAACGTGAGTTTTCGTTCCACTGA 6357
DB 3251 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAACGTGAGTTTTCGTTCCACTGA 3192
QY 6358 GGTGACAGCCCGTAGAAGATCAAGGATCTTCTGTGAGATCTTTTCTGCGCGTA 6417
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QY 6418 ATCTGCTGCTTGCACAAACCAAAATCCACCGCTACACGCGGTGTTTGTGCGGATCA 6477
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QY 6478 GAGTACCAACTCTTTTTCGAAAGTAACTGGCTTACAGAGCGGAGATACCAATACT 6537
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QY 6598 TACTCGCTCTGCTAATCTGTTTACAGTGGCTGCTGCCAGTGGCGATAGTGTGCTT 6657
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DB 2891 ACCGGTGTGACTCAAGACGATAGTTTACCGGATTAAGCGCGAGCGGTGCGGCTGAACGGGG 2832
QY 6718 GGTTCGTGACACAGCCGAGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAG 6777
DB 2831 GGTTCGTGACACAGCCGAGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAG 2772
QY 6778 CGTGACTATGAGAAACCGCAGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTA 6837
DB 2771 CGTGACTATGAGAAACCGCAGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTA 2712
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DB 2351 TGGCGGATTCATTAATGACGAGCTGGCACAGAGGTTTCCGACCTGGAAAGCGGAGTGAG 2292
QY 7258 CGCAACGCAATTAATGAGGATTAACCTCACTATTAGGACCCCGAGGCTTTACATTTATG 7317

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Db 6386 TG-----CITTTACAAGACTTGAAATTTTCTTGCAATAAACCGGGTCAATTGT 6339
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Qy 3239 AATTTTGGGACCTTAATGCTTCAACTAACTCCAGTAATTTCTTGCTGTAC-GAACAATCCA 3297
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Qy 3538 TCTGTTGGGAGATTACCGAATCAAAAATTTCAAGAAACCGAATCAAAAAGAAAT 3597
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Qy 3598 AAAAAAATGATGAATTAATTTGAAAGCTGTGTTAGTGTGCACTCTCAGTACAACTCT 3657
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Db 5651 CAAAGAAATGATAGCATTTGAGGATGAGACTAATCCAATGAGGAGTGGCAGCATATAG 5592
Qy 3958 AACAGCTAAGGGTAGTGTGAGGAGCATACGATACCCCGCATCGAATGGATATAT 4017
Db 5591 AACAGCTAAGGGTAGTGTGAGGAGCATACGATACCCCGCATCGAATGGATATAT 5532
Qy 4018 CACAGAGGTACTAGACTACCTTTTCACTTACATAAATAGACATATATATATATATATAT 4077
Db 5531 CACAGAGGTACTAGACTACCTTTTCACTTACATAAATAGACATATATATATATATATAT 5472
Qy 4078 AAGCATAAACAGCATATGCGGCTTCTCTCATGATATATATATATATATATATATATAT 4137
Db 5471 AAGCATAAACAGCATATGCGGCTTCTCTCATGATATATATATATATATATATATATAT 5412
Qy 4138 ATATAGGTCGAGCTGAAACAGTGTGATGTGCGCAGCTCGGTTGATTTTCGGAG 4197
Db 5411 ATATAGGTCGAGCTGAAACAGTGTGATGTGCGCAGCTCGGTTGATTTTCGGAG 5352

Qy 4198 CGCTCGTTTTCGGAACCGCTTTGAAAGTCTCTATTTCCGAAAGTCTCTATTTCTTAGAAAGTA 4257
Db 5351 CGCTCGTTTTCGGAACCGCTTTGAAAGTCTCTATTTCCGAAAGTCTCTATTTCTTAGAAAGTA 5292
Qy 4258 TAGGAACCTTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAGACGCACTTTCAAAAAC 4317
Db 5291 TAGGAACCTTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAGACGCACTTTCAAAAAC 5232
Qy 4318 CAAAAACGACCGGACTGTAAACGAGCTACTAAATATTCGAAATTCGAAATTCGAAATTC 4377
Db 5231 CAAAAACGACCGGACTGTAAACGAGCTACTAAATATTCGAAATTCGAAATTCGAAATTC 5172
Qy 4378 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTATATATCCCTATATATACTACCCA 4437
Db 5171 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTATATATCCCTATATATACTACCCA 5112
Qy 4438 TCCACCTTTGCTCTTGAACCTTGCATCTAATCTGAACTCGACCTCTACATTTTATGTTTATC 4497
Db 5111 TCCACCTTTGCTCTTGAACCTTGCATCTAATCTGAACTCGACCTCTACATTTTATGTTTATC 5052
Qy 4498 TCTAGTATTACTCTTTTGAACCAAAAATTTGTAGTAAAGACTATTCATAGAGTCAATCGAA 4557
Db 5051 TCTAGTATTACTCTTTTGAACCAAAAATTTGTAGTAAAGACTATTCATAGAGTCAATCGAA 4992
Qy 4558 AACAAATACAAAATGTAAACATTTCTTATACGTPAGTATATAGAGACAAAATAGAGAAAC 4617
Db 4991 AACAAATACAAAATGTAAACATTTCTTATACGTPAGTATATAGAGACAAAATAGAGAAAC 4932
Qy 4618 CGTTCATATTTTCTGACCAATGAAGATCATCAACGCTATCACTTTCTGTTTCAAAAGT 4677
Db 4931 CGTTCATATTTTCTGACCAATGAAGATCATCAACGCTATCACTTTCTGTTTCAAAAGT 4872
Qy 4678 ATGCGCAATCCACATCGGTATAGATATATATCGGGATGCTTTATCTTGAATAATGCA 4737
Db 4871 ATGCGCAATCCACATCGGTATAGATATATATCGGGATGCTTTATCTTGAATAATGCA 4812
Qy 4738 CCGCAGCTTCTGCTAGTAAATCAGTAAACCGGGAAGTGGAGTCAGCTTTTTTATGGAA 4797
Db 4811 CCGCAGCTTCTGCTAGTAAATCAGTAAACCGGGAAGTGGAGTCAGCTTTTTTATGGAA 4752
Qy 4798 GAGAAATAGACACCAAGTAGCTTCTTCTAACCCTTAACGACCTACAGTGCAGAAAGT 4857
Db 4751 GAGAAATAGACACCAAGTAGCTTCTTCTAACCCTTAACGACCTACAGTGCAGAAAGT 4692
Qy 4858 TATCAAGACATGCTATTATAGAGCGCACAAAGAGAGAAAAGTAACTAATCTAAGATGCTTG 4917
Db 4691 TATCAAGACATGCTATTATAGAGCGCACAAAGAGAGAAAAGTAACTAATCTAAGATGCTTG 4832
Qy 4918 TTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCTT 4977
Db 4631 TTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGTATAGATTCTT 4572
Qy 4978 TGTGTTAAAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAATAATGAGCTCAGATTC 5037
Db 4571 TGTGTTAAAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAATAATGAGCTCAGATTC 4512
Qy 5038 TTTGTTTGAATAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAGAGCAG 5097
Db 4511 TTTGTTTGAATAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAAATGAGAGCAG 4452
Qy 5098 TTTCTGTTTGTGTAATAATAGCGCTTTTCGCTGCTGCAATTTCTGTTCTGTAATAATGAGCTCA 5157
Db 4451 TTTCTGTTTGTGTAATAATAGCGCTTTTCGCTGCTGCAATTTCTGTTCTGTAATAATGAGCTCA 4392
Qy 5158 GATTTCTGTTTGAATAATAGCGCTCTCGGTTGCAATTTTGTGTTCTGTAATAATGAGAG 5217
Db 4391 GATTTCTGTTTGAATAATAGCGCTCTCGGTTGCAATTTTGTGTTCTGTAATAATGAGAG 4332
Qy 5218 CAGATGCTTCTGAGTGGCACTTTTTCGGGGAATGTCGGGGAACCCCTATTTCTGTTA 5277
Db 4331 CAGATGCTTCTGAGTGGCACTTTTTCGGGGAATGTCGGGGAACCCCTATTTCTGTTA 4272

QY 5278 TTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCTGATAATGCTT 5337
DB 4271 TTTTCTAAATACATTCBAATATGTATCCGCTCATGAGACAATAACCTGATAATGCTT 4212
QY 5338 CAATAATATGAAAGAGAGATGAGATATCAACATTTCCGTGTCGCCCTTATPCCC 5397
DB 4211 CAATAATATGAAAGAGAGATGAGATATCAACATTTCCGTGTCGCCCTTATPCCC 4152
QY 5398 TTTTGTGGGCAATTTGCGCTTCTGTTTGTCTCACCAGAAAGCTGGTGAAGTAAA 5457
DB 4151 TTTTGTGGGCAATTTGCGCTTCTGTTTGTCTCACCAGAAAGCTGGTGAAGTAAA 4092
QY 5458 GATGCTGAAGATCAGTTGGGTGACGAGTGGTTACATCCAACTGGATCTCAACAGCGGT 5517
DB 4091 GATGCTGAAGATCAGTTGGGTGACGAGTGGTTACATCGNACTGGATCTCAACAGCGGT 4032
QY 5518 AAGATCCTTGAGAGTTTTCGCCCGAAGAACGTTTTCATATGATGAGCACTTTTAAAGTT 5577
DB 4031 AAGATCCTTGAGAGTTTTCGCCCGAAGAACGTTTTCATATGATGAGCACTTTTAAAGTT 3972
QY 5578 CTGCTATGTGGCGGTATTTATCCGTTATTTGACCGCGGCAAGAGCAACTCGGTCCGCC 5637
DB 3971 CTGCTATGTGGCGGTATTTATCCGTTATTTGACCGCGGCAAGAGCAACTCGGTCCGCC 3912
QY 5638 ATACACTATTCTCAGAAATGACTTGGTTGAGTACTCAGCAGTCAAGAAAAGCATCTTACG 5697
DB 3911 ATACACTATTCTCAGAAATGACTTGGTTGAGTACTCAGCAGTCAAGAAAAGCATCTTACG 3852
QY 5698 GATGCTATGACAGTAAGAGAAATATGCAATGCTGCCATAACCAATGATGATAACACTGG 5757
DB 3851 GATGCTATGACAGTAAGAGAAATATGCAATGCTGCCATAACCAATGATGATAACACTGG 3792
QY 5758 GCCAACTTACTTCTGACAAACATCGGAGGACCGAGGAGCTTACCGCTTTTTCACAAAC 5817
DB 3791 GCCAACTTACTTCTGACAAACATCGGAGGACCGAGGAGCTTACCGCTTTTTCACAAAC 3732
QY 5818 ATGGGGATCATGTAACTCGCTTGTATGCTGGGAAACCGAGCTGAATGAAGCCATACCA 5877
DB 3731 ATGGGGATCATGTAACTCGCTTGTATGCTGGGAAACCGAGCTGAATGAAGCCATACCA 3672
QY 5878 AACGACGAGCTGACACACGATGCTGTAGCAATGCGCAACAGCTTGCAGCAACTATTA 5937
DB 3671 AACGACGAGCTGACACACGATGCTGTAGCAATGCGCAACAGCTTGCAGCAACTATTA 3612
QY 5938 ACTGGCGAATCTACTTCTAGCTTCCGCGCAACAAATTAAGTACGATGGAGGCGGAT 5997
DB 3611 ACTGGCGAATCTACTTCTAGCTTCCGCGCAACAAATTAAGTACGATGGAGGCGGAT 3552
QY 5998 AAAGTTGACGACCACTTCTCGCTCGGCCCTTCCGCTGGCTGGTTTATGCTGATAAA 6057
DB 3551 AAAGTTGACGACCACTTCTCGCTCGGCCCTTCCGCTGGCTGGTTTATGCTGATAAA 3492
QY 6058 TCTGAGCCGCTGAGCGTGGGTCTCGCGGTATCATTTGAGCACTTGGGGCCAGATGGTAAG 6117
DB 3491 TCTGAGCCGCTGAGCGTGGGTCTCGCGGTATCATTTGAGCACTTGGGGCCAGATGGTAAG 3432
QY 6118 CCCTCCCTGATCGTAGTTATCTACGACGGGAGTCAAGCAACTATGAGTGAACGAAT 6177
DB 3431 CCCTCCCTGATCGTAGTTATCTACGACGGGAGTCAAGCAACTATGAGTGAACGAAT 3372
QY 6178 AGACAGATCGCTGAGATAGTGGCTCACTGATTAAGCATTTGGTAACTGTGAGACCAAGTT 6237
DB 3371 AGACAGATCGCTGAGATAGTGGCTCACTGATTAAGCATTTGGTAACTGTGAGACCAAGTT 3312
QY 6238 TACTCATATATATTTAGATTTTAAATCACTTCAATTTTAAATTTAAAGATCTAGGTG 6297
DB 3311 TACTCATATATATTTAGATTTTAAATCACTTCAATTTTAAATTTAAAGATCTAGGTG 3252
QY 6298 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAAGTGAATTTTCTGTTCCACTGA 6357
DB 3251 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAAGTGAATTTTCTGTTCCACTGA 3192
QY 6358 GCGTCAGACCCCGTAGAAAAAGATCAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTA 6417

DB 3191 GCGTCAGACCCCGTAGAAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTA 3132
QY 6418 ATCTGCTGCTTGCACAAACAAACAAACCAACCTACCAGCGGTGGTTGTTGCGCGGATCAA 6477
DB 3131 ATCTGCTGCTTGCACAAACAAACAAACCAACCTACCAGCGGTGGTTGTTGCGCGGATCAA 3072
QY 6478 GAGCTACCAACTCTTTTTCCGAAGTAACTGGCTTTCAGCAGAGCGCAGATACCAAAATACT 6537
DB 3071 GAGCTACCAACTCTTTTTCCGAAGTAACTGGCTTTCAGCAGAGCGCAGATACCAAAATACT 3012
QY 6538 GTCTCTTCTAGTGTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCAGCTTACA 6597
DB 3011 GTCTCTTCTAGTGTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCAGCTTACA 2952
QY 6598 TACTCGCTCTGCTTAATCTGTTTACCAGTGGCTGCTGCCAGTGGCGGATAGCTCGTGTCTT 6657
DB 2951 TACTCGCTCTGCTTAATCTGTTTACCAGTGGCTGCTGCCAGTGGCGGATAGCTCGTGTCTT 2892
QY 6658 ACCGGGTTGAGCTCAAGACGATAGTTTACCGGATAAAGCGCAGCGGTCCGGCTGAACGCGG 6717
DB 2891 ACCGGGTTGAGCTCAAGACGATAGTTTACCGGATAAAGCGCAGCGGTCCGGCTGAACGCGG 2832
QY 6718 GGTTCGTGACACAGCCAGCTTGGAGCGAAACGACCTTACACCGAACTGAGATACTACAG 6777
DB 2831 GGTTCGTGACACAGCCAGCTTGGAGCGAAACGACCTTACACCGAACTGAGATACTACAG 2772
QY 6778 CGTGAGCTATGAGAAAGCGCACGCTTCCCGAAGGAGAAAGCGGACAGCTATCCGGTA 6837
DB 2771 CGTGAGCTATGAGAAAGCGCACGCTTCCCGAAGGAGAAAGCGGACAGCTATCCGGTA 2712
QY 6838 AGCGGAGGCTCGGAAACAGGAGAGCGCACGAGGAGCTTCCAGGGGGGAAACCGCTGGTAT 6897
DB 2711 AGCGGAGGCTCGGAAACAGGAGAGCGCACGAGGAGCTTCCAGGGGGGAAACCGCTGGTAT 2652
QY 6898 CTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCAATTTTGTGATGCTCG 6957
DB 2651 CTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCAATTTTGTGATGCTCG 2592
QY 6958 TCAGGGGGGGGAGCCTATGAGAAACCGCAGCAACCGGGGCTTTTACGGTTCCTGGCC 7017
DB 2591 TCAGGGGGGGGAGCCTATGAGAAACCGCAGCAACCGGGGCTTTTACGGTTCCTGGCC 2532
QY 7018 TTTTGTGCGCTTTTGTCTCATGTTCTTCTCTGCTGTTATCCCTGATTTCTGTGATTAAC 7077
DB 2531 TTTTGTGCGCTTTTGTCTCATGTTCTTCTCTGCTGTTATCCCTGATTTCTGTGATTAAC 2472
QY 7078 CGTATTAACCGCTTTTGTGATGAGTGTATACCGCTCGCGCAGCCGAAACGACCGAGCGCAGC 7137
DB 2471 CGTATTAACCGCTTTTGTGATGAGTGTATACCGCTCGCGCAGCCGAAACGACCGAGCGCAGC 2412
QY 7138 GAGTCACTGAGCGAGGAGGAGCGGCGCCCAATACGAAACCGCTCTCCCGCGGT 7197
DB 2411 GAGTCACTGAGCGAGGAGGAGCGGCGCCCAATACGAAACCGCTCTCCCGCGGT 2352
QY 7198 TGCGCGATTCATTAATGACGCTGCGCAGCAGAGTTTCCCGACTGGAAAGCGGCGAGTGAG 7257
DB 2351 TGCGCGATTCATTAATGACGCTGCGCAGCAGAGTTTCCCGACTGGAAAGCGGCGAGTGAG 2292
QY 7258 CGCAACGCAATTAATGAGTGTACTCTCACTATTAGGCAACCGGCTTTACCTTTATG 7317
DB 2291 CGCAACGCAATTAATGAGTGTACTCTCACTATTAGGCAACCGGCTTTACCTTTATG 2232
QY 7318 CTTCCGCTCCTATGTTGTGGAATTTGTGAGCGGATAACAAATTTTACACAGGAACAGC 7377
DB 2231 CTTCCGCTCCTATGTTGTGGAATTTGTGAGCGGATAACAAATTTTACACAGGAACAGC 2172
QY 7378 TATGACCATGATTACGCAAGCGCGCA 7404
DB 2171 TATGACCATGATTACGCAAGCTTGCA 2145

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; Sequence 27, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13414
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11582)
; OTHER INFORMATION: "N is A, G, C or T"
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: Plasmid
; US-09-945-917-27

Query Match 57.4%; Score 4492.6; DB 10; Length 13414;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

QY	1559	TCATGTAATTAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCGCTCTAAACCG	1618
DB	11004	TCATGTAATTAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCGCTCTAAACCG	10945
QY	1619	AAAAGGAAGAGTATGACAACTGAAGCTAGTGTCCCTATTTATTTTATTTATTTATGTTATGT	1678
DB	10944	AAAAGGAAGAGTATGACAACTGAAGCTAGTGTCCCTATTTATTTTATTTATTTATTTATGTTATGT	10885
QY	1679	TAGTATTAAGAACGTTATTTATTTATTTTCAAAATTTTCTTTTCTTTTCTGTCAGACGGCTGT	1738
DB	10884	TAGTATTAAGAACGTTATTTATTTATTTTCAAAATTTTCTTTTCTTTTCTGTCAGACGGCTGT	10825
QY	1739	ACGCATGTAACATTTACTGAAACCTTGTGAGAGGTTTTGGGACGCTCGAAGGCTT	1798
DB	10824	ACGCATGTAACATTTACTGAAACCTTGTGAGAGGTTTTGGGACGCTCGAAGGCTT	10765
QY	1799	TAATTTGGCGCGGTACCCAAATTCGCCCTTATAGTGTGATGATTAACGGCGCTCACTGCG	1858
DB	10764	TAATTTG-----CAAAGCTCGGGATCTCGAGCTCGCGAAAGCTTGGACGACTGCG	10715
QY	1859	CGTGTGTTTACACGTCGTGACTGGGAAACCTTGGCGTTTACCACTTTAATCGCCTTGC	1918
DB	10714	CGTGTGTTTACACGTCGTGACTGGGAAACCTTGGCGTTTACCACTTTAATCGCCTTGC	10655
QY	1919	AGCACATCCCTTCCGACGCTGGCGTAAATAGCGAAGGCGCGCACCGATCGCCCTTC	1978
DB	10654	AGCACATCCCTTCCGACGCTGGCGTAAATAGCGAAGGCGCGCACCGATCGCCCTTC	10595
QY	1979	CCAAAGTTGCGCAGCTGAAATGGCGGAAATGGCGGACCGCGCTGTAGCGGCGCATTAAG	2038
DB	10594	CCAAAGTTGCGCAGCTGAAATGGCGGAAATGGCGGACCGCGCTGTAGCGGCGCATTAAG	10535
QY	2039	CGCGCGGGGTGTTGTTACGCGCAGCTGACCGCTACACTTGCAGCGCCTAGCGCC	2098
DB	10534	CGCGCGGGGTGTTGTTACGCGCAGCTGACCGCTACACTTGCAGCGCCTAGCGCC	10475
QY	2099	CGCTCCTTTCGCTTCTTCCCTTCTTCTCGCACGTTTCCCGGCTTCCCGCTCAAGC	2158
DB	10474	CGCTCCTTTCGCTTCTTCCCTTCTTCTCGCACGTTTCCCGGCTTCCCGCTCAAGC	10415
QY	2159	TCTAAATCGGGGCTCCCTTTTAGGTTCCGATTTAGTGTCTTTACGCGACCTCGACCCCAA	2218

DB	10414	TCTAAATCGGGGCTCCCTTTTAGGTTCCGATTTAGTGTCTTTACGCGACCTCGACCCCAA	10355
QY	2219	AAAACCTTATAGGTTAGGTTACGTTACGTTAGTGGCCATCGCCTGATAGACGGTTTTTCG	2278
DB	10354	AAAACCTTATAGGTTAGGTTACGTTAGTGGCCATCGCCTGATAGACGGTTTTTCG	10295
QY	2279	CCCTTTGAGCTTGGAGTCCACGTTCTTTTAAATAGTGGACTCTTGTTCCAAATGGAAAC	2338
DB	10294	CCCTTTGAGCTTGGAGTCCACGTTCTTTTAAATAGTGGACTCTTGTTCCAAATGGAAAC	10235
QY	2339	ACTCAACCTATCTCGGCTATTTCTTTGATTTATAAGGATTTTGGCCATTTCCGCTTA	2398
DB	10234	ACTCAACCTATCTCGGCTATTTCTTTGATTTATAAGGATTTTGGCCATTTCCGCTTA	10175
QY	2399	TTGGTTAAAAAATGAGCTGATTTAAACAAATAATTTAAACGGAATTTTAAACAAATAATAAC	2458
DB	10174	TTGGTTAAAAAATGAGCTGATTTAAACAAATAATTTAAACGGAATTTTAAACAAATAATAAC	10115
QY	2459	GTTTACAAATTTCTGATGCGGTATTTCTCTCTTACGCACTGTGCGGTATTTTACACCGC	2518
DB	10114	GTTTACAAATTTCTGATGCGGTATTTCTCTCTTACGCACTGTGCGGTATTTTACACCGC	10055
QY	2519	ATAGGTAATAACTGATATAATAATTAAGAGCTCTAATTTGTGAGTTAGTATATATGC	2578
DB	10054	ATAGATCGCAAGTGCACAAACAATCTTAAATAAATACTACTCAGTAATAACCTATTTTC	9995
QY	2579	ATTACTTATAATAACAGTTTATTTTATTTTGTGCGCGCATCTTCTCAATAATAGTTCCTCA	2638
DB	9994	TTAGCAATTTTTCAGCAATTTGCTATTTTGTAGAGTCTTTTACCAATTTGTCTCCACA	9935
QY	2639	GCTGCTTTTCTGTAACTTCACTCTACCTCTACCTTTAGCATCCCTTCCCTTTGCAAAATAGTCC	2698
DB	9934	CTTCCGCTTACATCAAC-----ACCAATAACGC	9907
QY	2699	TCCTTCAACAATAATAATGTGAGTCTCTGTAGAGACCAATCATCACGGTTCTATATCTG	2758
DB	9906	CAATTAATCTAAGCGCATCACCAACAATTTCTTGGCGTCTGATCCACAGCTAAACATAAAT	9847
QY	2759	TTGACCAATGCTCTCCCTGCTCATCTAAACCCACACCGGCTGTCATAATCAACCAATC	2818
DB	9846	GTAAGCTTTGGGGCTCTCTTGGCTT-----CCAAACCGAGTCAGAAATCGAGTTCCNATC	9792
QY	2819	GTAACCTTTCATCTTCTTCAACCCATGCTCTTTTGGAGCAATAAAGCCGATAAACAAATCTTT	2878
DB	9791	CAAAAGTTTCACTGCTCCAC-----CTGCTTCTGAATCAACAAGGAAATAACGAATG	9738
QY	2879	GTCGCTTCTCGCAATGTCAACAGTACCTTATGATATTTCTCCAGTAGATAGGAGCCCTT	2938
DB	9737	AGGTTTCTGTGAAGCTGCACTGAGTAGTATGTTGAGTCTTTTGGAAATACGAGTCTTTT	9678
QY	2939	GCATGACAAATCTGCTAAACATCAAAAGGCTCTAGGTTCTCTTTGTTTACTTCTTCTGCGC	2998
DB	9677	-----AATACTGGGAAACCGAGGAACTCTTGATTTCTTGGACAGCTCATCTCCA	9626
QY	2999	CTGCTTCAAAACCGCTTAAACATACCTTGGGCGCACCAACCGTGTGATTCGTATGTCTGC	3058
DB	9625	TGCAGT-----TGACGATATCAATCGCGTAATCATTTGACAGAGCCAAACATCTCTC	9573
QY	3059	CAATTCGTGATTTCTGTATACACCGCGAGTACTGCAATTTTGTGATTTTACCAATGTC	3118
DB	9572	CTTAGGTTGATTTACGAAACACCGCAACCAAGTATTTTCGAGTGTGCTGAACTATTTTATA	9513
QY	3119	AGCAAAATTTCTGCTTCTCGAAGAGTAAATAATTTGACTTGGCGGATAATGCTTTTAGCGG	3178
DB	9512	TG-----CTTTTCAAGACTTGAAATTTTCTTGTCAATAACCGGGTCAATTTGT	9465
QY	3179	CTTAACTGTGCGCTCCATCGGAAATAATCAATCAAGATATCAATGTGTTTGTAGTAAACA	3238
DB	9464	TCTCTTCTTCTTGTGGGCACACATATAATCCAGCAAGTACAGCATCGGAATCTAG--AGCA	9407
QY	3239	AATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTCTTGGTGGTATC--GAAACATCA	3297
DB	9406	CAATTCGCGGCTCTGTCTCTGCAAGCGCAAACTTTTCAACCAATGGACAGAACTACCT	9347

QY 3298 ATGAAGCACACAGTTTGTGTTTTCGTCATGATATTAATAGCTTGGCAGCAACAG 3357
DB |||||
QY 9346 GTGAATTAATAACAGACACTCCAGCTGCCCTTGTGTGCTTAATACAGTATCTCAC 9287
DB |||||
QY 3358 GACTAGGATGATGACGACAGCTTCTTATATATGATGCTTTTCGACATGATTTATCTTGGTT 3417
DB |||||
QY 9286 GTGCTCAATAGTACCAATGCCCTCCCTCTTGGCCCTCTCC-----TTTTCCTT 9238
DB |||||
QY 3418 TCCTGCAGGTTTGTGCTGTCAGTTGGGTGAAGATACATGGGCAATTCATGTTTCCT 3477
DB |||||
QY 9237 TTTCCAGCGAATTAATCTTAATCGGCAAAAAGAAAGCTCCGGA-----T 9190
DB |||||
QY 3478 CAACACTACATATCGTATATATACCAATCTTAAGTCTGTGCTCTCTCTCTCTCTCTCT 3537
DB |||||
QY 9189 CAAGATTGCTAGTGAAGTGACAGCTATTTTCAATAAGAAATATCTTCACACTACTGCCA 9130
DB |||||
QY 3538 TCTGTTCCGAGATTACCGAATCAAAAATTTCAAAGAAACCGGAATCAAAAAGAAAT 3597
DB |||||
QY 9129 TCTGGCGTCATACTGCAAGAGTACACATATATTA-----CGATGCTGTCTATTAAAT 9078
DB |||||
QY 3598 AAAAAAATGATGAATGAATGAATGAAGCTGTGGTATGTGCACTCTCAGTACATCT 3657
DB |||||
QY 9077 GCTTCTTATATATATATATATATATATGCTGTGATCTATGTGCACTCTCAGTACATCT 9018
DB |||||
QY 3658 GCTCTGATGCCGATAGTTAAGCCAGCCCGACACCCGCAACACCCGCTGACGCGCCCT 3717
DB |||||
QY 9017 GCTCTGATGCCGATAGTTAAGCCAGCCCGACACCCGCAACACCCGCTGACGCGCCCT 8958
DB |||||
QY 3718 GACGGGCTGTCTGCTCCCGGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 3777
DB |||||
QY 8957 GACGGGCTGTCTGCTCCCGGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 8998
DB |||||
QY 3778 GATGTGTACAGGTTTTCACCGTCATCACCGAAACCGGGGAGACGAAAGGCGCTCTGTGA 3837
DB |||||
QY 8897 GCATGTGCAGAGGTTTTCACCGTCATCACCGAAACCGGGGAGACGAAAGGCGCTCTGTGA 8838
DB |||||
QY 3838 TACGCTATTTTATAGGTTAATGTGATGATAAATAGTTTCTTCTAGTATGATCCCAATAT 3897
DB |||||
QY 8837 TACGCTATTTTATAGGTTAATGTGATGATAAATAGTTTCTTCTAATATGATCCCAATAT 8778
DB |||||
QY 3898 CAAAGGAATGATAGCATTTGAAGGATGAGACTAATCCAAATTTGAGGAGTGGCAGCATATAG 3957
DB |||||
QY 8777 CAAAGGAATGATAGCATTTGAAGGATGAGACTAATCCAAATTTGAGGAGTGGCAGCATATAG 8718
DB |||||
QY 3958 AACAGCTAAAGGTAGTCTGAAAGAGCATACGATACCCCGCATGGAATGGGATATAT 4017
DB |||||
QY 8717 AACAGCTAAAGGTAGTCTGAAAGAGCATACGATACCCCGCATGGAATGGGATATAT 8658
DB |||||
QY 4018 CACAGGAGTACTAGACTACCTTTTATCTTACATATAAATAGACGATATAGTACGCAATTT 4077
DB |||||
QY 8657 CACAGGAGTACTAGACTACCTTTTATCTTACATATAAATAGACGATATAGTACGCAATTT 8598
DB |||||
QY 4078 AAGCAATAACCGCACTATGCGTTCTTCTCATGTATATATATATATACAGGCAACACGCGAG 4137
DB |||||
QY 8597 AAGCAATAACCGCACTATGCGTTCTTCTCATGTATATATATATATACAGGCAACACGCGAG 8538
DB |||||
QY 4138 ATATAGGTGCGACGTGAACAGTGAAGCTGTATGTGCGAGCTCGCGTTGCAATTTTCGGAAG 4197
DB |||||
QY 8537 ATATAGGTGCGACGTGAACAGTGAAGCTGTATGTGCGAGCTCGCGTTGCAATTTTCGGAAG 8478
DB |||||
QY 4198 CGCTGTTTTCGGAACCGTTTGAAGTTCCTTATTCGGAAGTTCCTATCTCTAGAAAGTA 4257
DB |||||
QY 8477 CGCTGTTTTCGGAACCGTTTGAAGTTCCTTATTCGGAAGTTCCTATCTCTAGAAAGTA 8418
DB |||||
QY 4258 TAGGAACCTCAGAGCGCTTTTGAACCCAAAGCGCTCTGAAGACGCACTTTTCAAAAAC 4317
DB |||||
QY 8417 TAGGAACCTCAGAGCGCTTTTGAACCCAAAGCGCTCTGAAGACGCACTTTTCAAAAAC 8358
DB |||||
QY 4318 CAAAAACGCGACGCTGTAAAGAGCTACTAAAATATTTGGGAATACCGCTTTCGCAAAACA 4377
DB |||||
QY 8357 CAAAAACGCGACGCTGTAAAGAGCTACTAAAATATTTGGGAATACCGCTTTCGCAAAACA 8298
DB |||||

QY 4378 TTGCTCAAAAGTATCTCTTTGCTATATATATCTCTGTGCTATATCTCTATATATACCTACCCA 4437
DB |||||
QY 8297 TTGCTCAAAAGTATCTCTTTGCTATATATATCTCTGTGCTATATCTCTATATATACCTACCCA 8238
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QY 4438 TCCACCTTTGCTCTCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCT 4497
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QY 8237 TCCACCTTTGCTCTCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCT 8178
DB |||||
QY 4498 TCTAGTATTACTCTTTAGACAAAAAATTTGTAGTAAGAACTATTCTATAGAGTGAATCGAA 4557
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QY 4558 AACAAATACGAAATGAAACATTTCTCTATACGTAATATATAGACAAAAATAGAAAGAAC 4617
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Db 5357 CTTCCGGCTCTTATGTTGTGGAATTTGTAGCGGATTAACAATTTTACACAGGAAACAGC 5298
QY 7378 TATGACCATGATTCGCAAGCGCGCA 7404
Db 5297 TATGACCATGATTCGCAAGCGCTTGA 5271

RESULT 8

US-09-845-917A-27/c
; Sequence 27, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845, 917A
; CURRENT FILING DATE: 2001-04-30


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; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13414
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; LOCATION: (11582)
; OTHER INFORMATION: "N is A, G, C or T"
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-845-917A-27

Query Match      57.4%; Score 4492.6; DB 10; Length 13414;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

QY 1559 TCATGTAATTAGTTATGTCAGCTTACATTCACGCCCTCCGCCACATCCGCTCAACCG 1618
Db 11004 TCATGTAATTAGTTATGTCAGCTTACATTCACGCCCTCCGCCACATCCGCTCAACCG 10945

QY 1619 AAAAGGAAGGAGTTAGACAACCTGAAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 1678
Db 10944 AAAAGGAAGGAGTTAGACAACCTGAAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 10885

QY 1679 TAGTATTAAGAACGTTATTTATATTTCAATTTTTCTTTTTTCTGTACAGCGGTGT 1738
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QY 1739 AGCATGTAAACATTATATCTGAACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT 1798
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QY 1799 TAAATTTGGCGGCTGACCAATTCGCCCTATAGTAGTCTGATTTACGCGGCTCACTGGC 1858
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QY 1859 CGTGTGTTTACAGCTGCTGATCGGAACCTTGGGTTACCCAACTTAATCGCCTTGC 1918
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QY 1919 AGCATATCCCTTTTCGCGAGCTGGCGTAATAGCGAAGAGCCCGACCGATCGCCCTTC 1978
Db 10654 AGCATATCCCTTTTCGCGAGCTGGCGTAATAGCGAAGAGCCCGACCGATCGCCCTTC 10595

QY 1979 CCAACAGTTGCGCAGCTGAAATGCGGAATGCGCGACGCGCTGTATAGCGCGCATTAAG 2038
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QY 2099 CGCTCTTTTCGCTTTCTTCCCTTCTCCTGCAAGCTTCCCGGCTTCCCGCTCAAGC 2158
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QY 2339 ACTCAACCTATCTCGGTCTATCTTTTGTATTAAGGGATTTTGGCGATTTTCGGCCTA 2398
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Db 6977 GATGCGATGACAGTAAGAGATTAATGAGTCTGCCATTAACCATGAGTATACACTGCG 6918
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Db 5297 TATGACCATGATTACGCCAAGCTTGCA 5271

RESULT 9

US-09-758-036-31
; Sequence 31, Application US/09758036
; Publication No. US20030190693A1
; GENERAL INFORMATION:
; APPLICANT: LEBERER, Ekkehard
; APPLICANT: LEEUW, Thomas
; APPLICANT: RITSCHER, Allegra
; TITLE OF INVENTION: POTASSIUM CHANNEL MUTANTS OF THE YEAST SACHAROMYCES CEREVISIAE
; TITLE OF INVENTION: USE FOR SCREENING EUKARYOTIC POTASSIUM CHANNELS
; FILE REFERENCE: 38005-0126
; CURRENT APPLICATION NUMBER: US/09758,036
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: DE 100 00 651.5
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 7772
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-758-036-31
Query Match 46.1%; Score 3610.2; DB 10; Length 7772;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3626; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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3880 CTTAGTATGATCAATATCAAGGAATGATAGCATTTGAAGGATGAGACTAATCCAATTG 3939
Db 61 CTTAG-ATGATCCANATCAAGGAATGATAGCATTTGAAGGATGAGACTAATCCAATTG 119
3940 AGGAGTGGCAGCATATAGAACACGCTAAAGGGTAGTCTGAAGGAAGCATACGATACCCCG 3999
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4420 CCTATATAACCTACCACTCACTTTGCTTCTGAACTTGCACTAATCACTGACCTCT 4479
Db 600 CCTATATAACCTACCACTCACTTTGCTTCTGAACTTGCACTAATCACTGACCTCT 659
4480 ACATTTTATGTTATCTCTAGTATATCTCTTTAGACAAAAAATTGATAGAACTA 4539
Db 660 ACATTTTATGTTATCTCTAGTATATCTCTTTAGACAAAAAATTGATAGAACTA 719
4540 TTCTATAGAGTGAATCGAAAAAATACGAAATGTAAACATTTCTATACGTAGTATATAG 4599
Db 720 TTCTATAGAGTGAATCGAAAAAATACGAAATGTAAACATTTCTATACGTAGTATATAG 779
4600 AGACAAATAAGAAAGAACCGTTTCATATTTTTCGCAATGAAGAAATCATCAACGCTATC 4659
Db 780 AGACAAATAAGAAAGAACCGTTTCATATTTTTCGCAATGAAGAAATCATCAACGCTATC 839
4660 ACTTTCTGTTTCAAAAGTATGCGCAATCCACATCGGTATAGATATAATCGGGGATGCTT 4719
Db 840 ACTTTCTGTTTCAAAAGTATGCGCAATCCACATCGGTATAGATATAATCGGGGATGCTT 899
4720 TTATCTTGAATAATGCAACCGCAGCTTCGCTAGTAAATCAGTAAACCGCGGAAGTGGAGT 4779
Db 900 TTATCTTGAATAATGCAACCGCAGCTTCGCTAGTAAATCAGTAAACCGCGGAAGTGGAGT 959
4780 CAGGCTTTTATGGAAGAGAAAAATAGACCAAAAGTAGCTTCTTCTAAACCTTAACCG 4839
Db 960 CAGGCTTTTATGGAAGAGAAAAATAGACCAAAAGTAGCTTCTTCTAAACCTTAACCG 1019
4840 ACCTACAGTCAAAAGTTATCAAGAGACTGCAATTTATAGGCGCAACAAAGGAGAAAAAA 4899
Db 1020 ACCTACAGTCAAAAGTTATCAAGAGACTGCAATTTATAGGCGCAACAAAGGAGAAAAAA 1079

4900 GTAATCTAAGATGCTTTGTAGAAAAATAGCGCTCTCGGATGCTATTTTGTAGAACAA 4959
Db 1080 GTAATCTAAGATGCTTTGTAGAAAAATAGCGCTCTCGGATGCTATTTTGTAGAACAA 1139
4960 AAAGAGTATAGATCTTTGTTGGTAAATAGCGCTCTCGCGTTGCATTTCTGTTCTGTA 5019
Db 1140 AAAGAGTATAGATCTTTGTTGGTAAATAGCGCTCTCGCGTTGCATTTCTGTTCTGTA 1199
5020 AAAATGCAGCTCAGATTTCTTTGTTGAAAAATAGCGCTCTCGCGTTGCATTTTCTGTTT 5079
Db 1200 AAAATGCAGCTCAGATTTCTTTGTTGAAAAATAGCGCTCTCGCGTTGCATTTTCTGTTT 1259
5080 ACAAATAAGAACAGATTTCTTTGTTGAAAAATAGCGCTTTTCGCGTTGCATTTCTGTTT 5139
Db 1260 ACAAATAAGAACAGATTTCTTTGTTGAAAAATAGCGCTTTTCGCGTTGCATTTCTGTTT 1319
5140 CTGTAATAATGAGCTCAGATTTCTTTGTTGAAAAATAGCGCTCTCGCGTTGCATTTT 5199
Db 1320 CTGTAATAATGAGCTCAGATTTCTTTGTTGAAAAATAGCGCTCTCGCGTTGCATTTT 1379
5200 GTTCTCAAAAATGAAGCACAGATGCTTTCTGAGGTGGCACTTTTCGGGAAATGTGCGC 5259
Db 1380 GTTCTCAAAAATGAAGCACAGATGCTTTCTGAGGTGGCACTTTTCGGGAAATGTGCGC 1439
5260 GGAACCCCTATTGTTTATTTTCTAAATACATTTCAAATATATGATCCGCTCATGAGACAA 5319
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5320 TAAACCTGATAATGCTTCAATAATATGAAAAAGAGATGATGATTTCAACATTTTC 5379
Db 1500 TAAACCTGATAATGCTTCAATAATATGAAAAAGAGATGATGATTTCAACATTTTC 1559
5380 CGTGTGCGCCTTATTCCCTTTTTCGCGCATTTTTCGCTTCTGTTTTCCTCACCCAGAA 5439
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5500 CTGGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCGCCGAGAAAGTTCCTCAATG 5559
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5620 GAGCAACTCGTTCGCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCACTC 5679
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5680 ACAGAAAGCATCTTACGATCGCATGACAGTAAGAAATTTAGCATGCTGCTGCTATAACC 5739
Db 1860 ACAGAAAGCATCTTACGATCGCATGACAGTAAGAAATTTAGCATGCTGCTGCTATAACC 1919
5740 ATGAGTGAATAACCTGCGGCACTTCTCTGACAAACCATCGGAGACCGAGGAGCTA 5799
Db 1920 ATGAGTGAATAACCTGCGGCACTTCTCTGACAAACCATCGGAGACCGAGGAGCTA 1979
5800 ACCGCTTTTTCACAACTGGGGATCATGTAACCTCGCTTTCGCTTGGGAAACCGGAG 5859
Db 1980 ACCGCTTTTTCACAACTGGGGATCATGTAACCTCGCTTTCGCTTGGGAAACCGGAG 2039
5860 CTGAATGAAGCATATACCAAAACGAGCGGTGACCAACGATGCTGTAGCAATGGCAACA 5919
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5920 ACGTTGCGCAAACTTAACTGCGCACTTCTTCTAGCTTCCCGCAACAAATTAATA 5979
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5980 GACTGATGAGGCGGATAAAGTTGAGGACCACTTCTCGCTCGGCCCTTCGGCTGCGC 6039

Db 2160 GACTGATGGAGCGGATAAAGTTGAGGACACTTCTGCGCTGCGCCCTTCCGCGTGGC 2219
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Qy 6160 ACTATGATGAACGAATAAGACAGATCGCTGAGATAGTGCTCTACTGATTAAGCATTTGG 6219
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Db 2460 TTTAAAGGATCTAGGTGAAGATCCCTTTTGTGATAATCTCATGACCAAAATCCCTTAAAGT 2519
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Db 2580 CTTTTTTTTCTGCGCTAATCTGCTGCTTGGCAACCAAAACCAACCGCTACCGCGGTG 2639
Qy 6460 GTTTGTTTCCGCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACTGGCTTCAGCAGA 6519
Db 2640 GTTTGTTTCCGCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACTGGCTTCAGCAGA 2699
Qy 6520 GCGAGATACCAATACTGCTCTCTAGTGTAGCGGTAGTTAGGCCACCACTTCAAGAAC 6579
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Qy 6640 GCGATAAGTCTGCTTACCGGGTTGGACTCAAGACGATAGTTTACCGGATAAGCGCAG 6699
Db 2820 GCGATAAGTCTGCTTACCGGGTTGGACTCAAGACGATAGTTTACCGGATAAGCGCAG 2879
Qy 6700 CGGTGCGGCTGAACCGGGGGTTCTGCAACAGCCAGCTTGGAGCGAACCACTTACAC 6759
Db 2880 CGGTGCGGCTGAACCGGGGGTTCTGCAACAGCCAGCTTGGAGCGAACCACTTACAC 2939
Qy 5760 GAACTGATACCTACAGCTGATATGAGAAAGCGCCAGCTTCCGAGGGGAGAAG 6819
Db 2940 GAACTGATACCTACAGCTGATATGAGAAAGCGCCAGCTTCCGAGGGGAGAAG 2999
Qy 6820 GCGGACAGGTATCCGGTAAAGCGGAGGTTCGGAACAGAGAGCGCACGAGGAGCTTCCA 6879
Db 3000 GCGGACAGGTATCCGGTAAAGCGGAGGTTCGGAACAGAGAGCGCACGAGGAGCTTCCA 3059
Qy 6880 GGGGGAACCGCTGTGTATCTTTATAGTCTGTGCGGGTTTCGCAACTCTGTAGCGGT 6939
Db 3060 GGGGGAACCGCTGTGTATCTTTATAGTCTGTGCGGGTTTCGCAACTCTGTAGCGGT 3119
Qy 6940 CGATTTTGTGATGCTCGTCAGGGGGGCGGACCTATCGAATAACCGCCAGCAACCGCGCC 6999
Db 3120 CGATTTTGTGATGCTCGTCAGGGGGGCGGACCTATCGAATAACCGCCAGCAACCGCGCC 3179
Qy 7000 TTTTACGGTCTCTGCGCTTTGCTGGCTTTTGTCTACATGTTCTTTTCTGCGGTATCC 7059
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Db 3240 CTTGATTTCTGTGATTAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCGCAGC 3299
Qy 7120 CGAACGACCGAGCGCAGGAGTCTAGTGAGCGAGGAAGCGGAGAGCGCCCAATACGCAAA 7179
Db 3300 CGAACGACCGAGCGCAGGAGTCTAGTGAGCGAGGAAGCGGAGAGCGCCCAATACGCAAA 3359
Qy 7180 CCGCTCTCTCCCGCGCTTGGCGGATTCATTAATGAGCTGGCAGCAGGTTTCCCGAC 7239
Db 3360 CCGCTCTCTCCCGCGCTTGGCGGATTCATTAATGAGCTGGCAGCAGGTTTCCCGAC 3419
Qy 7240 TGGAAAGCGGCGAGTGAGCGCAACGCAATTAATGAGTTACCTCATTAGGCAACC 7299
Db 3420 TGGAAAGCGGCGAGTGAGCGCAACGCAATTAATGAGTTACCTCATTAGGCAACC 3479
Qy 7300 CAGGCTTTACACTTTATGCTTCCGCTCCTATGTTGTGGAATTTGAGCGGATAACAA 7359
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Qy 7360 TTTTACACAGGAACAGCTATGACCATGATTTACCCAAAGCGGCAATTTAAACCTCATAA 7419
Db 3540 TTTTACACAGGAACAGCTATGACCATGATTTACCCAAAGCGGCAATTTAAACCTCATAA 3599
Qy 7420 AGGAAACAAAGCTGGAGCTCGTAGGAACAATTTT 7454
Db 3600 AGGAAACAAAGCTGGAGCTCAGTTTATCATTC 3634

RESULT 10

US-10-314-861-8/c
; Sequence 8, Application US/10314861
; Publication No. US20030148269A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Holzman, Thomas F.
; APPLICANT: Harlan, John Eric
; APPLICANT: Egan, David A.
; APPLICANT: Boko, Alexander M.
; APPLICANT: Solomon, Larry R.
; APPLICANT: Lador, Uri S.
; APPLICANT: Tang, Qing
; TITLE OF INVENTION: CENTRIFUGALLY-ENHANCED METHOD OF
; TITLE OF INVENTION: DETERMINING LIGAND/TARGET AFFINITY
; FILE REFERENCE: 6404.US.O1
; CURRENT APPLICATION NUMBER: US/10/314,861
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/270,427
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11912
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pBDEF3
; NAME/KEY: CDS
; LOCATION: (4616)...(7750)
; OTHER INFORMATION: Nucleotide sequence of plasmid pBDEF3
US-10-314-861-8

Query Match 45.3%; Score 3547.4; DB 15; Length 11912;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3551; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3848 TTTATAGTTTAAATGTCATGATAATAATATGTTTCTTAGTATGATCAATATCAAGGAAAT 3907
Db 11912 TTTATAGTTTAAATGTCATGATAATAATATGTTTCTTAGTATGATCAATATCAAGGAAAT 11853
Qy 3908 GATAGCATTCAGAGATGAGCTAATCCAAATTTGAGGTGGCAGCATATAGAACACCTAAA 3967
Db 11852 GATAGCATTCAGAGATGAGCTAATCCAAATTTGAGGTGGCAGCATATAGAACACCTAAA 11793

Qy	3968	GGGTAGTGTCTGAAGGAAGCATA	CGATACCCCGCATGGAAATGGATAA	TATATCACAGGAGGT	4027
Db	11792	GGGTAGTGTCTGAAGGAAGCATA	CGATACCCCGCATGGAAATGGATAA	TATATCACAGGAGGT	11733
Qy	4028	ACTAGACTACCTTTTCATCTCT	PACATAAATAGACGCATATAAGT	TACGCATTTTAAGCATAAAC	4087
Db	11732	ACTAGACTACCTTTTCATCTCT	PACATAAATAGACGCATATAAGT	TACGCATTTTAAGCATAAAC	11673
Qy	4088	ACGCATCTATGCCGTTCTTCT	CATGTATATATATACAGGC	AACACGCAGATATAGGTGC	4147
Db	11672	ACGCATCTATGCCGTTCTTCT	CATGTATATATATACAGGC	AACACGCAGATATAGGTGC	11613
Qy	4148	GACGTGAACAGTGAGCTGTAT	GTGCGCAGCTCGCGTTGCATTTT	CGGAAGCGCTCGTTTT	4207
Db	11612	GACGTGAACAGTGAGCTGTAT	GTGCGCAGCTCGCGTTGCATTTT	CGGAAGCGCTCGTTTT	11553
Qy	4208	CGGNAACGCTTTGNAAGTTT	CCTATTCCGAAGTTTCCCTAT	TCTCTAGAAAGTATAGNACTTC	4267
Db	11552	CGGNAACGCTTTGAAAGTTT	CCTATTCCGGAAGTTTCCCTAT	TCTCTAGAAAGTATAGNACTTC	11493
Qy	4268	AGAGCGCTTTTGAAGAAC	CAAAAGCGCTCTGGAAGCGCACT	TTTCAAAAACCAAAAACGCA	4327
Db	11492	AGAGCGCTTTTGAAGAAC	CAAAAGCGCTCTGGAAGCGCACT	TTTCAAAAACCAAAAACGCA	11433
Qy	4328	CCGGACTGTAAACGAGCTACT	ATAAATATTCGAATACCGCTT	CCACAAACATTTGCTCAAAA	4387
Db	11432	CCGGACTGTAAACGAGCTACT	ATAAATATTCGAATACCGCTT	CCACAAACATTTGCTCAAAA	11373
Qy	4388	GTATCTCTTTTGCTATATAT	CTCTGCTATATATCCCTATATA	ACCTACCGATCCACCTTTC	4447
Db	11372	GTATCTCTTTTGCTATATAT	CTCTGCTATATATCCCTATATA	ACCTACCGATCCACCTTTC	11313
Qy	4448	GCTCTTTGAACTTTGCATCT	ATAACTCGACCTCTACATTTT	TATGTTTATCTCTAGTATTA	4507
Db	11312	GCTCTTTGAACTTTGCATCT	ATAACTCGACCTCTACATTTT	TATGTTTATCTCTAGTATTA	11253
Qy	4508	CTCTTTAGACAAAAAATGT	AGTAAGAACTATTCATAGAGT	GAATCGAAAACCAATACGA	4567
Db	11252	CTCTTTAGACAAAAAATGT	AGTAAGAACTATTCATAGAGT	GAATCGAAAACCAATACGA	11193
Qy	4568	AAATGTAAACATTTTCTAT	ACGTAGTATATAGAGACAA	AAATAGAGAAGAACCGTTCATAT	4627
Db	11192	AAATGTAAACATTTTCTATA	CGTAGTATATAGAGACAA	AAATAGAGAAGAACCGTTCATAT	11133
Qy	4628	TTTCTGACCAATGAAGAA	TCAATCAACGCTATCACTT	CTTGTTTCAAAAAGTATCGCAATC	4687
Db	11132	TTTCTGACCAATGAAGAA	TCAATCAACGCTATCACTT	CTTGTTTCAAAAAGTATCGCAATC	11073
Qy	4688	CACATCGGTATAGATAAT	ATACGGGGATCGCTTTAT	CTTTGAAAAATGCACCCGAGCTT	4747
Db	11072	CACATCGGTATAGATAAT	ATACGGGGATCGCTTTAT	CTTTGAAAAATGCACCCGAGCTT	11013
Qy	4748	CGCTAGTAATCAGTAAAC	CGGGGAAGTGGAGTCA	GGCTTTTTTTTATGGAAGAAAAATAG	4807
Db	11012	CGCTAGTAATCAGTAAAC	CGGGGAAGTGGAGTCA	GGCTTTTTTTTATGGAAGAAAAATAG	10953
Qy	4808	ACACCAAGTAGCCTTCTT	CTTACCTTTAACCGACCT	TACAGTGCAAAAAGTTATCAAGAGA	4867
Db	10952	ACACCAAGTAGCCTTCTT	CTTACCTTTAACCGACCT	TACAGTGCAAAAAGTTATCAAGAGA	10893
Qy	4868	CTGCATTATAGACGCACA	AAAGGAGAAAAAAGTAAT	CTAAGATCGCTTTGTTGAAAAAT	4927
Db	10892	CTGCATTATAGACGCACA	AAAGGAGAAAAAAGTAAT	CTAAGATCGCTTTGTTGAAAAAT	10833
Qy	4928	AGGCTCTCGGGATGCA	TTTTTGTAGAACAAAAA	AGAGTATAGATTTCTTTGTTGGTAAA	4987
Db	10832	AGGCTCTCGGGATGCA	TTTTTGTAGAACAAAAA	AGAGTATAGATTTCTTTGTTGGTAAA	10773
Qy	4988	ATAGCGCTCTCGGTTG	CACTTTCTGTTCTGTA	AAAAATGCAGCTCAGATTTCTTTGTTGAA	5047
Db	10772	ATAGCGCTCTCGGTTG	CACTTTCTGTTCTGTA	AAAAATGCAGCTCAGATTTCTTTGTTGAA	10713
Qy	5048	AAATTAGCGCTCTCGG	TTGTCATTTTTTTGTTT	TATCAAAAATGAAGCACAGATTTCTTCGTTG	5107

10712	Db		AAATTAGCGCTCTCGCGTTGCAATTTTGTGTTTACAAAAATGAAGACACAGATTTCTTCGTTG	10653
5108	Qy		GTAAATAGCGCTTTCGCGTGCATTTCTGTGTTCTGTAAATAATGCAGCTCAGATCTCTTGT	5167
10652	Db		GTAAATAGCGCTTTCGCGTGCATTTCTGTGTTCTGTAAATAATGCAGCTCAGATCTCTTGT	10593
5168	Qy		TTGAAAAATTAGCGCTCTCGCGTTGCATTTTGTGTTCTACAAAAATGAAGACACAGATGCTTC	5227
10592	Db		TTGAAAAATTAGCGCTCTCGCGTTGCATTTTGTGTTCTACAAAAATGAAGACACAGATGCTTC	10533
5228	Qy		GTTTCAGGTGGCACTTTTTCGGGGAAATATGTGCGCGAAACCCCTATTTGTGTTTATTTTTCATAAA	5287
10532	Db		GTTTCAGGTGGCACTTTTTCGGGGAAATATGTGCGCGAAACCCCTATTTGTGTTTATTTTTCATAAA	10473
5288	Qy		TACATTTCAAAATATGATTCGGCTCATGAGACAAATACCTCGATTAATGCTTCAATAATATT	5347
10472	Db		TACATTTCAAAATATGATTCGGCTCATGAGACAAATACCTCGATTAATGCTTCAATAATATT	10413
5348	Qy		GA AAAAGGAGATATGAGTATTCAACATTTCCGTGTCGCCCTTATCCCTTTTTCGCG	5407
10412	Db		GA AAAAGGAGATATGAGTATTCAACATTTCCGTGTCGCCCTTATCCCTTTTTCGCG	10353
5408	Qy		CATTTTGCCTTCTCTGTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAAAGATGCTGAAG	5467
10352	Db		CATTTTGCCTTCTCTGTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAAAGATGCTGAAG	10293
5468	Qy		ATCAGTTGGGTGACAGAGTGGGTATATCGAATCTGATCTCAACAGCGGTAAATCCTTTG	5527
10292	Db		ATCAGTTGGGTGACAGAGTGGGTATATCGAATCTGATCTCAACAGCGGTAAATCCTTTG	10233
5528	Qy		AGAGTTTTCGCCCGGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTG	5587
10232	Db		AGAGTTTTCGCCCGGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTG	10173
5588	Qy		GGCGGTATTATCCCGTATTGACGGCGGCAAGAGCAACTCGGTGCGCGCATACACTATT	5647
10172	Db		GGCGGTATTATCCCGTATTGACGGCGGCAAGAGCAACTCGGTGCGCGCATACACTATT	10113
5648	Qy		CTCAGAACTACCTTGGTTGAGTACTCACAGTACAGAAAGCATCTTACGGATGGCATGA	5707
10112	Db		CTCAGAACTACCTTGGTTGAGTACTCACAGTACAGAAAGCATCTTACGGATGGCATGA	10053
5708	Qy		CAGTAAGAGAAATTATGCAGTGCTGCCATAAACCATGAGTGATAAACACTCGCGCCAACTTAC	5767
10052	Db		CAGTAAGAGAAATTATGCAGTGCTGCCATAAACCATGAGTGATAAACACTCGCGCCAACTTAC	9993
5768	Qy		TTCTGCAACACGATTCGGAGGACCGAAGGAGCTAAACCGCTTTTTTTCACAACATGCGGGATC	5827
9992	Db		TTCTGCAACACGATTCGGAGGACCGAAGGAGCTAAACCGCTTTTTTTCACAACATGCGGGATC	9933
5828	Qy		ATGTAATCTCGCTTGNATCGTTGGGAAACGGAGCTGAATGAAGCCATACCAACGACGAGC	5887
9932	Db		ATGTAATCTCGCTTGNATCGTTGGGAAACGGAGCTGAATGAAGCCATACCAACGACGAGC	9873
5888	Qy		GTGACACACGATGCTGTAGCAATGCGAAACAACTGCGCAAACTATTAATCTGGCGAAC	5947
9872	Db		GTGACACACGATGCTGTAGCAATGCGAAACAACTGCGCAAACTATTAATCTGGCGAAC	9813
5948	Qy		TACTTACTCTAGCTTCCCGGCAACAATTAAATAGACTGGATGGAGCGGATAAAGTTGCGAG	6007
9812	Db		TACTTACTCTAGCTTCCCGGCAACAATTAAATAGACTGGATGGAGCGGATAAAGTTGCGAG	9753
6008	Qy		GACCACCTTCGCGCTCGGCCCTTCGCGCTGGCTGTTTTTATGCTGATTAATCTCGAGCCG	6067
9752	Db		GACCACCTTCGCGCTCGGCCCTTCGCGCTGGCTGTTTTTATGCTGATTAATCTCGAGCCG	9693
6068	Qy		GTGAGCGTGGGTCTCGCGGTATCATTTGACGACACTGGGCGCAGATGGTAAGCCCTCCCGTA	6127
9692	Db		GTGAGCGTGGGTCTCGCGGTATCATTTGACGACACTGGGCGCAGATGGTAAGCCCTCCCGTA	9633
6128	Qy		TCGTAGTTATCTACGACGGGGAGTCAAGCAACTTATCGATGAACGAAATAGACAGATTCG	6187

Db 9632 TCGTAGTTATCTACACGAGCGGGAGTCAGGCAACTACTGATGAACAAATAGACAGATCG 9573
Qy 6188 CTGAGATAGTCCCTCACTGATTAAAGCAATGTGAACCTGTAGACCAAGCTTTACTCATATA 6247
Db 9572 CTGAGATAGTCCCTCACTGATTAAAGCAATGTGAACCTGTAGACCAAGCTTTACTCATATA 9513
Qy 6248 TACTTTAGATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTT 6307
Db 9512 TACTTTAGATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTT 9453
Qy 6308 TTGATAATCTCATGACCAAAATCCCTTAAGTAGATTTTCTGTTTCACTGAGCGTCAGACC 6367
Db 9452 TTGATAATCTCATGACCAAAATCCCTTAAGTAGATTTTCTGTTTCACTGAGCGTCAGACC 9393
Qy 6368 CCGTAGAAGATCAAGGATCTTCTGAGATCCCTTTTCTGCGGTAACTCTGCTGCT 6427
Db 9392 CCGTAGAAGATCAAGGATCTTCTGAGATCCCTTTTCTGCGGTAACTCTGCTGCT 9333
Qy 6428 TGCACAAACAAAAACCCCGCTACACGCGTGTGTTTGTTCGCGGATCAAGAGCTACCAA 6487
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Db 9272 CTCCTTTTCCGAAGTAAGTCTGCTTACAGAGCGCAGATACCAAAATCTGCTCTTAG 9213
Qy 6548 TGTAGCGGTAGTTAGGCGACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTC 6607
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Qy 6608 TGTAACTCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGCTTACCGGGTTGG 6667
Db 9152 TGTAACTCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGCTTACCGGGTTGG 9093
Qy 6668 ACTAAGACGATAGTTACCGGATAAGGCGCAGCGTCCGGCTGAAACCGGGGGTTCTGTCGA 6727
Db 9092 ACTAAGACGATAGTTACCGGATAAGGCGCAGCGTCCGGCTGAAACCGGGGGTTCTGTCGA 9033
Qy 6728 CACGCCAGCTTGAGCGGACGACTACCGACTCAGATACCTACAGCGTCAAGCTAT 6787
Db 9032 CACGCCAGCTTGAGCGGACGACTACCGACTCAGATACCTACAGCGTCAAGCTAT 6733
Qy 6788 GAGAAAGCGCCACGCTTCCGAAAGGAGAAAGCGCGACAGGTATCCGGTAAGCGCGCAGGG 6847
Db 8972 GAGAAAGCGCCACGCTTCCGAAAGGAGAAAGCGCGACAGGTATCCGGTAAGCGCGCAGGG 8913
Qy 6848 TCGGAAACAGGAGCGCAGGAGCTTCCAGGGGAGAAACGCTGTGATCTTTATAGTC 6907
Db 8912 TCGGAAACAGGAGCGCAGGAGCTTCCAGGGGAGAAACGCTGTGATCTTTATAGTC 8853
Qy 6908 CTGTCGGGTTTCCGACCTCTGACTTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGGG 6967
Db 8852 CTGTCGGGTTTCCGACCTCTGACTTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGGG 8793
Qy 6968 GGAGCCTATGGAAGAAACCGCAGCAACCGCGGCTTTTACGGTTCCTGCGCTTTTGTCTGGC 7027
Db 8792 GGAGCCTATGGAAGAAACCGCAGCAACCGCGGCTTTTACGGTTCCTGCGCTTTTGTCTGGC 8733
Qy 7028 CTTTGTCTCAGATGTTCTTCTGCTTATCCCTGATCTGTGGAATAACCGTATATACG 7087
Db 8732 CTTTGTCTCAGATGTTCTTCTGCTTATCCCTGATCTGTGGAATAACCGTATATACG 8673
Qy 7088 CTTTGTGAGTGAGCTGATACCGCTCCGCGCAGCGCAACCGAGCGGAGCGAGTCAGTGA 7147
Db 8672 CTTTGTGAGTGAGCTGATACCGCTCCGCGCAGCGCAACCGAGCGGAGCGAGTCAGTGA 8613
Qy 7148 GCGAGGAGCGGAGAGCGCCCAATACGCAACCGCCCTCTCCCGCGGCTTGGCGGATTC 7207
Db 8612 GCGAGGAGCGGAGAGCGCCCAATACGCAACCGCCCTCTCCCGCGGCTTGGCGGATTC 8553
Qy 7208 ATTAATGACGTGGCAGCAGAGTTTCCCGACTGCGAAGCGGGGAGTGAGCGCAACGCA 7267
Db 8552 ATTAATGACGTGGCAGCAGAGTTTCCCGACTGCGAAGCGGGGAGTGAGCGCAACGCA 8493

Qy 7268 TTAATGTAGTTACTCCTCACTCATTTAGGCACCCAGGCTTTACACTTTATGCTTCGGGCTC 7327
Db 8492 TTAATGTAGTTACTCCTCACTCATTTAGGCACCCAGGCTTTACACTTTATGCTTCGGGCTC 8433
Qy 7328 CTAATGTGTGTGAATTTGTGAGCGGATAACAATTTTCAACAGGAAACAGCTATGACCATG 7387
Db 8432 GTATGTGTGTGAATTTGTGAGCGGATAACAATTTTCAACAGGAAACAGCTATGACCATG 8373
Qy 7388 ATTACGCCAAGCGCGCA 7404
Db 8372 ATTACGCCAAGCTTGCA 8356

RESULT 11

US-10-228-785-9
; Sequence 9, Application US/10228785
; Publication No. US20030186443A1
; GENERAL INFORMATION:
; APPLICANT: VEIDE, JENNY
; APPLICANT: SANDBERG, ANN-SOFIE
; TITLE OF INVENTION: PHYTASE ACTIVE YEAST
; FILE REFERENCE: 6821
; CURRENT APPLICATION NUMBER: US/10/228,785
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: SE 0200911-6
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9210
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic plasmid
; OTHER INFORMATION: PYX212 nucleotide sequence
US-10-228-785-9

Query Match 42.48; Score 3318.6; DB 15; Length 9210;

Best Local Similarity 74.8%; Pred. No. 0;
Matches 4787; Conservative 0; Mismatches 769; Indels 847; Gaps 16;

Qy 1851 TCACGTGCGCGTCTGTTTACAAACGTCGTGACTGGGAAACCCCTGGCGTTACCCAACTTAAT 1910
Db 1095 TCACGTGCGCGTCTGTTTACAAACGTCGTGACTGGGAAACCCCTGGCGTTACCCAACTTAAT 1154
Qy 1911 CGCCTTGACGACATCCCTTTTCGCGAGCTGGCGTAATAGCGAGGCGCCGACCGAT 1970
Db 1155 CGCCTTGACGACATCCCTTTTCGCGAGCTGGCGTAATAGCGAGGCGCCGACCGAT 1214
Qy 1971 CGCCTTCCCAACAGTTGCGCAGCTCAATGGCGAATGGCGCGAGCGCCCTGTAGCGCG 2030
Db 1215 CGCCTTCCCAACAGTTGCGCAGCTCAATGGCGAATGGCGCGAGCGCCCTGTAGCGCG 1274
Qy 2031 GCATTAGCGCGCGGCTGTGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCC 2090
Db 1275 GCATTAGCGCGCGGCTGTGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCC 1334
Qy 2091 CTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTTCGCGACGTTCCGCGGCTTTCC 2150
Db 1335 CTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTTCGCGACGTTCCGCGGCTTTCC 1394
Qy 2151 CGTCAAGCTCTAATCCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTAGGGCACCTC 2210
Db 1395 CGTCAAGCTCTAATCCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTAGGGCACCTC 1454
Qy 2211 GACCCCAAAAACCTTGATTAGGGTGATGGTTACGCTAGTGGGCCATCGCCCTGTAGAGC 2270
Db 1455 GACCCCAAAAACCTTGATTAGGGTGATGGTTACGCTAGTGGGCCATCGCCCTGTAGAGC 1514
Qy 2271 GTTTTTCGCGCTTGAAGTGGAGTCCAGTCTTTTAAATAGTGAAGCTTTGTTCCAAACT 2330

1515	Db	GT	TTTTCGCCCTTTGACGTTGGAGTCCACGGTTCTTTAAATAGTGGACATCTCTGTGTTCCAAACT	1574
2331	Qy	GG	AACACACTCAACCCCTATCTCGGTCTATTCTTTTGAATTTATAAGGGATTTTTCGGGATT	2390
1575	Db	GG	AACACACTCAACCCCTATCTCGGTCTATTCTTTTGAATTTATAAGGGATTTTTCGGGATT	1634
2391	Qy	TC	GGCCTATTGGTTTAAAAATGAGCTGATTTTAAACAAAATTTTAAACGGAAATTTTAAACAAA	2450
1635	Db	TC	GGCCTATTGGTTTAAAAATGAGCTGATTTTAAACAAAATTTTAAACGGAAATTTTAAACAAA	1694
2451	Qy	AT	ATTACGGTTTACAAATTCCTGATCGGGTATTTTCTCTTACGATCTCTGCGGGTATTTT	2510
1695	Db	AT	ATTACGGTTTACAAATTCCTGATCGGGTATTTTCTCTTACGATCTCTGCGGGTATTTT	1754
2511	Qy	CAC	ACGCATAGGGTAAATACTGATATAAATTAATTTGAAGCTCTAAATTTGTGAGTTTAGT	2570
1755	Db	CAC	ACGCATAGGGTAAATACTGATATAAATTTGAAGCTCTAAATTTGTGAGTTTAGT	1814
2571	Qy	AT	CATGCATTTACTTTAATAACAGTTTTTTTGTGTTTGTGGCGGCATCTTCTCAAAATAT	2630
1815	Db	AT	CATGCATTTACTTTAATAACAGTTTTTTTGTGTTTGTGGCGGCATCTTCTCAAAATAT	1874
2631	Qy	GC	TTCACGCTCTCTTTTCTGTAAAGTTTACCCCTCTACCTTTAGCATCCCTTCCTCTTGCA	2690
1875	Db	GC	TTCACGCTCTCTTTTCTGTAAAGTTTACCCCTCTACCTTTAGCATCCCTTCCTCTTGCA	1934
2691	Qy	AA	TAGTCTCTTCCAAACAATAAATGTCAGATCCTGTAGAGACCAATCATCCACGGTT	2750
1935	Db	AA	TAGTCTCTTCCAAACAATAAATGTCAGATCCTGTAGAGACCAATCATCCACGGTT	1994
2751	Qy	CT	ATCTGTTGACCCAAATGGTCTCCCTGTGTCAATCTAAACCCACACCGGGTGTCAATAATC	2810
1995	Db	CT	ATCTGTTGACCCAAATGGTCTCCCTGTGTCAATCTAAACCCACACCGGGTGTCAATAATC	2054
2811	Qy	AA	CCAAATCGTAAACCTTTCATCTCTCCACCCATGTCTCTTTGAGCAATAAAGCCGATACA	2870
2055	Db	AA	CCAAATCGTAAACCTTTCATCTCTCCACCCATGTCTCTTTGAGCAATAAAGCCGATACA	2114
2871	Qy	AA	ATCTTTGTGCGCTCTTCGCAATGTCAACAGTACCCCTTAGTATATCTCCAGTAGATAGG	2930
2115	Db	AA	ATCTTTGTGCGCTCTTCGCAATGTCAACAGTACCCCTTAGTATATCTCCAGTAGATAGG	2174
2931	Qy	GAG	CCCTTGATGACAAATTCGTCTAACATCAAAAGGCGCTCTAGGTTCCCTTTGTTACTTCT	2990
2175	Db	GAG	CCCTTGATGACAAATTCGTCTAACATCAAAAGGCGCTCTAGGTTCCCTTTGTTACTTCT	2234
2991	Qy	TC	TGCGCGCTGCTTCAAAACGCTTAAATACCTGGGCGCCACACACCGTGTGCATTCGTA	3050
2235	Db	TC	TGCGCGCTGCTTCAAAACGCTTAAATACCTGGGCGCCACACACCGTGTGCATTCGTA	2294
3051	Qy	AT	GTCGCCCAATTCGTCTATTCTGTATACACCCGACAGTACTGCAATTTGACTGTATTA	3110
2295	Db	AT	GTCGCCCAATTCGTCTATTCTGTATACACCCGACAGTACTGCAATTTGACTGTATTA	2354
3111	Qy	CCA	ATGTCAGCAAAATTTCTGTCTTCGAAGAGTAAAAAATTTGTACTTGGCGGATAATGCC	3170
2355	Db	CCA	ATGTCAGCAAAATTTCTGTCTTCGAAGAGTAAAAAATTTGTACTTGGCGGATAATGCC	2414
3171	Qy	TT	TAGCGGCTTAATGTGCGCCTCCATCGAAAAATCAGTCAAGATATCCATGTGTTTTT	3230
2415	Db	TT	TAGCGGCTTAATGTGCGCCTCCATCGAAAAATCAGTCAAGATATCCATGTGTTTTT	2474
3231	Qy	AG	TAAAACAAATTTTGGGACCTTAATGCTTTCAACTCAAGTAAATCTTTGGTGGTACGA	3290
2475	Db	AG	TAAAACAAATTTTGGGACCTTAATGCTTTCAACTCAAGTAAATCTTTGGTGGTACGA	2534
3291	Qy	ACA	TCCAATGAAGCACCAAGTTTGTGTTTTTGTGTCATGATATTAATAATAGCTTGGCA	3350
2535	Db	ACA	TCCAATGAAGCACCAAGTTTGTGTTTTTGTGTCATGATATTAATAATAGCTTGGCA	2594
3351	Qy	GCA	ACAGCACTAGGATGAGTAGACGACGTTTCTTATATAGTACGTTTCGACATGATTTAT	3410
2595	Db	GCA	ACAGCACTAGGATGAGTAGACGACGTTTCTTATATAGTACGTTTTCGACATGATTTAT	2654

Qy	3411	CTTCGGTTTCTCGAGGTTTTTGTGTCGTGAGTTGGTTAAGAATACTGGGCAATTTTCAT	3470
Db	2655	CTTCGGTTTCTCGAGGTTTTTGTGTCGTGAGTTGGTTAAGAATACTGGGCAATTTTCAT	2714
Qy	3471	GTTCCTTTCAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCCTTCCTTCGT	3530
Db	2715	GTTCCTTTCAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCCTTCCTTCGT	2774
Qy	3531	TCTTCCTCTGTTCCGGAGATTACCGAATCAAAAAATTTCAAAGAAACCGAAATCAAAA	3590
Db	2775	TCCTTCCTCTGTTCCGGAGATTACCGAATCAAAAAATTTCAAAGAAACCGAAATCAAAA	2834
Qy	3591	AAAGAAATAAAAAAATAATGATGAATTTGAAATGAAAGCTGTGTGATGTGTCATCTCAGT	3650
Db	2835	AAAGAAATAAAAAAATAATGATGAATTTGAAATGAAAGCTGTGTGATGTGTCATCTCAGT	2894
Qy	3651	ACAATCTGCTCTGATCGCGATAGTTAAGCCAGCCCGCACCCCGCCACACACCGCTGAC	3710
Db	2895	ACAATCTGCTCTGATCGCGATAGTTAAGCCAGCCCGCACCCCGCCACACACCGCTGAC	2954
Qy	3711	GCGCCCTGACCGGCTGTCTGCTCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC	3770
Db	2955	GCGCCCTGACCGGCTGTCTGCTCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC	3014
Qy	3771	GGGAGCTGCATGTGTACAGAGTTTTTCAACCGTCAATCCGAAACCGCGAGACGAAAGGC	3830
Db	3015	GGGAGCTGCATGTGTACAGAGTTTTTCAACCGTCAATCCGAAACCGCGAGACGAAAGGC	3074
Qy	3831	CTCGTGATACGCCATTTTTTATAGTTTAATGTGCATGATTAATATGTTTCTTTA	3883
Db	3075	CTCGTGATACGCCATTTTTTATAGTTTAATGTGCATGATTAATATGTTTCTTTAGACGTGC	3134
Qy	3884	-----	3883
Db	3135	GCGCGCTCTAGAACTAGTGGATCAATTCACGGCAATAGACTATAGTACTAGTACTCCGT	3194
Qy	3884	-----GTATGATCCAAATATCAAAGGAAATGATAGCAATTGAAGGATG-----	3924
Db	3195	CTACTGTACGATACACTTCCGCTCAGGTCTTCTGCTCTTTAAACGAGGCTTACCACCTTT	3254
Qy	3925	-----AGCTAATCCAAATGTAGGAGTGGCAGCATATAGAACAGCTAAAGGGTAGTCT	3977
Db	3255	TGTTACTCTTATGATCCAGCTCAGCAAGGCACTGTGATCTAAGATTCTATCTTCGCGAT	3314
Qy	3978	GAAGGAGCATACGATACCCCGCATGGAAATGGGATATATACAGAGGTACTAGACTAC	4037
Db	3315	GTAGTAAACTAGCTAGACCCGAGAAAGAGACTAGAATGCAAAAGGCATCTTCTACAAATG	3374
Qy	4038	CTTTCATCCT-----ACATAAATAGACGCATATATAAGTACGCATT	4076
Db	3375	CTGCCATCATTAATTATCCGATGTGACGCTGCAGTCTCTCAATGATATCGAATACGCTTT	3434
Qy	4077	TAGACATAAACCGCACTATGC-----CGTCTCTCTCAT	4110
Db	3435	GAGGAGATACAGCTTAATATCCGACAAACTGTTTTTACAGATTTTACGATCTGTGTTAC	3494
Qy	4111	GTATATATATACAGGCAACACGAGATATAGTGGCGTGCAACAGTACGCTGTATGT	4170
Db	3495	CCATCATTTGAATTTTGAACATCCGAACCTGGAGTTTTTCCCTGAAACAGATGATATTT	3554
Qy	4171	GCGCAGCTCGGTTGCAATTTTCGGAAGCGCTCGTTTTTCGAAACGCTTTTGAAGTCTCAT	4230
Db	3555	GAACCTGTATAATAATATATAGTCTAGCGCTTTTACGGAAGACAAATGATATGTTTCGTT	3614
Qy	4231	TCCGAAGTTCCTATCTCTAGAAAGTATAGGAACCTTCAGAGCG-----	4273
Db	3615	CCTGGAAACCTATTCGATCTATTGCAATAGGTAATCTTTCGACGTCCCGGTTTCAT	3674
Qy	4274	-----	4273
Db	3675	TTTTCGGTTTTCCATCTTTCGACTTCAATAGCATATCTTTGTTAAACGAAGATCTGTGCTT	3734

QY 4274 -CTTTTGAACCAAAAGCGCTCTGAAGCGCACT----- 4307
Db 3735 CATTTTGTAGAACAAAATGCAACGCGAGCGCTAAATTTTCAAACAAGAACTGAGC 3794
QY 4308 -----TTCAAAAACCAAAACGCGAGCTGTAAAGAGCTACTAAATAT 4354
Db 3795 TGCATTTTACAGAACAGAAATGCAACGCGAAAGCGCTATTTTACCAACGAAGATCTGT 3854
QY 4355 TCGAATACCGCTTCCACAAACATTTGCTCAAAAG-----TATCTCTTTGCTATATATCTC 4409
Db 3855 GCTTCATTTTGTAAAAAACAATAATGCAACGCGAGCGCTAAATTTTCAACAAGAAATC 3914
QY 4410 TGTGCTATATCCCTATATAACCTAC-----COATCAACCTT 4445
Db 3915 TGAAGCTGCAATTTTACAGAACAGAAATGCAACGCGAGAGCGCTATTTTACCAACAAGAA 3974
QY 4446 TCGCTCCTTGAACCTTGCATCTAAA-----CTCGACCTCTA 4480
Db 3975 TCTATACCTTCTTTTGTCTTACAAAATGCAATCCGAGAGCGCTATTTTCTAACAAAG 4034
QY 4481 CATTTTGTATGTTTATCTCTAGTATTTACTCTTTAGACAAAAAATTTGTAGTAAGAACTAT 4540
Db 4035 CATCTTAGATTAATTTTCTCTTTTGTGCGCTCTATATGCACTCTCTTGATAACTTT 4094
QY 4541 TCATAGAGTGAATCGAAAAACAATACGAAAAATGTAAACAATTTCTATACGTAGTATAGA 4600
Db 4095 TTGCACTGTAGGTCGTTAAGGTTAGAAGAGGCTACTTTTGTGTCTATTTTCTCTTCCA 4154
QY 4601 GACAAA-----TAGAAGAAACCGTTTCATAATTTT 4630
Db 4155 TAAAAAAGCCTGACTCCACTTTCCGCGGTTTACTGATTTACTAGCGAAGCTCGCGGTGCAT 4214
QY 4631 CTGACCAATGAAGAAATCATCAACGCTATCACTTTCTGTTCAACAAGTATGCGCAATCCAC 4690
Db 4215 TTTTTCAGATTAAGGCATCCCGAATATATTTCTATACCGATTTGGATTTGCGCATCTTT 4274
QY 4691 ATCGGTATAGAAATAAATCGGGATGCGCTTTATCTTG-----AAAAATGCAAC 4739
Db 4275 GTGAACAGAAAGTGATAGCGTTGATGATTTCTTCAATTTGTCAGAAAAATATGACCGTTTC 4334
QY 4740 CGCAGCTTCGCTAGTAATACAGTAAGCGGGAAGTGGAGTCAGGCTTTTATTTATGGAAGA 4799
Db 4335 TTCTATTTTGTCTCTATATACTACGTATAGGAATGTTTACATTTTCGTATTTGTTTCGA 4394
QY 4800 GAAAAATAGACCAAAAGTAGCCTCTCTTCACTTTAAACGGACCTACAGTGCAAAAAGTTA 4859
Db 4395 TTCACCTATGATAGTTCTTCTACTACAATTTTTTTTGTCTAAAGAGTAATACTAGAGATA 4454
QY 4860 TCAAGAGACTGCATTTATAGAGCGCAAAAGGAGAAAAAAGTAATCTAAGATGCTTTGTT 4919
Db 4455 ACATAAAAAATGTAGAGGTGCAAGTTTATGATGCAAGTTCAGAGGCGAAAGGTGGATGGT 4514
QY 4920 AGAAAAATAGCGCTCTCGGAGTGCATTTTGTGTAGAACAAA----- 4959
Db 4515 AGTTATATAGGGATATAGCACAGAGATATATAGCAAAAGAGATACTTTTGTAGCAATGTTT 4574
QY 4960 ---AAGAGATAGATCTTTTGTGTAAATAGCGCTCTCGGTTGCAATTTCTGTCT 5016
Db 4575 GTGGAAGCGGTATTCGCAATATTTTGTAGTCTGCTTACAGTCCGCTGCGTTTGTGGTTT 4634
QY 5017 GTAAAAATCGAGC-TCAGATTTCTTTGTTTGAATAATAGCGCTCTCGGTTGCAATTTTGTG 5075
Db 4635 TTGAAAGTCGCTCTTCAGAGCGCTTTTGGTTTCAAAAGCGCTCTGAAGTTCCTATACTT 4694
QY 5076 TTTTCAAAAAATGAAGCACAGATT----- 5099
Db 4695 TCTAGAGAAATAGGAACCTTCGGAATAGGAACCTTCAAGAGGTTTCCGAAAAACGAGCGCTTCC 4754
QY 5100 -----CTTCGTTGGTAAATAGCG 5118
Db 4755 GAAAAATGCAACGCGAGCTGCGCACATACAGCTCACTGTTACGTGCGACCTATATCTGCG 4814
QY 5119 CTTTGGCGTTGCAATTTCTGTTCTGTAAAAATGCAAGTCTCAGATTTCTTTGTTG----- 5170

Db 4815 TGTGCTGTATATATATATATATACATGAGAAGAACGGCATAGTGCCTGTTTATGCTTTAAATG 4874
QY 5171 ----- 5170
Db 4875 CGTACTTATATGCGTCTATTTATGTAGATGAAAAGTAGTCTAGTACCTCTCTGTGATATT 4934
QY 5171 ----- 5170
Db 4935 ATCCCAATTCATGCGGGGTATCGTATGCTTCTTCAGCACATACCCTTTAGCTGTTCTATA 4994
QY 5171 ----- 5170
Db 4995 TGTGCCACTCTCAATTTGATTAGTCTCATCTTCAATGCTATCATTTCTCTTTGATATT 5054
QY 5171 ----- 5170
Db 5055 GGATCATATGATAGTACCGAGAAAACATAGTCGGAAGTAGTATCAGGTATTGCTGTTATC 5114
QY 5171 -----AA 5172
Db 5115 TGATGAGTATACGTTGTCTGCGCCACGCGCAGAACACGCTTATCGTCTCAATTTCCACACA 5174
QY 5173 AAATTAGCGCTCTGCGGTTGCAATTTTGTCTTCTAATAATGAAGCACAGATGCTTCGT --- 5229
Db 5175 ACATTTAGTCAACTCCGTTAGGCCCTTCATTTGAAGAAAATGAGTTCATCAAAATGCTCTTCCA 5234
QY 5230 ----- 5229
Db 5235 ATGTGAGATTTTGGGCCAATTTTTATAGCAAAAGATTGAATAAGGGCGCAATTTTCTTCAAA 5294
QY 5230 -----TCAGTGGCACCTTTTTCGGGGAAATGTGCGCGGAA 5263
Db 5295 GCTGCGGCCGCACTCTCACTAGTAGCTCAGGTGGCACTTTTTCGGGAAATGTGCGCGGAA 5354
QY 5264 CCCTATTTGTTTATTTTCTTAATAATTCATAATATGATTCGCTCTATGACACAAATTAAC 5323
Db 5355 CCCCTATTTGTTTATTTTCTTAATAATTCATAATATGATTCGCTCTATGACACAAATTAAC 5414
QY 5324 CCTGATAAATGCTTCAATAATATTTGAAAAGGAGATGATCAGTATTTCAACAATTTCCGCTG 5383
Db 5415 CGTGATAAATGCTTCAATAATATTTGAAAAGGAGATGATGAGTATTTCAACAATTTCCGCTG 5474
QY 5384 TCGCCCTTATTTCCCTTTTTCGGGCATTTTTCCTCTCTCTTTTTCCTCACCCAGAAAACGC 5443
Db 5475 TCGCCCTTATTTCCCTTTTTCGGGCATTTTTCCTCTCTCTTTTTCCTCACCCAGAAAACGC 5534
QY 5444 TGTGAAAGTAAAGATGCTGAAGATCAGTTTGGGTGCAACGAGTGGGTTTACATCGAACTGG 5503
Db 5535 TGTGAAAGTAAAGATGCTGAAGATCAGTTTGGGTGCAACGAGTGGGTTTACATCGAACTGG 5594
QY 5504 ATCTCAACGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTTCCAATGATGA 5563
Db 5595 ATCTCAACGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTTCCAATGATGA 5654
QY 5564 GCATTTTAAAGTTCCTCTATGTCGCGCGGTATTTATCCCGTATTTGACGCCGCGGCAAGAGC 5623
Db 5655 GCATTTTAAAGTTCCTCTATGTCGCGCGGTATTTATCCCGTATTTGACGCCGCGGCAAGAGC 5714
QY 5624 AACTCGGTTCGCCGATACACTATTTCTCAGAAATGACTTTGGTTGAGTACTCACAGTCAAG 5683
Db 5715 AACTCGGTTCGCCGATACACTATTTCTCAGAAATGACTTTGGTTGAGTACTCACAGTCAAG 5774
QY 5684 AAAAGCATCTTAGGATGGCATGACAGTAAAGAAATTTATGAGTCTGCTGCCATTAACATGA 5743
Db 5775 AAAAGCATCTTAGGATGGCATGACAGTAAAGAAATTTATGAGTCTGCTGCCATTAACATGA 5834
QY 5744 GTGATAACACTGGGCCAACTTACTCTGACAAAGTTCGAGGACCGAAGAGCTTAAACCG 5803
Db 5835 GTGATAACACTGGGCCAACTTACTCTGACAAAGTTCGAGGACCGAAGAGCTTAAACCG 5894
QY 5804 CTTTGTGCAACAATCGGGGATCATGTAATTCGCTTGTGATCTGCTTGTGGAAACCGGAGCTGA 5863

Db 5895 CTTTTTGGACAACATGGGGATCATGTAACTCGCCTTGATCGTTTGGGAACCGAGCTGA 5954
Qy 5864 ATGAAGCCTATACAAACGACGAGGTGACACCAAGATGCTGTAGCAATGGCAACACGCT 5923
Db 5955 ATGAAGCCTATACAAACGACGAGGTGACACCAAGATGCTGTAGCAATGGCAACACGCT 6014
Qy 5924 TGGCGCAAACTATTAACTGGGAACTACTTACTTACTTACTTCTCCGGCAACAAATTAATAGCT 5983
Db 6015 TGGCGCAAACTATTAACTGGGAACTACTTACTTACTTCTCCGGCAACAAATTAATAGCT 6074
Qy 5984 GGAATGAGGCGGATAAAGTTGACGAGCACTTCTGCGCTCGGCCCTTTCGGGCTGGCTGGT 6043
Db 6075 GGAATGAGGCGGATAAAGTTGACGAGCACTTCTGCGCTCGGCCCTTTCGGGCTGGCTGGT 6134
Qy 6044 TTATTGCTGATAAATCTGGAGCGGCTGAGCGTGGGTCTCGCGGTATCATTTGACGACTGG 6103
Db 6135 TTATTGCTGATAAATCTGGAGCGGCTGAGCGTGGGTCTCGCGGTATCATTTGACGACTGG 6194
Qy 6104 GGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAGAGCGGGAGTCAAGCAACTA 6163
Db 6195 GGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAGAGCGGGAGTCAAGCAACTA 6254
Qy 6164 TGGATCAACGAATAGACAGATCGCTGAGATAGTGCCTCACTGATTTAAGCATTGTGTAAC 6223
Db 6255 TGGATCAACGAATAGACAGATCGCTGAGATAGTGCCTCACTGATTTAAGCATTGTGTAAC 6314
Qy 6224 TGTGAGCAAAAGTTTACTCATATATATCTTTAGATGATTTAAATCTCAATTTTAAATTA 6283
Db 6315 TGTGAGCAAAAGTTTACTCATATATATCTTTAGATGATTTAAATCTCAATTTTAAATTA 6374
Qy 6284 AAAGATCTAGGTGAAGATCTTTTGTGATAATCTCATGATCAAAATCTCCCTTAAAGTGGT 6343
Db 6375 AAAGATCTAGGTGAAGATCTTTTGTGATAATCTCATGATCAAAATCTCCCTTAAAGTGGT 6434
Qy 6344 TTTCTGTTCCACTGAGCGTCAGACCCGCTGAGAAAGATCAAGGATCTTCTTGAGATCCCT 6403
Db 6435 TTTCTGTTCCACTGAGCGTCAGACCCGCTGAGAAAGATCAAGGATCTTCTTGAGATCCCT 6494
Qy 6404 TTTTCTGCGCGTAATCTGCTGCTGCAACAAACAAACCAACCGCTACACGCGGTGGTT 6463
Db 6495 TTTTCTGCGCGTAATCTGCTGCTGCAACAAACAAACCAACCGCTACACGCGGTGGTT 6554
Qy 6464 GTTTGCGGATCAAGAGTCAACCACTCTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGC 6523
Db 6555 GTTTGCGGATCAAGAGTCAACCACTCTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGC 6614
Qy 6524 AGATACAAATCTGCTCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAACTCTG 6583
Db 6615 AGATACAAATCTGCTCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAACTCTG 6674
Qy 6584 TAGCACCGCTACATACCTCGCTCTGTAATCTGTTTACAGTGGCTGTGCCAGTGGCG 6643
Db 6675 TAGCACCGCTACATACCTCGCTCTGTAATCTGTTTACAGTGGCTGTGCCAGTGGCG 6734
Qy 6644 ATAAGTCTGTCTTACCGGGTGGACTCAAGACGATAGTTTACCGGATAAGCGCAGCGGT 6703
Db 6735 ATAAGTCTGTCTTACCGGGTGGACTCAAGACGATAGTTTACCGGATAAGCGCAGCGGT 6794
Qy 6704 CGGGCTGAACGGGGGTTGTGCAACAGCCAGCTTGGAGCGAAACGACCTACACCGAAC 6763
Db 6795 CGGGCTGAACGGGGGTTGTGCAACAGCCAGCTTGGAGCGAAACGACCTACACCGAAC 6854
Qy 6764 TGAGATACCTACAGCTGAGCTATGAGAAGCGCCACGCTTCCGGAAGGAGAGAGCGG 6823
Db 6855 TGAGATACCTACAGCTGAGCTATGAGAAGCGCCACGCTTCCGGAAGGAGAGAGCGG 6914
Qy 6824 ACAGGTATCCGGTAAGCGGCGAGGCTCGGAACAGGAGCGCAACGAGGAGCTTCCAGGGG 6883
Db 6915 ACAGGTATCCGGTAAGCGGCGAGGCTCGGAACAGGAGCGCAACGAGGAGCTTCCAGGGG 6974
Qy 6884 GAAACGCTGGTATCTTTATGCTCTGTGGGTTTCCGCACTCTGACTTGGAGCTCGAT 6943
Db 6975 GAAACGCTGGTATCTTTATGCTCTGTGGGTTTCCGCACTCTGACTTGGAGCTCGAT 7034

Qy 6944 TTTTGTGATGCTCGTTCAGGGGGCGGAGCCTATGGAATAACGCCAGCAACGCCGCGCTTTT 7003
Db 7035 TTTTGTGATGCTCGTTCAGGGGGCGGAGCCTATGGAATAACGCCAGCAACGCCGCGCTTTT 7094
Qy 7004 TAGGTTCTCGGCTTTTGTCTGCGCTTTTGTCTACATGTTCTTCTCGGTATCCCTG 7063
Db 7095 TAGGTTCTCGGCTTTTGTCTGCGCTTTTGTCTACATGTTCTTCTCGGTATCCCTG 7154
Qy 7064 ATTCTGTGATAAACCGTATTACCGCTTTTGTGAGTGAGCTGATACCGCTCGCCGAGCGAA 7123
Db 7155 ATTCTGTGATAAACCGTATTACCGCTTTTGTGAGTGAGCTGATACCGCTCGCCGAGCGAA 7214
Qy 7124 CGACGAGCGCAGCGAGTCACTGAGCGAGGAAGCGGAAGCGCCCAATAACGAAACCGC 7183
Db 7215 CGACGAGCGCAGCGAGTCACTGAGCGAGGAAGCGGAAGCGCCCAATAACGAAACCGC 7274
Qy 7184 CTCTCCCGCGGTTGGCGGATTCATTAATGAGCTGCGACGACGAGTTTCCGACTGGA 7243
Db 7275 CTCTCCCGCGGTTGGCGGATTCATTAATGAGCTGCGACGAGTTTCCGACTGGA 7334
Qy 7244 AAGCGGCGAGTCAAGCGCAACGCAATTAATGAGTTACCTCACTCAATAGGCAACCCAGG 7303
Db 7335 AAGCGGCGAGTCAAGCGCAACGCAATTAATGAGTTACCTCACTCAATAGGCAACCCAGG 7394
Qy 7304 CTTTACATTTATGCTTCCGGCTCTCTATGTTGTGGAATTTGTAGCGGATAACTTTTC 7363
Db 7395 CTTTACATTTATGCTTCCGGCTCTCTATGTTGTGGAATTTGTAGCGGATAACTTTTC 7454
Qy 7364 ACACAGGAACAGCTATGACCATGATTACGCCAAGCGCGAAT 7406
Db 7455 ACACAGGAACAGCTATGACCATGATTACGCCAAGCTCGAAT 7497

RESULT 12

US-10-228-785-3
; Sequence 3, Application US/10228785
; Publication No. US20030186443A1
; GENERAL INFORMATION:
; APPLICANT: ANDLID, THOMAS
; APPLICANT: VEIDE, JENNY
; APPLICANT: SANDBERG, ANN-SOFIE
; TITLE OF INVENTION: PHYTASE ACTIVE YEAST
; FILE REFERENCE: 6821
; CURRENT APPLICATION NUMBER: US/10/228,785
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: SE 0200911-6
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9715
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic plasmid
; OTHER INFORMATION: pYX212 nucleotide sequence
US-10-228-785-3

Query Match 42.4%; Score 3318.6; DB 15; Length 9715;
Best Local Similarity 74.8%; Pred. No. 0;
Matches 4787; Conservative 0; Mismatches 769; Indels 847; Gaps 16;
Qy 1851 TCACTGGCGCTGTTTTTACAACTGCTGAGTGGGAACCCCTGGCTTACCCAACTTAAT 1910
Db 1599 TCACTGGCGCTGTTTTTACAACTGCTGAGTGGGAACCCCTGGCTTACCCAACTTAAT 1658
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Db 1659 CGCTTTCAGCAGCATCCCTCTTTCGCCAGCTGGCGTAATAGCAAGAGCGCCGACCGAT 1718
Qy 1971 CGCCCTTCCCAACAGTTGCGCAGCTGAATGGCGAATGGCGGACGCGCCCTGTAGCGG 2030

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Db 1899 CGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGTTCCGATTTAGTCTTTACGGCACCTC 1958
Qy 2211 GACCCCAAAAATCTGATTTAGGGTGTATGTTTACGTAGTGGCCATCGCCCTGTATAGAG 2270
Db 1959 GACCCCAAAAATCTGATTTAGGGTGTATGTTTACGTAGTGGCCATCGCCCTGTATAGAG 2018
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Qy 2331 GGAACAACACTCAACCCCTATCTCGGTCTATCTTTTGAATTTAAGGATTTTCCCGATT 2390
Db 2079 GGAACAACACTCAACCCCTATCTCGGTCTATCTTTTGAATTTAAGGATTTTCCCGATT 2138
Qy 2391 TCGGCTATTGGTTAAATAATGAGCTGATTTTAAACAAAATTTTAAACGGAATTTTAAACAA 2450
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Qy 2451 ATATTAAAGCTTTTACAAATTTCTGTAGTGGGTATTTTCTCTTACGCATCTGTGCGGTATTT 2510
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Qy 2631 GCTTCCAGCTGCTTTTCTGTAAAGCTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCA 2690
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Qy 2751 CTATAGTGTGACCAATGCGTCTCCCTGTGTCATCTAAACCCACACCGGTTCTATATC 2810
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Qy 2811 AACCAATGTAACCTTCTCTTCCACCATGTCCTTTTGGAGCAATAAAGCCGATAACA 2870
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Qy 2871 AAATCTTTGTCGCTCTTCCGAATGCAACAGTACCTTTAGTATATTTCCAGTATAGTAGG 2930
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Qy 2931 GAGCCCTTGCAATCTGCTAAATCAAAAGGCTCTAGTTCCTTTGTTACTTCT 2990
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Qy 2991 TCTGCGGCTGCTTCAAAACCGTCTAAATACCTGCGGCCACACACCGGTGTGCAATCGTA 3050
Db 2739 TCTGCGGCTGCTTCAAAACCGTCTAAATACCTGCGGCCACACACCGGTGTGCAATCGTA 2798
Qy 3051 ATGTCTGCCCAATCTGCTATTCTGTATACACCGCAGAGTACTGCAATTTGACTGTATTA 3110
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Db 2919 TTTAGCGGCTTAATCTGTGCGCTCATCGAAAAAATCAGTCAATATATCCACATGTGTTTTT 2978
Qy 3231 AGTAAACAAAATTTTGGGACCTTAATGCTTCAACTAATCCAGTAAATCTTCTGCTGATGAT 3290
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Qy 3291 ACATCCAAATGAAGCACACAAAGTTTGTGCTTTTCTGTCATGATATTAATAGCTTTGGCA 3350
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Db 3399 ACAATCTGCTCTGATGCGCATAGTTAAGCCAGCCCGGACACCCGCGCAACCCGCTGAC 3458
Qy 3711 GCGCCCTGACGGGCTTCTGCTCCCGCATCCGCTTACAGCAAGCTGTGACGCTTCC 3770
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Qy 3831 CTGCTGATACGCTTATTTTATAGTTTAAATGTCTATGATATAATAGTTTCTTTA 3883
Db 3579 CTGCTGATACGCTTATTTTATAGTTTAAATGTCTATGATATAATAGTTTCTTTAGACGTG 3638
Qy 3884 ----- 3883
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Qy 3884 -----GTATGATCCAATATCAAGGAAATGATAGCATTTGAAGATG----- 3924
Db 3699 CTACTGTACGATACACTTCCGCTCAGGTCCTTTGCTTTTAAACGAGGCTTACCACCTTTT 3758
Qy 3925 -----AGACTAATCCAAATTTAGGAGTGGCAGCATATAGAAACAGCTAAAGGGTAGTGT 3977
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Qy 3978 GAAGGAAGCATACGATACCCCGCATGGAAATGGGTAATATACAGGAGGTACTAGACTAC 4037
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Qy 4038 CTTTTCATCCT-----ACATAAATAGACGATATAAGTACGCATT 4076
Db 3879 CTGCCATCATTTATTCGGATGTGACGCTGACGCTTCTCAATGATATTTTCAATACGCTTT 3938

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Db 3939 GAGGAGATACAGCCTAATATCCGACAAACCTGTTTTACAGATTTCAGTCTGTTAC 3998
QY 4111 GTATATATATATACAGCAACACGATAGTGCAGCTGAAACAGTGCATGTATGT 4170
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QY 4231 TCCGAAGTTCCTATTTCTAGAAAGTATAGGAACCTTCAGAGCG----- 4273
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QY 4274 ----- 4273
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QY 4601 GACAAA-----TAGAAGAAACCGTTCAATATTT 4630
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QY 5017 GTAAAAATCGAGC-TCAGATTTCTTTGTTGAAAAAATAGCGCTCTCGCGTTGCAATTTT 5075
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Qy 6584 TAGACCGGCTACATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6643
Db 7179 TAGACCGGCTACATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7238

Qy 6644 ATAAGTCTGTCTTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGCGCAGCGGT 6703
Db 7239 ATAAGTCTGTCTTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGCGCAGCGGT 7298
Qy 6704 CGGCTGAAACGCGGGGTTCTGTGACACAGCCAGCTTTGGAGCGAACGACTTACACCGAAC 6763
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Qy 6764 TGAGATACCTACAGCGTGAAGTATGAAAGCGCCAGCTTCCGAAAGGAGAAAGCGG 6823
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Qy 6884 GAAACGCTCGTATCTTTATAGTCTGTGCGGTTTCCGCACTCTGACTTGAAGCGTCAAT 6943
Db 7479 GAAACGCTCGTATCTTTATAGTCTGTGCGGTTTCCGCACTCTGACTTGAAGCGTCAAT 7538
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Db 7599 TACGGTTCTCGGCTTTTGTGCTGCTCATGTTTCTTCTGCTGCTTATCCCTG 7658
Qy 7064 ATCTGTGATTAACCGTATTACCGCTTTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 7123
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Db 7719 CGACGAGCGCAGCTCAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7778
Qy 7184 CTCTCCCGCGCGTGTGCGGATTCATTAATGACGCTGCGACGACGAGGTTTCCCGACTGA 7243
Db 7779 CTCTCCCGCGCGTGTGCGGATTCATTAATGACGCTGCGACGACGAGGTTTCCCGACTGA 7838
Qy 7244 AAGCGGAGTGTAGGCGCAACGAAATTAATGTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 7303
Db 7839 AAGCGGAGTGTAGGCGCAACGAAATTAATGTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 7898
Qy 7304 CTTTACACTTTATGCTTCCGCTCTATGTTGTGGAATTTGTGAGCGGATAACAATTTTC 7363
Db 7899 CTTTACACTTTATGCTTCCGCTCTATGTTGTGGAATTTGTGAGCGGATAACAATTTTC 7958
Qy 7364 ACACAGGAAACAGCTATGACCATGATTACGCAAGCGCGCAAT 7406
Db 7959 ACACAGGAAACAGCTATGACCATGATTACGCAAGCTCGAAAT 8001

RESULT 13

US-10-340-447-3/c
; Sequence 3, Application US/10340447
; Publication No. US20040002115A1
; GENERAL INFORMATION:
; APPLICANT: FRAISSIGNES, Pauline
; APPLICANT: GRATZER, Sabine
; APPLICANT: LEBERER, Ekkehard
; TITLE OF INVENTION: METHOD OF IDENTIFYING PROTEIN CAMS (CONSTITUTIVELY ACTIVE
; TITLE OF INVENTION: MUTANTS)
; FILE REFERENCE: DEAN2002/0003 USNP
; CURRENT APPLICATION NUMBER: US/10340,447
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: DE 02000733.2
; PRIOR FILING DATE: 2002-01-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6831

[illegible]

6791 AAAGCGCCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGTAAGCGGACGGGTGC 6850
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1861 TTGAGTGAGTGATACGCTCGCGGCGGAAACGAGCGAGTCAAGTCAAGTCAAGTCAAGTCA 1920
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Db |||||
1921 AGAAGCGGAGAGCGGCGGCGGAAACGAGCGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1980
Qy AATGCACTGCGGACGAGCGGTTCCGAGCTGGAAGCGGCGAGTCAAGTCAAGTCAAGTCAAGTCA 7270
Db |||||
1981 AATGCACTGCGGACGAGCGGTTCCGAGCTGGAAGCGGCGAGTCAAGTCAAGTCAAGTCAAGTCA 2040
Qy ATGAGTGAGTGATACGCTTATAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7330
Db |||||
2041 ATGAGTGAGTGATACGCTTATAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100
Qy TGTGTTGTTGAATTTGAGCGGATTAACAATTTACAGAGAAACAGTATGACCATGATT 7390
Db |||||
2101 TGTGTTGTTGAATTTGAGCGGATTAACAATTTACAGAGAAACAGTATGACCATGATT 2160
Qy ACCGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7444
Db |||||
2161 ACCGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7514

RESULT 15

US-10-343-303-1
; Sequence 1, Application US/10343303
; Publication No. US20040038394A1
; GENERAL INFORMATION:
; APPLICANT: Mogen Biotechnology Research Institute
; APPLICANT: Pan-Gen Biotech Laboratories Inc.
; TITLE OF INVENTION: Expression vector for animal cell
; FILE REFERENCE: opp010629kr
; CURRENT APPLICATION NUMBER: US/10/343,303
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: KR10-2000-43996
; PRIOR FILING DATE: 2000-07-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: KopatentIn 1.55
; SEQ ID NO 1
; LENGTH: 6287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pMS vector sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(419)
; OTHER INFORMATION: SV40virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3305)..(6269)

; OTHER INFORMATION: Human beta globin MAR element
US-10-343-303-1

Query Match 28.2%; Score 2204.6; DB 13; Length 6287;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5230 TCAGTGGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTATTTGTTTATTTCTAAATA 5289
Db 1080 TCAGTGGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTATTTGTTTATTTCTAAATA 1139
Qy 5290 CATTTCAATATGATCGCTCATGAGCAATATACCTGTAAATGCTTCAATATATTTGA 5349
Db 1140 CATTTCAATATGATCGCTCATGAGCAATATACCTGTAAATGCTTCAATATATTTGA 1199
Qy 5350 AAAAGGAAAGATGATAGTATTCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCA 5409
Db 1200 AAAAGGAAAGATGATAGTATTCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCA 1259
Qy 5410 TTTTGCCTTCTCTGTTTTGCTCACCCAGAAACGCTGCTGTAAGATGCTGAAGAT 5469
Db 1260 TTTTGCCTTCTCTGTTTTGCTCACCCAGAAACGCTGCTGTAAGATGCTGAAGAT 1319
Qy 5470 CAGTTGGGTGCACGAGTGGGTTACATCGAATCGAATCGAATCGAATCGAATCGAATCGAAT 5529
Db 1320 CAGTTGGGTGCACGAGTGGGTTACATCGAATCGAATCGAATCGAATCGAATCGAATCGAAT 1379
Qy 5530 AGTTTTCGGCGCCGAGAAAGCTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGC 5589
Db 1380 AGTTTTCGGCGCCGAGAAAGCTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGC 1439
Qy 5590 GCGGTATTATCCCGTATTGACGCGGCGGCAAGAGCAACTCGGTCGCGCATACATATTCT 5649
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Qy 5650 CAGAAATGACTTGGTTGAGTACTCACCAGTCAAGAAAGATCTTACGGATGCGATGACA 5709
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Qy 5710 GTAAAGAAATTTATGCAAGTCTGCTGCAATAACCATGAGTATAACACTGCGGCAACTTACTT 5769
Db 1560 GTAAAGAAATTTATGCAAGTCTGCTGCAATAACCATGAGTATAACACTGCGGCAACTTACTT 1619
Qy 5770 CTGACAAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTTCGCAACATGCGGAGTATCAT 5829
Db 1620 CTGACAAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTTCGCAACATGCGGAGTATCAT 1679
Qy 5830 GTAACTCGGCTTGATCGTTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGAGAGCGT 5889
Db 1680 GTAACTCGGCTTGATCGTTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGAGAGCGT 1739
Qy 5890 GACACCAACGATGCTCTGAGCAATGGAACAAACGCTGCGGCAAACTATTAACTGGCGAACTA 5949
Db 1740 GACACCAACGATGCTCTGAGCAATGGAACAAACGCTGCGGCAAACTATTAACTGGCGAACTA 1799
Qy 5950 CTTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGAGTGGAGCGGATTAAGTTTCAGGA 6009
Db 1800 CTTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGAGTGGAGCGGATTAAGTTTCAGGA 1859
Qy 6010 CCACTTCTGCGCTCGGCGCTTCCGCGTGGCTGTTTATTTGCTGATTAATCTGAGCGCGT 6069
Db 1860 CCACTTCTGCGCTCGGCGCTTCCGCGTGGCTGTTTATTTGCTGATTAATCTGAGCGCGT 1919
Qy 6070 GAGCGTGGGTCTCGCGGTATCATTTGAGCACTTGGGCGGAGATGTAAGCCCTCCCGTATC 6129
Db 1920 GAGCGTGGGTCTCGCGGTATCATTTGAGCACTTGGGCGGAGATGTAAGCCCTCCCGTATC 1979
Qy 6130 GTAGTTATCTACAGCGGGGAGTCAAGCAACTATGAGTGAACGAAATAGACAGATCGCT 6189
Db 1980 GTAGTTATCTACAGCGGGGAGTCAAGCAACTATGAGTGAACGAAATAGACAGATCGCT 2039
Qy 6190 GAGATAGTGGCTCACTGATTAAGCAATTTGATTAAGCAATCTGTCAGCAAGTCTTACTATATA 6249
Db |||||

Db 2040 GAGATAGTGTCCTACTGATTAAAGCATTTGGTAACGTCTCAGACCAGTTTACTCATATATA 2099
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Db 2100 CTTTAGATTGATTTAAAGCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTT 2159
Qy 6310 GATAATCTCATGACCAAAATCCCTTAACTGAGTTTTCCTTCCACTGAGCGTCAAGCCCC 6369
Db 2160 GATAATCTCATGACCAAAATCCCTTAACTGAGTTTTCCTTCCACTGAGCGTCAAGCCCC 2219
Qy 6370 GTAGAAAGATCAAGGATCTCTCTGAGATCCTTTTTTTTTCGCGGTAATCTGCTGCTTG 6429
Db 2220 GTAGAAAGATCAAGGATCTCTCTGAGATCCTTTTTTTTTCGCGGTAATCTGCTGCTTG 2279
Qy 6430 CAAACAAAACCAACACCGCTACACGCGTGGTTGTTTTCGCGGATCAAGAGCTACCAACT 6489
Db 2280 CAAACAAAACCAACACCGCTACACGCGTGGTTGTTTTCGCGGATCAAGAGCTACCAACT 2339
Qy 6490 CTTTTTCCGAAGGTAACCTGGCTTACGACAGCGCAGATACCAAAATACCTCTTCTAGTG 6549
Db 2340 CTTTTTCCGAAGGTAACCTGGCTTACGACAGCGCAGATACCAAAATACCTCTTCTAGTG 2399
Qy 6550 TAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTG 6609
Db 2400 TAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTG 2459
Qy 6610 CTAATCCTGTTACCAAGTGGCTGCTCCAGTGGCGATAGTCTGTCTTTACCGGGTTGGAC 6669
Db 2460 CTAATCCTGTTACCAAGTGGCTGCTCCAGTGGCGATAGTCTGTCTTTACCGGGTTGGAC 2519
Qy 6670 TCAAGACGATAGTTACCGGATAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTGCACA 6729
Db 2520 TCAAGACGATAGTTACCGGATAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTGCACA 2579
Qy 6730 CAGCCGAGCTTGGAGCAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGA 6789
Db 2580 CAGCCGAGCTTGGAGCAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGA 2639
Qy 6790 GAAAGCGCCACGCTTCCGAGGGAGAAAGCGGACAGTATCCGGTAAGCGCGAGGGTC 6849
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Qy 6850 GGAACAGGAGAGCGCAGAGGAGCTTCCAGGGGAAACGGCTGTGTATCTTTATAGTCT 6909
Db 2700 GGAACAGGAGAGCGCAGAGGAGCTTCCAGGGGAAACGGCTGTGTATCTTTATAGTCT 2759
Qy 6910 GTCCGGTTTCGCACTCTGACTGAGCGTCGATTTTGTGATGCTCGTAGGGGGGGGG 6969
Db 2760 GTCCGGTTTCGCACTCTGACTGAGCGTCGATTTTGTGATGCTCGTAGGGGGGGGG 2819
Qy 6970 AGCTATGAAAAACGCCAGCAACCGGCTTTTACGGTTCTTGGCCCTTTTGTGGCCT 7029
Db 2820 AGCTATGAAAAACGCCAGCAACCGGCTTTTACGGTTCTTGGCCCTTTTGTGGCCT 2879
Qy 7030 TTTGCTCACATGTTCTTCTCGGTTATCCCTGATTTCTGTGGATAACCGTATTACCGCC 7089
Db 2880 TTTGCTCACATGTTCTTCTCGGTTATCCCTGATTTCTGTGGATAACCGTATTACCGCC 2939
Qy 7090 TTTGAGTAGCTGATACCGCTCGCCGACCGCAACGACCGAGCGGAGTCAAGTGAAC 7149
Db 2940 TTTGAGTAGCTGATACCGCTCGCCGACCGCAACGACCGAGCGGAGTCAAGTGAAC 2999
Qy 7150 GAGGAAGCGGAAGAGCGCCCAATAGCAACCGCCTCTCCCGCGGTTGGCCGATTCAAT 7209
Db 3000 GAGGAAGCGGAAGAGCGCCCAATAGCAACCGCCTCTCCCGCGGTTGGCCGATTCAAT 3059
Qy 7210 TAATGAGCTGGCAGACAGAGTTTCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATT 7269
Db 3060 TAATGAGCTGGCAGACAGAGTTTCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATT 3119
Qy 7270 AATGTAGTTACTCATCTATTAGGACCCAGGCTTTACATTTATGCTTCCGGCTCCT 7329
Db 3120 AATGTAGTTACTCATCTATTAGGACCCAGGCTTTACATTTATGCTTCCGGCTCCT 3179

Qy 7330 ATGTTGTGTGGAATTTGTAGCGGATAACAATTTTCAACAGGAAACAGCTATGACCATGAT 7389
Db 3180 ATGTTGTGTGGAATTTGTAGCGGATAACAATTTTCAACAGGAAACAGCTATGACCATGAT 3239
Qy 7390 TAGCCGAAGCGCGCAATTAACCTCTCACTAAGGGAAACAAAAGCTTGGAGCTC 7440
Db 3240 TAGCCGAAGCTCGAAATTAACCTCTCACTAAGGGAAACAAAAGCTTGGAGCTC 3290

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